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(54) Title: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR ANALYSIS OF GENE EXPRESSION IN HUMAN PLACENTA

(57) Abstract: A single exon nucleic acid microarray comprising a plurality of single exon nucleic acid probes for measuring gene expression in a sample derived from human placenta is described. Also described are single exon nucleic acid probes expressed in the placenta and their use in methods for detecting gene expression.



HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR ANALYSIS OF GENE EXPRESSION IN HUMAN PLACENTA

CROSS REFERENCE TO RELATED APPLICATIONS

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The present application is a continuation-in-part of U.S. patent application serial nos. 09/632,366, filed August 3, 2000 and 09/608,408, filed June 30, 2000; claims the benefit under 35 U.S.C. s 119(e) of U.S.provisional patent application serial nos. 60/236,359, filed September 27, 2000, 60/234,687, filed September 21, 2000, 60/207,456, filed May 26, 2000, and 60/180,312, filed February 4, 2000; and further claims the benefit under 35 U.S.C. s 119(a) of UK patent application no. 0024263.6, filed October 4, 2000, the disclosures of which are incorporated herein by reference in their entireties.

REFERENCE TO SEQUENCE LISTING AND INCORPORATION BY REFERENCE THEREOF

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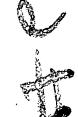
The present application includes a Sequence Listing in electronic format, filed pursuant to PCT Administrative Instructions 801 - 806 on a single CD-R disc, in triplicate, containing a file pto\_PLACENTA.txt, created 24

25 January 2001, having 26,548,337 bytes. The Sequence Listing contained in said file on said disc is incorporated herein by reference in its entirety.

Field of the Invention

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The present invention relates to genome-derived single exon microarrays useful for verifying the expression of regions of genomic DNA predicted to encode protein. In particular, the present invention relates to unique genomederived single exon nucleic acid probes expressed in human











placenta and single exon nucleic acid microarrays that include such probes.

#### Background of the Invention

For almost two decades following the invention of general techniques for nucleic acid sequencing, Sanger et al., Proc. Natl. Acad. Sci. USA 70(4):1209-13 (1973); Gilbert et al., Proc. Natl. Acad. Sci. USA 70(12):3581-4 (1973), these techniques were used principally as tools to further the understanding of proteins — known or suspected — about which a basic foundation of biological knowledge had already been built. In many cases, the cloning effort that preceded sequence identification had been both informed and directed by that antecedent biological understanding.

For example, the cloning of the T cell receptor for antigen was predicated upon its known or suspected cell type-specific expression, by its suspected membrane association, and by the predicted assembly of its gene via T cell-specific somatic recombination. Subsequent sequencing efforts at once confirmed and extended understanding of this family of proteins. Hedrick et al., Nature 308(5955):153-8 (1984).

More recently, however, the development of high
throughput sequencing methods and devices, in concert with
large public and private undertakings to sequence the human
and other genomes, has altered this investigational
paradigm: today, sequence information often precedes
understanding of the basic biology of the encoded protein
product.

One of the approaches to large-scale sequencing is predicated upon the proposition that expressed sequences — that is, those accessible through isolation of mRNA — are of greatest initial interest. This "expressed sequence tag" ("EST") approach has already yielded vast

amounts of sequence data (see for example Adams et al.,

Science 252:1651 (1991); Williamson, Drug Discov. Today

4:115 (1999)). For nucleic acids sequenced by this

approach, often the only biological information that is

5 known a priori with any certainty is the likelihood of

biologic expression itself. By virtue of the species and

tissue from which the mRNA had originally been obtained,

most such sequences are also annotated with the identity of

the species and at least one tissue in which expression

10 appears likely.

More recently, the pace of genomic sequencing has accelerated dramatically. When genomic DNA serves as the initial substrate for sequencing efforts, expression cannot be presumed; often the only a priori biological information about the sequence includes the species and chromosome (and perhaps chromosomal map location) of origin.

With the ever-accelerating pace of sequence accumulation by directed, EST, and genomic sequencing approaches — and in particular, with the accumulation of sequence information from multiple genera, from multiple species within genera, and from multiple individuals within a species — there is an increasing need for methods that rapidly and effectively permit the functions of nucleic sequences to be elucidated. And as such functional information accumulates, there is a further need for methods of storing such functional information in meaningful and useful relationship to the sequence itself; that is, there is an increasing need for means and apparatus for annotating raw sequence data with known or predicted functional information.

Although the increase in the pace of genomic sequencing is due in large part to technological changes in sequencing strategies and instrumentation, Service, Science 280:995 (1998); Pennisi, Science 283: 1822-1823 (1999),

35 there is an important functional motivation as well.

While it was understood that the EST approach would rarely be able to yield sequence information about the noncoding portions of the genome, it now also appears the EST approach is capable of capturing only a fraction of a genome's actual expression complexity.

For example, when the C. elegans genome was fully sequenced, gene prediction algorithms identified over 19,000 potential genes, of which only 7,000 had been found by EST sequencing. C. elegans Sequencing Consortium, 10 Science 282:2012 (1998). Analogously, the recently completed sequence of chromosome 2 of Arabidopsis predicts over 4000 genes, Lin et al., Nature, 402:761 (1999), of which only about 6% had previously been identified via EST sequencing efforts. Although the human genome has the 15 greatest depth of EST coverage, it is still woefully short of surrendering all of its genes. One recent estimate suggests that the human genome contains more than 146,000 genes, which would at this point leave greater than half of the genes undiscovered. It is now predicted that many 20 genes, perhaps 20 to 50%, will only be found by genomic sequencing.

There is, therefore, a need for methods that permit the functional regions of genomic sequence — and most importantly, but not exclusively, regions that

25 function to encode genes — to be identified.

Much of the coding sequence of the human genome is not homologous to known genes, making detection of open reading frames ("ORFs") and predictions of gene function difficult. Computational methods exist for predicting coding regions in eukaryotic genomes. Gene prediction programs such as GRAIL and GRAIL II, Uberbacher et al., Proc. Natl. Acad. Sci. USA 88(24):11261-5 (1991); Xu et al., Genet. Eng. 16:241-53 (1994); Uberbacher et al., Methods Enzymol. 266:259-81 (1996); GENEFINDER, Solovyev et al., Nucl. Acids. Res. 22:5156-63 (1994); Solovyev et al.,

Ismb 5:294-302 (1997); and GENESCAN, Burge et al., J. Mol.
Biol. 268:78-94 (1997), predict many putative genes without
known homology or function. Such programs are known,
however, to give high false positive rates. Burset et al.,
Genomics 34:353-367 (1996). Using a consensus obtained by
a plurality of such programs is known to increase the
reliability of calling exons from genomic sequence.
Ansari-Lari et al., Genome Res. 8(1):29-40 (1998)

Identification of functional genes from genomic

10 data remains, however, an imperfect art. For example, in
reporting the full sequence of human chromosome 21, the
Chromosome 21 Mapping and Sequencing Consortium reports
that prior bioinformatic estimates of human gene number may
need to be revised substantially downwards. Nature

405:311-199 (2000); Reeves, Nature 405:283-284 (2000).

Thus, there is a need for methods and apparatus that permit the functions of the regions identified bioinformatically — and specifically, that permit the expression of regions predicted to encode protein — readily to be confirmed experimentally.

Recently, the development of nucleic acid microarrays has made possible the automated and highly parallel measurement of gene expression. Reviewed in Schena (ed.), DNA Microarrays: A Practical Approach

25 (Practical Approach Series), Oxford University Press (1999) (ISBN: 0199637768); Nature Genet. 21(1)(suppl):1 - 60 (1999); Schena (ed.), Microarray Biochip: Tools and Technology, Eaton Publishing Company/BioTechniques Books Division (2000) (ISBN: 1881299376).

It is common for microarrays to be derived from cDNA/EST libraries, either from those previously described in the literature, such as those from the I.M.A.G.E. consortium, Lennon et al., Genomics 33(1):151-2 (1996), or from the construction of "problem specific" libraries targeted at a particular biological question, R.S. Thomas

et al., Cancer Res. (in press). Such microarrays by definition can measure expression only of those genes found in EST libraries, and thus have not been useful as probes for genes discovered solely by genomic sequencing.

microarrays to answer certain biological questions has been demonstrated for the yeast Saccharomyces cerevisiae. De Risi et al., Science 278:680 (1997). The vast majority of yeast nuclear genes, approximately 95% however, are single exon genes, i.e., lack introns, Lopez et al., RNA 5:1135-1137 (1999); Goffeau et al., Science 274:563-67 (1996), permitting coding regions more readily to be identified. Whole genome nucleic acid microarrays have not generally been used to probe gene expression from more complex eukaryotic genomes, and in particular from those averaging more than one intron per gene.

Given the substantial impact on human morbidity and mortality of diseases directly caused by genetic defect, and given the profound influence of genetic factors on the predisposition, onset, and/or aggressiveness of most, if not all human diseases, there has long been interest in efficient and safe means for early detection of gene defects and polymorphisms that cause, are associated with, or are implicated in development of disease.

Recently, techniques have been developed that permit direct sampling of placenta earlier in pregnancy. There is a need for methods and apparatus that permit analysis of placenta samples for the prediction and diagnosis of diseases caused by genetic defect,

30 particularly those with polygenic etiology.

#### Summary of the Invention

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The present invention solves these and other

problems in the art by providing methods and apparatus for predicting, confirming, and displaying functional information derived from genomic sequence. The present invention also provides apparatus for verifying the expression of putative genes identified within genomic sequence.

In particular, the invention provides novel genome-derived single exon nucleic acid microarrays useful for verifying the expression of putative genes identified within genomic sequence.

The present invention also provides compositions and kits for the ready production of nucleic acids identical in sequence to, or substantially identical in sequence to, probes on the genome-derived single exon microarrays of the present invention.

Accordingly, in a first aspect of the invention, there is provided a spatially-addressable set of single exon nucleic acid probes for measuring gene expression in a sample derived from human placenta, comprising a plurality of single exon nucleic acid probes according to any one of the nucleotide sequences set out in SEQ ID NOs: 1 - 13,232 or a complementary sequence, or a portion of such a sequence.

By plurality is meant at least two, suitably at least 20, most suitably at least 100, preferably at least 1000 and, most preferably, upto 5000.

In one embodiment of the first aspect, each of said plurality of probes is separately and addressably amplifiable.

In an alternative embodiment, each of said plurality of probes is separately and addressably isolatable from said plurality.

In a preferred embodiment, each of said plurality of probes is amplifiable using at least one common primer.

35 Preferably, each of said plurality of probes is amplifiable

using a first and a second common primer.

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In yet another embodiment, said set of single exon nucleic acid probes comprises between 50 - 20,000 probes, for example, 50 - 5000.

5 Suitably, said set of single exon nucleic acid probes comprises at least 50 - 1000 discrete single exon nucleic acid probes having a sequence as set out in any of SEQ ID NOS.: 1 - 26,232 or a complimentary sequence, or a portion of such a sequence.

10 Preferably, the average length of the single exon nucleic acid probes is between 200 and 500 bp. It is preferred that the average length should be at least 200bp, suitably at least 250bp, most suitably at least 300bp, preferably at least 400bp and, most preferably, 500 bp.

In another embodiment, the single exon nucleic acid probes lack prokaryotic and bacteriophage vector sequence. It is preferred that at least 50%, suitably at least 60%, most suitably at least 70%, preferably at least 75%, more preferably at least 80, 85, 90, 95 or 99% of said 20 single exon nucleic acid probes lack prokaryotic and bacteriophage vector sequence.

In another preferred embodiment, said single exon nucleic acid lack homopolymeric stretches of A or T. It is preferred that at least 50%, suitably at least 60%, most 25 suitably at least 70%, preferably at least 75%, more preferably at least 80, 85, 90, 95 or 99% of said single exon nucleic acid probes lack homopolymeric stretches of A or T.

Preferably, a spatially-addressable set of single 30 exon nucleic acid probes in accordance with the first aspect of the invention is is addressably disposed upon a substrate.

Suitable substrates include a filter membrane which may, preferably, be nitrocellulose or nylon. The 35 nylon may preferably, be positively-charged. Other suitable

substrates include glass, amorphous silicon, crystalline silicon, and plastic. Further suitable materials include polymethylacrylic, polyethylene, polypropylene, polyacrylate, polymethylmethacrylate, polyvinylchloride, polytetrafluoroethylene, polystyrene, polycarbonate, polyacetal, polysulfone, celluloseacetate, cellulosenitrate, nitrocellulose, and mixtures thereof.

In a second aspect of the invention, there is provided a microarray comprising a spatially addressable set of single exon nucleic acid probes in accordance with the first aspect of the invention.

In one embodiment, a genome-derived single-exon microarray is packaged together with such an ordered set of amplifiable probes corresponding to the probes, or one or more subsets of probes, thereon. In alternative embodiments, the ordered set of amplifiable probes is packaged separately from the genome-derived single exon microarray.

In another aspect, the invention provides genome20 derived single exon nucleic acid probes useful for gene
expression analysis, and particularly for gene expression
analysis by microarray. In particular embodiments of this
aspect, the present invention provides human single-exon
probes that include specifically-hybridizable fragments of
25 SEQ ID Nos. 13,233 - 26,232, wherein the fragment
hybridizes at high stringency to an expressed human gene.
In particular embodiments, the invention provides single
exon probes comprising SEQ ID Nos. 1 - 13,232.

Accordingly, in a third aspect of the invention,

there is provided a single exon nucleic acid probe for
measuring human gene expression in a sample derived from
human placenta which is a nucleic acid molecule comprising
a nucleotide sequence as set out in any of SEQ ID NOs.: 1

13,232 or a complementary sequence or a fragment thereof
wherein said probe hybridizes at high stringency to a

nucleic acid expressed in the human placenta.

In one embodiment, a single exon nucleic acid probe in accordance with the third aspect comprises a nucleotide sequence as set out in any of SEQ ID NOs.:

13,233 - 26,232 or a complementary sequence or a fragment thereof.

In a fourth aspect of the invention, there is provided a single exon nucleic acid probe for measuring human gene expression in a sample derived from human placenta which is a nucleic acid molecule having a sequence encoding a peptide comprising a peptide sequence as set out in any of SEQ ID NOs.: 26,233 - 38,837 or a complementary sequence or a fragment thereof wherein said probe hybridizes at high stringency to a nucleic acid expressed in the human placenta.

Preferably, a single exon nucleic acid probe in accordance with the third or fourth aspects of the invention comprises between at least 15 and 50 contiguous nucleotides of said SEQ ID NO:. It is preferred that the single exon nucleic acid probe comprises at least 15, suitably at least 20, more suitably at least 25 or preferably at least 50 contiguous nucleotides of said SEQ ID NO:.

In another preferred embodiment, a single exon

15 nucleic acid probe in accordance with the third or fourth
 aspects of the invention is between 3kb and 25kb in length.

It is preferred that said probe is no more than 3kb,
 suitably no more than 5kb, more suitably no more than 10kb,
 preferably 15kb, more preferably 20kb or, most preferably,

30 no more than 20kb in length.

Preferably, a single exon nucleic acid probe in accordance with either the fifth or sixth aspect of the invention is DNA, preferably single-stranded DNA, RNA or PNA.

35 In another embodiment of either the third or

fourth aspect of the invention, a single exon nucleic acid probe is detectably labeled. Suitable detectable labels include a radionuclide, a fluorescent label or a first member of a specific binding pair. Suitable fluorescent labels include dyes such as cyanine dyes, preferably Cy3 and Cy5 although other suitable dyes will be known to those skilled in the art.

In a particularly preferred embodiment, a single exon nucleic acid probe in accordance with either the third or fourth aspect of the invention lacks prokaryotic and bacteriophage vector sequence. In yet another embodiment, a single exon nucleic acid probe in accordance with either the third or fourth aspect of the invention lacks homopolymeric stretches of A or T.

In a fifth aspect of the invention, there is provided an amplifiable nucleic acid composition, comprising:

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the single exon nucleic acid probe in accordance with either of the third or fourth aspects of the invention; and at least one nucleic acid primer;

wherein said at least one primer is sufficient to prime enzymatic amplification of said probe.

In an sixth aspect of the invention, there is provided a method of measuring gene expression in a sample derived from human placenta, comprising:

contacting the single exon microarray in accordance with the second aspect of the invention, with a first collection of detectably labeled nucleic acids, said first collection of nucleic acids derived from mRNA of human placenta; and then

measuring the label detectably bound to each probe of said microarray.

In a seventh aspect of the invention, there is provided a method of identifying exons in a eukaryotic genome, comprising:

algorithmically predicting at least one exon from genomic sequence of said eukaryote; and then

detecting specific hybridization of detectably labeled nucleic acids to a single exon probe,

wherein said detectably labeled nucleic acids are derived from mRNA from the placenta of said eukaryote, said probe is a single exon probe having a fragment identical in sequence to, or complementary in sequence to, said predicted exon, said probe is included within a single exon microarray in accordance with the first aspect of the invention, and said fragment is selectively hybridizable at high stringency.

In a eighth aspect of the invention, there is provided a method of assigning exons to a single gene,

15 comprising:

identifying a plurality of exons from genomic sequence in accordance with the seventh aspect of the invention; and then

measuring the expression of each of said exons in
20 a plurality of tissues and/or cell types using
hybridization to single exon microarrays having a probe
with said exon,

wherein a common pattern of expression of said exons in said plurality of tissues and/or cell types indicates that the exons should be assigned to a single gene.

In an ninth aspect of the invention, there is provided a nucleic acid sequence as set out in any of SEQ ID NOs: 1 - 26,232 wherein said sequence encodes a peptide.

In a tenth aspect of the invention, there is provided a peptide encoded by a sequence comprising a sequence as set out in any of SEQ ID NOs: 13,233 - 26,232, or a complementary sequence or coding portion thereof.

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In a preferred embodiment, a peptide may be served by a sequence comprising a sequence set out in any

of SEQ ID NOS.: 1 -13,232 .

In a further aspect, the invention provides peptides comprising an amino acid sequence translated from the DNA fragments, said amino acid sequences comprising SEQ ID NOS.: 26,233 - 38,837.

Accordingly in a eleventh aspect of the invention there is provided a peptide comprising a sequence as set out in any of SEQ ID NOs: 26,233 - 38,837, or fragment thereof.

In another aspect, the invention provides means for displaying annotated sequence, and in particular, for displaying sequence annotated according to the methods and apparatus of the present invention. Further, such display can be used as a preferred graphical user interface for electronic search, query, and analysis of such annotated sequence.

# Detailed Description of the Invention

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#### Definitions

As used herein, the term "microarray" and phrase "nucleic acid microarray" refer to a substrate-bound collection of plural nucleic acids, hybridization to each of the plurality of bound nucleic acids being separately detectable. The substrate can be solid or porous, planar or non-planar, unitary or distributed.

"nucleic acid microarray" include all the devices so called
in Schena (ed.), DNA Microarrays: A Practical Approach
(Practical Approach Series), Oxford University Press (1999)
(ISBN: 0199637768); Nature Genet. 21(1)(suppl):1 - 60
(1999); and Schena (ed.), Microarray Biochip: Tools and
Technology, Eaton Publishing Company/BioTechniques Books
Division (2000) (ISBN: 1881299376). As so defined, the

term "microarray" and phrase "nucleic acid microarray"
further include substrate-bound collections of plural
nucleic acids in which the nucleic acids are distributably
disposed on a plurality of beads, rather than on a unitary
planar substrate, as is described, inter alia, in Brenner
et al., Proc. Natl. Acad. Sci. USA 97(4):166501670 (2000);
in such case, the term "microarray" and phrase "nucleic
acid microarray" refer to the plurality of beads in
aggregate.

10 As used herein with respect to a nucleic acid microarray, the term "probe" refers to the nucleic acid that is, or is intended to be, bound to the substrate; in such context, the term "target" thus refers to nucleic acid intended to be bound thereto by Watson-Crick

15 complementarity. As used herein with respect to solution phase hybridization, the term "probe" refers to the nucleic acid of known sequence that is detectably labeled.

As used herein, the expression "probe comprising SEQ ID NO.", and variants thereof, intends a nucleic acid probe, at least a portion of which probe has either (i) the sequence directly as given in the referenced SEQ ID NO., or (ii) a sequence complementary to the sequence as given in the referenced SEQ ID NO., the choice as between sequence directly as given and complement thereof dictated by the requirement that the probe hybridize to mRNA.

As used herein, the term "open reading frame" and the equivalent acronym "ORF" refer to that portion of an exon that can be translated in its entirety into a sequence of contiguous amino acids i.e. a nucleic acid sequence that, in at least one reading frame, does not possess stop codons; the term does not require that the ORF encode the entirety of a natural protein.

As used herein, the term "amplicon" refers to a PCR product amplified from human genomic DNA, containing the predicted exon.

As used herein the term "exon" refers to the consensus prediction of the various exon and gene predicting algorithms i.e. a nucleic acid sequence bioinformatically predicted to encode a portion of a natural protein.

As used herein, the term "peptide" refers to a sequence of amino acids. The sequences referred to as PEPTIDE SEQ ID NOS.: are the predicted peptide sequences that would be translated from one of the exons, or a portion thereof set out in exon SEQ ID NOS.: The codons encoding the peptide are wholly contained within the exon.

As used herein, a "portions" of a defined nucleotide sequence or sequences can be and, preferably, are fragments unique to that sequence or to one or a combination of those sequences. A fragment unique to a nucleic acid molecule is one that is a signature for the larger nucleic acid molecule.

As used herein, the phrase "expression of a probe" and its linguistic variants means that the ORF 20 present within the probe, or its complement, is present within a target mRNA.

As used herein, "stringent conditions" refers to parameters well known to those skilled in the art. When a nucleic acid molecule is said to be hybridisable to another of a given sequence under "stringent conditions" it is meant that it is homologous to the given sequence.

As used herein, the phrase "specific binding pair" intends a pair of molecules that bind to one another with high specificity. Binding pairs are said to exhibit specific binding when they exhibit avidity of at least 10<sup>7</sup>, preferably at least 10<sup>8</sup>, more preferably at least 10<sup>9</sup> liters/mole. Nonlimiting examples of specific binding pairs are: antibody and antigen; biotin and avidin; and biotin and streptavidin.

As used herein with respect to the visual display

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of annotated genomic sequence, the term "rectangle" means any geometric shape that has at least a first and a second border, wherein the first and second borders each are capable of mapping uniquely to a point of another visual object of the display.

As used herein, a "Mondrian" means a visual display in which a single genomic sequence is annotated with predicted and experimentally confirmed functional information.

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### Brief Description of the Drawings

The present invention is further illustrated with reference to the following non-limiting figures and examples in which:

FIG. 1 illustrates a process for predicting functional regions from genomic sequence, confirming the functional activity of such regions experimentally, and associating and displaying the data so obtained in meaningful and useful relationship to the original sequence data;

FIG. 2 further elaborates that portion of the process schematized in FIG. 1 for predicting functional regions from genomic sequence;

FIG. 3 illustrates a Mondrian visual display; FIG. 4 presents a Mondrian showing a hypothetical

annotated genomic sequence;

FIG. 5 is a histogram showing the distribution of 30 ORF length and PCR products as obtained, with ORF length shown in black and PCR product length shown in dotted lines;

FIG. 6 is a histogram showing the distribution, among exons predicted according to the methods described, of expression as measured using simultaneous two color

hybridization to a genome-derived single exon microarray. The graph shows the number of sequence-verified products that were either not expressed ("0"), expressed in one or more but not all tested tissues ("1" - "9"), or expressed in all tissues tested ("10");

FIG. 7 is a pictorial representation of the expression of verified sequences that showed expression with signal intensity greater than 3 in at least one tissue, with: FIG. 7A showing the expression as measured by microarray hybridization in each of the 10 measured tissues, and the expression as measured "bioinformatically" by query of EST, NR and SwissProt databases; with FIG. 7B showing the legend for display of physical expression (ratio) in FIG. 7A; and with FIG. 7C showing the legend for scoring EST hits as depicted in FIG. 7A;

FIG. 8 shows a comparison of normalized CY3 signal intensity for arrayed sequences that were identical to sequences in existing EST, NR and SwissProt databases or that were dissimilar (unknown), where black denotes the signal intensity for all sequence-verified products with a BLAST Expect ("E") value of greater than 1e-30 (1 x 10<sup>-30</sup>) ("unknown") and a dotted line denotes sequence-verified spots with a BLAST expect ("E") value of less than 1e-30 (1 x 10<sup>-30</sup>) ("known");

FIG. 9 presents a Mondrian of BAC AC008172 (bases 25,000 to 130,000), containing the carbamyl phosphate synthetase gene (AF154830.1); and

FIG. 10 is a Mondrian of BAC A049839.

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Methods and Apparatus for Predicting, Confirming,

Annotating, and Displaying Functional Regions From Genomic

Sequence Data

FIG. 1 is a flow chart illustrating in broad

outline a process for predicting functional regions from genomic sequence, confirming and characterizing the functional activity of such regions experimentally, and then associating and displaying the information so obtained 5 in meaningful and useful relationship to the original sequence data.

The initial input into process 10 of the present invention is drawn from one or more databases 100 containing genomic sequence data. Because genomic sequence 10 is usually obtained from subgenomic fragments, the sequence data typically will be stored in a series of records corresponding to these subgenomic sequenced fragments. Some fragments will have been catenated to form larger contiguous sequences ("contigs"); others will not. A 15 finite percentage of sequence data in the database will typically be erroneous, consisting inter alia of vector sequence, sequence created from aberrant cloning events, sequence of artificial polylinkers, and sequence that was erroneously read.

Each sequence record in database 100 will minimally contain as annotation a unique sequence identifier (accession number), and will typically be annotated further to identify the date of accession, species of origin, and depositor. Because database 100 can 25 contain nongenomic sequence, each sequence will typically be annotated further to permit query for genomic sequence. Chromosomal origin, optionally with map location, can also be present. Data can be, and over time increasingly will be, further annotated with additional information, in part through use of the present invention, as described below. Annotation can be present within the data records, in information external to database 100 and linked to the records thereto, or through a combination of the two.

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Databases useful as genomic sequence database 100 in the present invention include GenBank, and particularly

include several divisions thereof, including the htgs(draft), NT (nucleotide, command line), and NR (nonredundant) divisions. GenBank is produced by the National Institutes of Health and is maintained by the National Center for Biotechnology Information (NCBI). Databases of genomic sequence from species other than human, such as mouse, rat, Arabidopsis, C. elegans, C. brigsii, Drosophila, zebra fish, and other higher eukaryotic organisms will also prove useful as genomic sequence database 100.

Sequence database 100 is then input into one or more processes 200 for identification of regions therein that are predicted to have a biological function as specified by the user. Such functions include, but are not limited to, encoding protein, regulating transcription, regulating message transport after transcription into mRNA, regulating message splicing after transcription into mRNA, of regulating message degradation after transcription into mRNA, of regulating message degradation after transcription into to mRNA, and the like. Other functions include directing somatic recombination events, contributing to chromosomal stability or movement, contributing to allelic exclusion or X chromosome inactivation, and the like.

The particular genomic sequence to be input into process 200 will depend upon the function for which relevant sequence is to be identified as well as upon the approach chosen for such identification. Process step 200 can be iterated to identify different functions within a given genomic region. In such case, the input often will be different for the several iterations.

Sequences predicted to have the requisite function by process 200 are then input into process 300, where a subset of the input sequences suitable for experimental confirmation is identified. Experimental confirmation can involve physical and/or bioinformatic

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assay. Where the subsequent experimental assay is bioinformatic, rather than physical, there are fewer constraints on the sequences that can be tested, and in this latter case therefore process 300 can output the 5 entirety of the input sequence.

The subset of sequences output from process 300 is then used in process 400 for experimental verification and characterization of the function predicted in process 200, which experimental verification can, and often 10 will, include both physical and bioinformatic assay.

Process 500 annotates the sequence data with the functional information obtained in the physical and/or bioinformatic assays of process 400. Such annotation can be done using any technique that usefully relates the 15 functional information to the sequence, as, for example, by incorporating the functional data into the sequence data record itself, by linking records in a hierarchical or relational database, by linking to external databases, by a combination thereof, or by other means well known within 20 the database arts. The data can even be submitted for incorporation into databases maintained by others, such as GenBank, which is maintained by NCBI.

As further noted in FIG. 1, additional annotation can be input into process 500 from external sources 600.

The annotated data is then displayed in process 800, either before, concomitantly with, or after optional storage 700 on nontransient media, such as magnetic disk, optical disc, magnetooptical disk, flash memory, or the like.

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FIG. 1 shows that the experimental data output from process 400 can be used in each preceding step of process 10: e.g., facilitating identification of functional sequences in process 200, facilitating identification of an experimentally suitable subset thereof in process 300, and 35 facilitating creation of physical and/or informational

substrates for, and performance of subsequent assay, of functional sequences in process 400.

Information from each step can be passed directly to the succeeding process, or stored in permanent or 5 interim form prior to passage to the succeeding process. Often, data will be stored after each, or at least a plurality, of such process steps. Any or all process steps can be automated.

FIG. 2 further elaborates the prediction of 10 functional sequence within genomic sequence according to process 200.

Genomic sequence database 100 is first queried 20 for genomic sequence.

The sequence required to be returned by query 20 15 will depend, in the first instance, upon the function to be identified.

For example, genomic sequences that function to encode protein can be identified inter alia using gene prediction approaches, comparative sequence analysis 20 approaches, or combinations of the two. In gene prediction analysis, sequence from one genome is input into process 200 where at least one, preferably a plurality, of algorithmic methods are applied to identify putative coding regions. In comparative sequence analysis, by contrast, 25 corresponding, e.g., syntenic, sequence from a plurality of sources, typically a plurality of species, is input into process 200, where at least one, possibly a plurality, of algorithmic methods are applied to compare the sequences and identify regions of least variability.

The exact content of query 20 will also depend upon the database queried. For example, if the database contains both genomic and nongenomic sequence, perhaps derived from multiple species, and the function to be determined is protein coding regions in human genomic 35 sequence, the query will accordingly require that the

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sequence returned be genomic and derived from humans.

Query 20 can also incorporate criteria that compel return of sequence that meets operative requirements of the subsequent analytical method. Alternatively, or in addition, such operative criteria can be enforced in subsequent preprocess step 24.

For example, if the function sought to be identified is protein coding, query 20 can incorporate criteria that return from genomic sequence database 100 only those sequences present within contigs sufficiently long as to have obviated substantial fragmentation of any given exon among a plurality of separate sequence fragments.

Such criteria can, for example, consist of a

required minimal individual genomic sequence fragment
length, such as 10 kb, more typically 20 kb, 30 kb, 40kb,
and preferably 50 kb or more, as well as an optional
further or alternative requirement that sequence from any
given clone, such as a bacterial artificial chromosome

("BAC"), be presented in no more than a finite maximal
number of fragments, such as no more than 20 separate
pieces, more typically no more than 15 fragments, even more
typically no more than about 10 - 12 fragments.

Results using the present invention have shown

25 that genomic sequence from bacterial artificial chromosomes
(BACs) is sufficient for gene prediction analysis according
to the present invention if the sequence is at least 50 kb
in length, and if additionally the sequence from any given
BAC is presented in fewer than 15, and preferably fewer

30 than 10, fragments. Accordingly, query 20 can incorporate
a requirement that data accessioned from BAC sequencing be
in fewer than 15, preferably fewer than 10, fragments.

An additional criterion that can be incorporated into the query can be the date, or range of dates, of sequence accession. Although the process has been

described above as if genomic sequence database 100 were static, it is of course understood that the genomic sequence databases need not be static, and indeed are typically updated on a frequent, even hourly, basis. Thus, as further described in Examples 1 and 2, infra, it is possible to query the database for newly added sequence, either newly added after an absolute date, or newly added relative to a prior analysis performed using the methods and apparatus of the present invention. In this way, the process herein described can incorporate a dynamic, temporal component.

One utility of such temporal limitation is to identify, from newly accessioned genomic sequence, the presence of novel genes, particularly those not previously identified by EST sequencing (or other sequencing efforts that are similarly based upon gene expression). As further described in Example 1, such an approach has shown that newly accessioned human genomic sequence, when analyzed for sequences that function to encode protein, readily identifies genes that are novel over those in existing EST and other expression databases. This makes the methods of the present invention extremely powerful gene discovery tools. And as would be appreciated, such gene discovery can be performed using genomic sequence from species other than human.

If query 20 incorporates multiple criteria, such as above-described, the multiple criteria can be performed as a series of separate queries or as a single query, depending in part upon the query language, the complexity of the query, and other considerations well known in the database arts.

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If query 20 returns no genomic sequence meeting the query criteria, the negative result can be reported by process 22, and process 200 (and indeed, entire process 10) ended 23, as shown. Alternatively, or in addition to

report and termination of the initial inquiry, a new query 20 can be generated that takes into account the initial negative result.

When query 20 returns sequence meeting the query criteria, the returned sequence is then passed to optional preprocessing 24, suitable and specific for the desired analytical approach and the particular analytical methods thereof to be used in process 25.

Preprocessing 24 can include processes suitable 10 for many approaches and methods thereof, as well as processes specifically suited for the intended subsequent analysis.

Preprocessing 24 suitable for most approaches and methods will include elimination of sequence irrelevant to, or that would interfere with, the subsequent analysis. Such sequence includes repetitive sequence, such as Alu repeats and LINE elements, vector sequence, artificial sequence, such as artificial polylinkers, and the like. Such removal can readily be performed by identification and subsequent masking of the undesired sequence.

Identification can be effected by comparing the genomic sequence returned by query 20 with public or private databases containing known repetitive sequence, vector sequence, artificial sequence, and other artifactual sequence. Such comparison can readily be done using programs well known in the art, such as CROSS\_MATCH, or by proprietary sequence comparison programs the engineering of which is well within the skill in the art.

Alternatively, or in addition, undesirable,

including artifactual, sequence can be identified
algorithmically without comparison to external databases
and thereafter removed. For example, synthetic polylinker
sequence can be identified by an algorithm that identifies
a significantly higher than average density of known

restriction sites. As another example, vector sequence can

be identified by algorithms that identify nucleotide or codon usage at variance with that of the bulk of the genomic sequence.

Once identified, undesired sequence can be Removal can usefully be done by masking the undesired sequence as, for example, by converting the specific nucleotide references to one that is unrecognized by the subsequent bioinformatic algorithms, such as "X". Alternatively, but at present less preferred, the undesired sequence can be excised from the returned genomic sequence, leaving gaps.

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Preprocessing 24 can further include selection from among duplicative sequences of that one sequence of highest quality. Higher quality can be measured as a lower 15 percentage of, fewest number of, or least densely clustered occurrence of ambiguous nucleotides, defined as those nucleotides that are identified in the genomic sequence using symbols indicating ambiguity. Higher quality can also or alternatively be valued by presence in the longest contig.

Preprocessing 24 can, and often will, also include formatting of the data as specifically appropriate for passage to the analytical algorithms of process 25. Such formatting can and typically will include, inter alia, 25 addition of a unique sequence identifier, either derived from the original accession number in genomic sequence database 100, or newly applied, and can further include additional annotation. Formatting can include conversion from one to another sequence listing standard, such as conversion to or from FASTA or the like, depending upon the input expected by the subsequent process.

Preprocessing, which can be optional depending upon the function desired to be identified and the informational requirements of the methods for effecting such identification, is followed by sequence processing 25,

where sequences with the desired function are identified within the genomic sequence.

As mentioned above, such functions can include, but are not limited to, encoding protein, regulating

5 transcription, regulating message transport after transcription into mRNA, regulating message splicing after transcription, of regulating message degradation, and the like. Other functions include directing somatic recombination events, contributing to chromosomal stability or movement, contributing to allelic exclusion or X chromosome inactivation, or the like.

The methods of the present invention are particularly useful for gene discovery, that is, for identifying, from genomic sequence, regions that function to encode genes, and in a particularly useful embodiment, for identifying regions that function to encode genes not hitherto identified by expression-based or directed cloning and sequencing. In conjunction with verification using the novel single exon microarrays of the present invention, as further described below, the methods herein described become powerful gene discovery tools.

Accordingly, in a preferred embodiment of the present invention, process 25 is used to identify putative coding regions. Two preferred approaches in process 25 for identifying sequence that encodes putative genes are gene prediction and comparative sequence analysis.

Gene prediction can be performed using any of a number of algorithmic methods, embodied in one or more software programs, that identify open reading frames (ORFs) using a variety of heuristics, such as GRAIL, DICTION, and GENEFINDER. Comparative sequence analysis similarly can be performed using any of a variety of known programs that identify regions with lower sequence variability.

As further described in Example 1, below, gene 35 finding software programs yield a range of results. For

the newly accessioned human genomic sequence input in Example 1, for example, GRAIL identified the greatest percentage of genomic sequence as putative coding region, 2% of the data analyzed; GENEFINDER was second, calling 1%; and DICTION yielded the least putative coding region, with 0.8% of genomic sequence called as coding region.

Increased reliability can be obtained when consensus is required among several such methods. Although discussed herein particularly with respect to exon calling, consensus among methods will in general increase reliability of predicting other functions as well.

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Thus, as indicated by query 26, sequence processing 25, optionally with preprocessing 24, can be repeated with a different method, with consensus among such iterations determined and reported in process 27.

Process 27 compares the several outputs for a given input genomic sequence and identifies consensus among the separately reported results. The consensus itself, as well as the sequence meeting that consensus, is then stored in process 29a, displayed in process 29b, and/or output to process 300 for subsequent identification of a subset thereof suitable for assay.

Multiple levels of consensus can be calculated and reported by process 27. For example, as further

25 described in Example 1, infra, process 27 can report consensus as between all specific pairs of methods of gene prediction, as consensus among any one or more of the pairs of methods of gene prediction, or as among all of the gene prediction algorithms used. Thus, in Example 1, process 27 reported that GRAIL and GENEFINDER programs agreed on 0.7% of genomic sequence, that GRAIL and DICTION agreed on 0.5% of genomic sequence, and that the three programs together agreed on 0.25% of the data analyzed. Put another way, 0.25% of the genomic sequence was identified by all three of the programs as containing putative coding region.

Furthermore, consensus can be required among different approaches to identifying a chosen function.

For example, if the function desired to be identified is coding of protein sequence, and a first used approach to exon calling is gene prediction, the process can be repeated on the same input sequence, or subset thereof, with another approach, such as comparative sequence analysis. In such a case, where comparative sequence analysis follows gene prediction, the comparison can be performed not only on genomic nucleic acid sequence, but additionally or alternatively can be performed on the predicted amino acid sequence translated from the ORFs prior identified by the gene prediction approach.

Although shown as an iterative process, the

15 multiple analyses required to achieve consensus can be done
in series, in parallel, or some combination thereof.

Predicted functional sequence, optionally representing a consensus among a plurality of methods and approaches for determination thereof, is passed to process 300 for identification of a subset thereof for functional assay.

In the preferred embodiment of the methods of the present invention, wherein the function sought to be identified is protein coding, process 300 is used to identify a subset thereof suitable for experimental verification by physical and/or bioinformatic approaches.

For example, putative ORFs identified in process 200 can be classified, or binned, bioinformatically into putative genes. This binning can be based inter alia upon consideration of the average number of exons/gene in the species chosen for analysis, upon density of exons that have been called on the genomic sequence, and other empirical rules. Thereafter, one or more among the genespecific ORFs can be chosen for subsequent use in gene expression assay.

Where such subsequent gene expression assay uses amplified nucleic acid, considerations such as desired amplicon length, primer synthesis requirements, putative exon length, sequence GC content, existence of possible 5 secondary structure, and the like can be used to identify and select those ORFs that appear most likely successfully to amplify. Where subsequent gene expression assay relies upon nucleic acid hybridization, whether or not using amplified product, further considerations involving 10 hybridization stringency can be applied to identify that subset of sequences that will most readily permit sequencespecific discrimination at a chosen hybridization and wash stringency. One particular such consideration is avoidance of putative exons that span repetitive sequence; such 15 sequence can hybridize spuriously to nonspecific message, reducing specific signal in the hybridization.

For bioinformatic assay, there are fewer constraints on the sequences that can be tested experimentally, and in this latter case therefore process 300 can output the entirety of the input sequence.

The subset of sequences identified by process 300 as suitable for use in assay is then used in process 400 to create the physical and/or informational substrate for experimental verification of the predictions made in process 200, and thereafter to assay those substrates.

As mentioned, the methods of the present invention are particularly useful for identifying potential coding regions within genomic sequence. In a preferred embodiment of process 400, therefore, the expression of the sequences predicted to encode protein is verified. The combination of the predictive and experimental methods provides a powerful gene discovery engine.

Thus, in another aspect, the present invention provides methods and apparatus for verifying the expression of putative genes identified within genomic sequence. In

particular, the invention provides a novel method of verifying gene expression in which expression of predicted ORFs is measured and confirmed using a novel type of nucleic acid microarray, the genome-derived single exon nucleic acid microarrays of the present invention.

Putative ORFs as predicted by a consensus of gene calling, particularly gene prediction, algorithms in process 200, and as further identified as suitable by process 300, are amplified from genomic DNA using the polymerase chain reaction (PCR). Although PCR is conveniently used, other amplification approaches can also be used.

Amplification schemes can be designed to capture the entirety of each predicted ORF in an amplicon with

15 minimal additional (that is, intronic or intergenic) sequence. Because ORFs predicted from human genomic sequence using the methods of the present invention differ in length, such an approach results in amplicons of varying length.

20 However, most predicted ORFs are shorter than 500 bp in length, and although amplicons of at least about 100 or 200 base pairs can be immobilized as probes on nucleic acid microarrays, early experimental results using the methods of the present invention have suggested that longer amplicons, at least about 400 or 500 base pairs, are more effective. Furthermore, certain advantages derive from application to the microarray of amplicons of defined size.

Therefore, amplification schemes can alternatively, and preferably, be designed to amplify regions of defined size, preferably at least about 300, 400 or 500 bp, centered about each predicted ORF. Such an approach results in a population of amplicons of limited size diversity, but that typically contain intronic and/or intergenic nucleic acid in addition to putative ORF.

Conversely, somewhat fewer than 10% of ORFs

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predicted from human genomic sequence according to the methods of the present invention exceed 500 bp in length. Portions of such extended ORFs, preferably at least about 300,400 or 500 bp in length, can be amplified. However, it has been discovered that the percentage success at amplifying pieces of such ORFs is low, and that such putative exons are more effectively amplified when larger fragments, at least about 1000 or 1500 bp, and even as large as 2000 bp are amplified.

The putative ORFs selected in process 300 are
thus input into one or more primer design programs, such as
PRIMER3 (available online for use at
http://www-genome.wi.mit.edu/cgi-bin/primer/), with a goal
of amplifying at least about 500 base pairs of genomic
sequence centered within or about ORFs predicted to be no
more than about 500 bp, or at least about 1000 - 1500 bp of
genomic sequence for ORFs predicted to exceed 500 bp in
length, and the primers synthesized by standard techniques.
Primers with the requisite sequences can be purchased
commercially or synthesized by standard techniques.

Conveniently, a first predetermined sequence can be added commonly to the ORF-specific 5' primer and a second, typically different, predetermined sequence commonly added to each 3' ORF-unique primer. This serves to immortalize the amplicon, that is, serves to permit further amplification of any amplicon using a single set of primers complementary respectively to the common 5' and common 3' sequence elements. The presence of these "universal" priming sequences further facilitates later sequence verification, providing a sequence common to all amplicons at which to prime sequencing reactions. The common 5' and 3' sequences further serve to add a cloning site should any of the ORFs warrant further study.

Such predetermined sequence is usefully at least about 10, 12 or 15 nt in length, and usually does not

exceed about 25 nt in length. The "universal" priming sequences used in the examples presented *infra* were each 16 nt long.

The genomic DNA to be used as substrate for 5 amplification will come from the eukaryotic species from which the genomic sequence data had originally been obtained, or a closely related species, and can conveniently be prepared by well known techniques from somatic or germline tissue or cultured cells of the 10 organism. See, e.g., Short Protocols in Molecular Biology : A Compendium of Methods from Current Protocols in Molecular Biology, Ausubel et al. (eds.), 4th edition (April 1999), John Wiley & Sons (ISBN: 047132938X) and Maniatis et al., Molecular Cloning: A Laboratory Manual, 15 2<sup>nd</sup> edition (December 1989), Cold Spring Harbor Laboratory Press (ISBN: 0879693096). Many such prepared genomic DNAs are available commercially, with the human genomic DNAs additionally having certification of donor informed consent.

20 Although the intronic and intergenic material flanking putative coding regions in the amplicons could potentially interfere with hybridizations during microarray experiments, we have found, surprisingly, that differential expression ratios are not significantly affected. Rather, 25 the predominant effect of exon size is to alter the absolute signal intensity, rather than its ratio. Equally surprising, the art had suggested that single exon probes would not provide sufficient signal intensity for high stringency hybridization analyses; we find that such probes not only provide adequate signal, but have substantial advantages, as herein described.

After partial purification, as by size exclusion spin column, with or without confirmation as to amplicon quality as by gel electrophoresis, each amplicon (single exon probe) is disposed in an array upon a support

substrate.

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Methods for creating microarrays by deposition and fixation of nucleic acids onto support substrates are well known in the art (Reviewed by Schena et al., see above).

Typically, the support substrate will be glass, although other materials, such as amorphous or crystalline silicon or plastics. Such plastics include polymethylacrylic, polyethylene, polypropylene,

10 polyacrylate, polymethylmethacrylate, polyvinylchloride, polytetrafluoroethylene, polystyrene, polycarbonate, polyacetal, polysulfone, celluloseacetate, cellulosenitrate, nitrocellulose, or mixtures thereof, can also be used. Typically, the support will be rectangular,

15 although other shapes, particularly circular disks and even spheres, present certain advantages. Particularly advantageous alternatives to glass slides as support substrates for array of nucleic acids are optical discs, as described in WO 98/12559.

The amplified nucleic acids can be attached covalently to a surface of the support substrate or, more typically, applied to a derivatized surface in a chaotropic agent that facilitates denaturation and adherence by presumed noncovalent interactions, or some combination thereof.

Robotic spotting devices useful for arraying nucleic acids on support substrates can be constructed using public domain specifications (The MGuide, version 2.0, http://cmgm.stanford.edu/pbrown/mguide/index.html), or can conveniently be purchased from commercial sources (MicroArray GenII Spotter and MicroArray GenIII Spotter, Molecular Dynamics, Inc., Sunnyvale, CA). Spotting can also be effected by printing methods, including those using ink jet technology.

As is well known in the art, microarrays

typically also contain immobilized control nucleic acids.

For controls useful in providing measurements of background signal for the genome-derived single exon microarrays of the present invention, a plurality of E. coli genes can readily be used. As further described in Example 1, 16 or 32 E. coli genes suffice to provide a robust measure of background noise in such microarrays.

As is well known in the art, the amplified product disposed in arrays on a support substrate to create a nucleic acid microarray can consist entirely of natural nucleotides linked by phosphodiester bonds, or alternatively can include either nonnative nucleotides, alternative internucleotide linkages, or both, so long as complementary binding can be obtained in the hybridization. If enzymatic amplification is used to produce the immobilized probes, the amplifying enzyme will impose certain further constraints upon the types of nucleic acid analogs that can be generated.

Although particularly described herein as using
high density microarrays constructed on planar substrates,
the methods of the present invention for confirming the
expression of ORFs predicted from genomic sequence can use
any of the known types of microarrays, as herein defined,
including lower density planar arrays, and microarrays on
nonplanar, nonunitary, distributed substrates.

For example, gene expression can be confirmed using hybridization to lower density arrays, such as those constructed on membranes, such as nitrocellulose, nylon, and positively-charged derivatized nylon membranes.

30 Further, gene expression can also be confirmed using nonplanar, bead-based microarrays such as are described in Brenner et al., Proc. Natl. Acad. Sci. USA 97(4):166501670 (2000); U.S. Patent No. 6,057,107; and U.S. Patent No. 5,736,330. In theory, a packed collection of such beads provides in aggregate a higher density of nucleic acid

probe than can be achieved with spotting or lithography techniques on a single planar substrate.

Planar microarrays on solid substrates, however, provide certain useful advantages, including high throughput and compatibility with existing readers. For example, each standard microscope slide can include at least 1000, typically at least 2000, preferably 5000 and upto 10,000 - 50,000 or more nucleic acid probes of discrete sequence. The number of sequences deposited will depend on their required application.

Each putative gene can be represented in the array by a single predicted ORF. Alternatively, genes can be represented by more than one predicted ORF. For purposes of measuring differential splicing, more than one predicted ORF will be provided for a putative gene. And as is well known in the art, each probe of defined sequence, representing a single predicted ORF, can be deposited in a plurality of locations on a single microarray to provide redundancy of signal.

The genome-derived single exon microarrays described above differ in several fundamental and advantageous ways from microarrays presently used in the gene expression art, including (1) those created by deposition of mRNA-derived nucleic acids, (2) those created by in situ synthesis of oligonucleotide probes, and (3) those constructed from yeast genomic DNA.

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Most nucleic acid microarrays that are in use for study of eukaryotic gene expression have as immobilized probes nucleic acids that are derived — either directly or indirectly — from expressed message. As discussed above, it is common, for example, for such microarrays to be derived from cDNA/EST libraries, either from those previously described in the literature, see Lennon et al., or from the de novo construction of "problem specific" libraries targeted at a particular biological question,

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R.S. Thomas et al., Cancer Res. (in press). Such microarrays are herein collectively denominated "EST microarrays".

Such EST microarrays by definition can measure 5 expression only of those genes found in EST libraries, shown herein to represent only a fraction of expressed genes. Furthermore, such libraries - and thus microarrays based thereupon - are biased by the tissue or cell type of message origin, by the expression levels of the respective 10 genes within the tissues, and by the ability of the message successfully to have been reverse-transcribed and cloned.

Thus, as further discussed in Example 1, the methods of the present invention enable sequences that do not appear in EST or other expression databases to be 15 determined - subsequently arrayed for expression measurements could not, therefore, have been represented as probes on an EST microarray. And as further demonstrated in the examples, infra, the remaining population of genes identified from genomic sequence by the methods of the present invention — that is, the one third of sequences that had previously been accessioned in EST or other expression databases - are biased toward genes with higher expression levels.

Representation of a message in an EST and/or cDNA 25 library depends upon the successful reverse transcription, optionally but typically with subsequent successful cloning, of the message. This introduces substantial bias into the population of probes available for arraying in EST microarrays.

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In contrast, neither reverse transcription nor cloning is required to produce the probes arrayed on the genome-derived single exon microarrays of the present invention. And although the ultimate deposition of a probe on the genome-derived single exon microarray of the present 35 invention depends upon a successful amplification from

genomic material, a priori knowledge of the sequence of the desired amplicon affords greater opportunity to recover any given probe sequence recalcitrant to amplification than is afforded by the requirement for successful reverse transcription and cloning of unknown message in EST approaches.

Thus, the genome-derived single exon microarrays of the present invention present a far greater diversity of probes for measuring gene expression, with far less bias, than do EST microarrays presently used in the art.

As a further consequence of their ultimate origin from expressed message, the probes in EST microarrays often contain poly-A (or complementary poly-T) stretches derived from the poly-A tail of mature mRNA. These homopolymeric stretches contribute to cross-hybridization, that is, to a spurious signal occasioned by hybridization to the homopolymeric tail of a labeled cDNA that lacks sequence homology to the gene-specific portion of the probe.

In contrast, the probes arrayed in the genomederived single exon microarrays of the present invention
lack homopolymeric stretches derived from message
polyadenylation, and thus can provide more specific signal.
Typically, at least about 50, 60 or 75% of the probes on
the genome-derived single exon microarrays of the present
invention lack homopolymeric regions consisting of A or T,
where a homopolymeric region is defined for purposes herein
as stretches of 25 or more, typically 30 or more, identical
nucleotides.

A further distinction, which also affects the specificity of hybridization, is occasioned by the typical derivation of EST microarray probes from cloned material. Because much of the probe material disposed as probes on EST microarrays is excised or amplified from plasmid, phage, or phagemid vectors, EST microarrays typically include a fair amount of vector sequence, more so when the

probes are amplified, rather than excised, from the vector.

In contrast, the vast majority of probes in the genome-derived single exon microarrays of the present invention contain no prokaryotic or bacteriophage vector 5 sequence, having been amplified directly or indirectly from genomic DNA. Typically, therefore, at least about 50, 60, 70 or 80% or more of individual exon-including probes disposed on a genome-derived single exon microarray of the present invention lack vector sequence, and particularly 10 lack sequences drawn from plasmids and bacteriophage. Preferably, at least about 85, 90 or more than 90% of exonincluding probes in the genome-derived single exon microarray of the present invention lack vector sequence. With attention to removal of vector sequences through 15 preprocessing 24, percentages of vector-free exon-including probes can be as high as 95 - 99%. The substantial absence of vector sequence from the genome-derived single exon microarrays of the present invention results in greater specificity during hybridization, since spurious cross-20 hybridization to a probe vector sequence is reduced.

As a further consequence of excision or amplification of probes from vectors in construction of EST microarrays, the probes arrayed thereon often contain artificial sequence, derived from vector polylinker

25 multiple cloning sites, at both 5' and 3' ends. The probes disposed upon the genome-derived single exon microarrays need have no such artificial sequence appended thereto.

As mentioned above, however, the ORF-specific primers used to amplify putative ORFs can include

30 artificial sequences, typically 5' to the ORF-specific primer sequence, useful for "universal" (that is, independent of ORF sequence) priming of subsequent amplification or sequencing reactions. When such "universal" 5' and/or 3' priming sequences are appended to the amplification primers, the probes disposed upon the

genome-derived single exon microarray will include artificial sequence similar to that found in EST microarrays. However, the genome-derived single exon microarray of the present invention can be made without such sequences, and if so constructed, presents an even smaller amount of nonspecific sequence that would contribute to nonspecific hybridization.

Yet another consequence of typical use of cloned material as probes in EST microarrays is that such microarrays contain probes that result from cloning artifacts, such as chimeric molecules containing coding region of two separate genes. Derived from genomic material, typically not thereafter cloned, the probes of the genome-derived single exon microarrays of the present invention lack such cloning artifacts, and thus provide greater specificity of signal in gene expression measurements.

A further consequence of the cloned origin of probes on many EST microarrays is that the individual probes often have disparate sizes, which can cause the optimal hybridization stringency to vary among probes on a single microarray. In contrast, as discussed above, the probes arrayed on the genome-derived single exon microarrays of the present invention can readily be designed to have a narrow distribution in sizes, with the range of probe sizes no greater than about 10% of the average size, typically no greater than about 5% of the average probe size.

Because of their origin from fully- or partially30 spliced message, probes disposed upon EST arrays will often include multiple exons. The percentage of such exonspanning probes in an EST microarray can be calculated, on average, based upon the predicted number of exons/gene for the given species and the average length of the immobilized probes. For human genes, the near-complete sequence of

human chromosome 22, Dunham et al., Nature 402(6761):489-95 (1999), predicts that human genes average 5.5 exons/gene. Even with probes of 200 - 500 bp, the vast majority of human EST microarray probes include more than one exon.

In contrast, by virtue of their origin from algorithmically identified ORFs in genomic sequence, the probes in the genome-derived single exon microarrays of the present invention can consist of individual exons. Thus, in contrast to EST microarrays, at least about 50, 60, 70, 75, 80, 85, 95 or 99% of probes deposited in the genomederived microarray of the present invention consist of, or include, no more than one predicted ORF.

This provides the ability, not readily achieved using EST microarrays, to use the genome-derived single exon microarrays of the present invention to measure tissue-specific expression of individual exons, which in turn allows differential splicing events to be detected and characterized, and in particular, allows the correlation of differential splicing to tissue-specific expression patterns.

Furthermore, the exons that are represented in EST microarrays are often biased toward the 3' or 5' end of their respective genes, since sequencing strategies used for EST identification are so biased. In contrast, no such 3' or 5' bias necessarily inheres in the selection of exons for disposition on the genome-derived single exon microarrays of the present invention.

Conversely, the probes provided on the genomederived single exon microarrays of the present invention

typically, but need not necessarily, include intronic
and/or intergenic sequence that is absent from EST
microarrays, which are derived from mature mRNA.

Typically, at least about 50, 60, 70, 80 or 90% of the
exon-including probes on the genome-derived single exon

microarrays of the present invention include sequence drawn

from noncoding regions. As discussed above, the additional presence of noncoding region does not significantly interfere with measurement of gene expression, and provides the additional opportunity to assay prespliced RNA, and thus measure such phenomena such as nuclear export control.

The genome-derived single exon microarrays of the present invention are also quite different from in situ synthesis microarrays, where probe size is severely constrained by inadequacies in the photolithographic synthesis process.

Typically, probes arrayed on in situ synthesis microarrays are limited to a maximum of about 25 bp. As a well known consequence, hybridization to such chips must be performed at low stringency. In order, therefore, to achieve unambiguous sequence-specific hybridization results, the in situ synthesis microarray requires substantial redundancy, with concomitant programmed arraying for each probe of probe analogues with altered (i.e., mismatched) sequence.

In contrast, the longer probe length of the genome-derived single exon microarrays of the present invention allows much higher stringency hybridization and wash. Typically, therefore, exon-including probes on the genome-derived single exon microarrays of the present invention average at least about 100, 200, 300, 400 or 500 bp in length. By obviating the need for substantial probe redundancy, this approach permits a higher density of probes for discrete exons or genes to be arrayed on the microarrays of the present invention than can be achieved for in situ synthesis microarrays.

A further distinction is that the probes in in situ synthesis microarrays typically are covalently linked to the substrate surface. In contrast, the probes disposed on the genome-derived microarray of the present invention typically are, but need not necessarily be, bound

noncovalently to the substrate.

Furthermore, the short probe size on in situ microarrays causes large percentage differences in the melting temperature of probes hybridized to their complementary target sequence, and thus causes large percentage differences in the theoretically optimum stringency across the array as a whole.

In contrast, the larger probe size in the microarrays of the present invention create lower percentage differences in melting temperature across the range of arrayed probes.

A further significant advantage of the microarrays of the present invention over in situ synthesized arrays is that the quality of each individual probe can be confirmed before deposition. In contrast, the quality of probes cannot be assessed on a probe-by-probe basis for the in situ synthesized microarrays presently being used.

The genome-derived single exon microarrays of the present invention are also distinguished over, and present substantial benefits over, the genome-derived microarrays from lower eukaryotes such as yeast. Lashkari et al., Proc. Natl. Acad. Sci. USA 94:13057-13062 (1997).

Only about 220 - 250 of the 6100 or so nuclear

genes in Saccharomyces cerevisiae — that is, only about 4

- 5% — have standard, spliceosomal, introns, Lopez et al.,

Nucl. Acids Res. 28:85-86 (2000); Spingola et al., RNA

5(2):221-34 (1999). Furthermore, the entire yeast genome
has already been sequenced. These two facts permit the

ready amplification and disposition of single-ORF amplicons
on such microarray without the requirement for antecedent
use of gene prediction and/or comparative sequence
analyses.

Thus, a significant aspect of the present invention is the ability to identify and to confirm

expression of predicted coding regions in genomic sequence drawn from eukaryotic organisms that have a higher percentage of genes having introns than do yeast such as Saccharomyces cerevisiae, particularly in genomic sequence drawn from eukaryotes in which at least about 10, 20 or 50% of protein-encoding genes have introns. In preferred embodiments, the methods and apparatus of the present invention are used to identify and confirm expression of novel genes from genomic sequence of eukaryotes in which the average number of introns per gene is at least about one, two or three or more.

After the physical substrate is prepared, experimental verification of predicted function is performed.

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In a preferred embodiment of the present invention, where the function sought to be identified in genomic sequence is protein coding, experimental verification is performed by measuring expression of the putative ORFs, typically through nucleic acid hybridization experiments, and in particularly preferred embodiments, through hybridization to genome-derived single exon microarrays prepared as above- described.

Expression is conveniently measured and expressed for each probe in the microarray as a ratio of the

25 expression measured concurrently in a plurality of mRNA sources, according to techniques well known in the microarray art, Reviewed in Schena et al., and as further described in Example 2, below. The mRNA source for the reference against which specific expression is measured can be drawn from a homogeneous mRNA source, such as a single cultured cell-type, or alternatively can be heterogeneous, as from a pool of mRNA derived from multiple tissues and/or cell types, as further described in Example 2, infra.

mRNA can be prepared by standard techniques, see

35 Ausubel et al. and Maniatis et al., or purchased

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commercially. The mRNA is then typically reversetranscribed in the presence of labeled nucleotides: the index source (that in which expression is desired to be measured) is reverse transcribed in the presence of 5 nucleotides labeled with a first label, typically a fluorophore (fluorochrome; fluor; fluorescent dye); the reference source is reverse transcribed in the presence of a second label, typically a fluorophore, typically fluorometrically-distinguishable from the first label. As 10 further described in Example 2, infra, Cy3 and Cy5 dyes prove particularly useful in these methods. After partial purification of the index and reference targets, hybridization to the probe array is conducted according to standard techniques, typically under a coverslip.

After wash, microarrays are conveniently scanned using a commercial microarray scanning device, such as a Gen3 Scanner (Molecular Dynamics, Sunnyvale, CA). Data on expression is then passed, with or without interim storage, to process 500, where the results for each probe are 20 related to the original sequence.

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Often, hybridization of target material to the genome-derived single exon microarray will identify certain of the probes thereon as of particular interest. Thus, it is often desirable that the user be able readily to obtain 25 sufficient quantities of an individual probe, either for subsequent arrayed deposition upon an additional support substrate, often as part of a microarray having a plurality of probes so identified, or alternatively or additionally as a solitary solid-phase or solution-phase probe, for 30 further use.

Thus, in another aspect, the present invention provides compositions and kits for the ready production of nucleic acids identical in sequence to, or substantially identical in sequence to, probes on the genome-derived 35 single exon microarrays of the present invention.

In this aspect, a small quantity of each probe is disposed, typically without attachment to substrate, in a spatially-addressable ordered set, typically one per well of a microtiter dish. Although a 96 well microtiter plate 5 can be used, greater efficiency is obtained using higher density arrays, such as are provided by microtiter plates having 384, 864, 1536, 3456, 6144, or 9600 wells, and although microtiter plates having physical depressions (wells) are conveniently used, any device that permits addressable withdrawal of reagent from fluidlynoncommunicating areas can be used.

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In this aspect of the invention, therefore, a fluidly noncommunicating addressable ordered set of individual probes, corresponding to those on a genome-15 derived single exon microarray, is provided, with each probe in sufficient quantity to permit amplification, such as by PCR. As earlier mentioned, the ORF-specific 5' primers used for genomic amplification can have a first common sequence added thereto, and the ORF-specific 3' 20 primers used for genomic amplification can have a second, different, common sequence added thereto, thus permitting, in this preferred embodiment, the use of a single set of 5' and 3' primers to amplify any one of the probes from the amplifiable ordered set.

Each discrete amplifiable probe can also be packaged with amplification primers, solutes, buffers, etc., and can be provided in dry (e.g., lyophilized) form or wet, in the latter case typically with addition of agents that retard evaporation.

In another aspect of the present invention, a genome-derived single-exon microarray is packaged together with such an ordered set of amplifiable probes corresponding to the probes, or one or more subsets of probes, thereon. In alternative embodiments, the ordered set of amplifiable probes is packaged separately from the

genome-derived single exon microarray.

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In some embodiments, the microarray and/or ordered probe set are further packaged with recordable media that provide probe identification and addressing information, and that can additionally contain annotation information, such as gene expression data. Such recordable media can be packaged with the microarray, with the ordered probe set, or with both.

If the microarray is constructed on a substrate

10 that incorporates recordable media, such as is described in

international patent application no. WO 98/12559, then

separate packaging of the genome-derived single exon

microarray and the bioinformatic information is not

required.

The amount of amplifiable probe material should be sufficient to permit at least one amplification sufficient for subsequent hybridization assay.

Although the use of high density genome-derived microarrays on solid planar substrates is presently a preferred approach for the physical confirmation and characterization of the expression of sequences predicted to encode protein, other types of microarrays (as herein defined) can also be used.

Furthermore, as earlier mentioned, experimental
verification of the function predicted from genomic
sequence in process 200 can be bioinformatic, rather than,
or additional to, physical verification.

For example, where the function desired to be identified is protein coding, the predicted ORFs can be compared bioinformatically to sequences known or suspected of being expressed.

Thus, the sequences output from process 300 (or process 200), can be used to query expression databases, such as EST databases, SNP ("single nucleotide") polymorphism") databases, known cDNA and mRNA sequences,

SAGE ("serial analysis of gene expression") databases, and more generalized sequence databases that allow query for expressed sequences. Such query can be done by any sequence query algorithm, such as BLAST ("basic local alignment search tool"). The results of such query — including information on identical sequences and information on nonidentical sequences that have diffuse or focal regions of sequence homology to the query sequence — can then be passed directly to process 500, or used to inform analyses subsequently undertaken in process 200, process 300, or process 400.

Experimental data, whether obtained by physical or bioinformatic assay in process 400, is passed to process 500 where it is usefully related to the sequence data

15 itself, a process colloquially termed "annotation". Such annotation can be done using any technique that usefully relates the functional information to the sequence, as, for example, by incorporating the functional data into the record itself, by linking records in a hierarchical or 20 relational database, by linking to external databases, or by a combination thereof. Such database techniques are well within the skill in the art.

The annotated sequence data can be stored locally, uploaded to genomic sequence database 100, and/or displayed 800.

The methods and apparatus of the present invention rapidly produce functional information from genomic sequence. Coupled with the escalating pace at which sequence now accumulates, the rapid pace of sequence annotation produces a need for methods of displaying the information in meaningful ways.

FIG. 3 shows visual display 80 presenting a single genomic sequence annotated according to the present invention. Because of its nominal resemblance to artistic works of Piet Mondrian, visual display 80 is alternatively

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described herein as a "Mondrian".

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Each of the visual elements of display 80 is aligned with respect to the genomic sequence being annotated (hereinafter, the "annotated sequence"). Given 5 the number of nucleotides typically represented in an annotated sequence, representation of individual nucleotides would rarely be readable in hard copy output of display 80. Typically, therefore, the annotated sequence is schematized as rectangle 89, extending from the left 10 border of display 80 to its right border. By convention herein, the left border of rectangle 89 represents the first nucleotide of the sequence and the right border of rectangle 89 represents the last nucleotide of the sequence.

As further discussed below, however, the Mondrian visual display of annotated sequence can serve as a convenient graphical user interface for computerized representation, analysis, and query of information stored electronically. For such use, the individual nucleotides 20 can conveniently be linked to the X axis coordinate of rectangle 89. This permits the annotated sequence at any point within rectangle 89 readily to be viewed, either automatically - for example, by time-delayed appearance of a small overlaid window upon movement of a cursor or other 25 pointer over rectangle 89 - or through user intervention, as by clicking a mouse or other pointing device at a point in rectangle 89.

Visual display 80 is generated after user specification of the genomic sequence to be displayed. 30 Such specification can consist of or include an accession number for a single clone (e.g., a single BAC accessioned into GenBank), wherein the starting and stopping nucleotides are thus absolutely identified, or alternatively can consist of or include an anchor or 35 fulcrum point about which a chosen range of sequence is

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anchored, thus providing relative endpoints for the sequence to be displayed. For example, the user can anchor such a range about a given chromosomal map location, gene name, or even a sequence returned by query for similarity 5 or identity to an input query sequence. When visual display 80 is used as a graphical user interface to computerized data, additional control over the first and last displayed nucleotide will typically be dynamically selectable, as by use of standard zooming and/or selection tools. 10

Field 81 of visual display 80 is used to present the output from process 200, that is, to present the bioinformatic prediction of those sequences having the desired function within the genomic sequence. Functional 15 sequences are typically indicated by at least one rectangle 83 (83a, 83b, 83c), the left and right borders of which respectively indicate, by their X-axis coordinates, the starting and ending nucleotides of the region predicted to have function.

Where a single bioinformatic method or approach identifies a plurality of regions having the desired function, a plurality of rectangles 83 is disposed horizontally in field 81. Where multiple methods and/or approaches are used to identify function, each such method 25 and/or approach can be represented by its own series of horizontally disposed rectangles 83, each such horizontally disposed series of rectangles offset vertically from those representing the results of the other methods and approaches.

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Thus, rectangles 83a in FIG. 3 represent the functional predictions of a first method of a first approach for predicting function, rectangles 83b represent the functional predictions of a second method and/or second approach for predicting that function, and rectangles 83c represent the predictions of a third method and/or

approach.

results from DICTION.

Where the function desired to be identified is protein coding, field 81 is used to present the bioinformatic prediction of sequences encoding protein.

5 For example, rectangles 83a can represent the results from GRAIL or GRAIL II, rectangles 83b can represent the results from GENEFINDER, and rectangles 83c can represent the

Optionally, and preferably, rectangles 83

10 collectively representing predictions of a single method and/or approach are identically colored and/or textured, and are distinguishable from the color and/or texture used for a different method and/or approach.

Alternatively, or in addition, the color, hue,

density, or texture of rectangles 83 can be used further to
report a measure of the bioinformatic reliability of the
prediction. For example, many gene prediction programs
will report a measure of the reliability of prediction.

Thus, increasing degrees of such reliability can be
indicated, e.g., by increasing density of shading. Where
display 80 is used as a graphical user interface, such
measures of reliability, and indeed all other results
output by the program, can additionally or alternatively be
made accessible through linkage from individual rectangles
83, as by time-delayed window ("tool tip" window), or by
pointer (e.g., mouse)-activated link.

As earlier described, increased predictive reliability can be achieved by requiring consensus among methods and/or approaches to determining function. Thus, field 81 can include a horizontal series of rectangles 83 that indicate one or more degrees of consensus in predictions of function.

Although FIG. 3 shows three series of
horizontally disposed rectangles in field 81, display 80
can include as few as one such series of rectangles and as

many as can discriminably be displayed, depending upon the number of methods and/or approaches used to predict a given function.

Furthermore, field 81 can be used to show

5 predictions of a plurality of different functions.

However, the increased visual complexity occasioned by such display makes more useful the ability of the user to select a single function for display. When display 80 is used as a graphical user interface for computer query and analysis, such function can usefully be indicated and user-selectable, as by a series of graphical buttons or tabs (not shown in FIG. 3).

Rectangle 89 is shown in FIG. 3 as including interposed rectangle 84. Rectangle 84 represents the portion of annotated sequence for which predicted functional information has been assayed physically, with the starting and ending nucleotides of the assayed material indicated by the X axis coordinates of the left and right borders of rectangle 84. Rectangle 85, with optional inclusive circles 86 (86a, 86b, and 86c) displays the results of such physical assay.

Although a single rectangle 84 is shown in FIG.

3, physical assay is not limited to just one region of annotated genomic sequence. It is expected that an

25 increasing percentage of regions predicted to have function by process 200 will be assayed physically, and that display 80 will accordingly, for any given genomic sequence, have an increasing number of rectangles 84 and 85, representing an increased density of sequence annotation.

Where the function desired to be identified is protein coding, rectangle 84 identifies the sequence of the probe used to measure expression. In embodiments of the present invention where expression is measured using genome-derived single exon microarrays, rectangle 84 identifies the sequence included within the probe

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immobilized on the support surface of the microarray. noted supra, such probe will often include a small amount of additional, synthetic, material incorporated during amplification and designed to permit reamplification of the 5 probe, which sequence is typically not shown in display 80.

Rectangle 87 is used to present the results of bioinformatic assay of the genomic sequence. For example, where the function desired to be identified is protein coding, process 400 can include bioinformatic query of 10 expression databases with the sequences predicted in process 200 to encode exons. And as earlier discussed, because bioinformatic assay presents fewer constraints than does physical assay, often the entire output of process 200 can be used for such assay, without further subsetting 15 thereof by process 300. Therefore, rectangle 87 typically need not have separate indicators therein of regions submitted for bioinformatic assay; that is, rectangle 87 typically need not have regions therein analogous to rectangles 84 within rectangle 89.

Rectangle 87 as shown in FIG. 3 includes smaller rectangles 880 and 88. Rectangles 880 indicate regions that returned a positive result in the bioinformatic assay, with rectangles 88 representing regions that did not return such positive results. Where the function desired to be 25 predicted and displayed is protein coding, rectangles 880 indicate regions of the predicted exons that identify sequence with significant similarity in expression databases, such as EST, SNP, SAGE databases, with rectangles 88 indicating genes novel over those identified in existing expression data bases.

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Rectangles 880 can further indicate, through color, shading, texture, or the like, additional information obtained from bioinformatic assay.

For example, where the function assayed and 35 displayed is protein coding, the degree of shading of

rectangles 880 can be used to represent the degree of sequence similarity found upon query of expression databases. The number of levels of discrimination can be as few as two (identity, and similarity, where similarity has a user-selectable lower threshold). Alternatively, as many different levels of discrimination can be indicated as can visually be discriminated.

Where display 80 is used as a graphical user interface, rectangles 880 can additionally provide links directly to the sequences identified by the query of expression databases, and/or statistical summaries thereof. As with each of the precedingly-discussed uses of display 80 as a graphical user interface, it should be understood that the information accessed via display 80 need not be resident on the computer presenting such display, which often will be serving as a client, with the linked information resident on one or more remotely located servers.

Rectangle 85 displays the results of physical 20 assay of the sequence delimited by its left and right borders.

Rectangle 85 can consist of a single rectangle, thus indicating a single assay, or alternatively, and increasingly typically, will consist of a series of rectangles (85a, 85b, 85c) indicating separate physical assays of the same sequence.

Where the function assayed is gene expression, and where gene expression is assayed as herein described using simultaneous two-color fluorescent detection of

hybridization to genome-derived single exon microarrays, individual rectangles 85 can be colored to indicate the degree of expression relative to control. Conveniently, shades of green can be used to depict expression in the sample over control values, and shades of red used to depict expression less than control, corresponding to the

spectra of the Cy3 and Cy5 dyes conventionally used for respective labeling thereof. Additional functional information can be provided in the form of circles 86 (86a, 86b, 86c), where the diameter of the circle can be used to indicate expression intensity. As discussed *infra*, such relative expression (expression ratios) and absolute expression (signal intensity) can be expressed using normalized values.

Where display 80 is used as a graphical user

interface, rectangle 85 can be used as a link to further information about the assay. For example, where the assay is one for gene expression, each rectangle 85 can be used to link to information about the source of the hybridized mRNA, the identity of the control, raw or processed data

from the microarray scan, or the like.

gene prediction and gene expression for a hypothetical BAC, showing conventions used in the Examples presented infra.

BAC sequence ("Chip seq.") 89 is presented, with the

physically assayed region thereof (corresponding to rectangle 84 in FIG. 3) shown in white. Algorithmic gene predictions are shown in field 81, with predictions by GRAIL shown, predictions by GENEFINDER, and predictions by DICTION shown. Within rectangle 87, regions of sequence that, when used to query expression databases, return identical or similar sequences ("EST hit") are shown as white rectangles (corresponding to rectangles 880 in FIG.

3), gray indicates low homology, and black indicates unknowns (where black and gray would correspond to rectangles 88 in FIG. 3).

Although FIGS. 3 and 4 show a single stretch of sequence, uninterrupted from left to right, longer sequences are usefully represented by vertical stacking of such individual Mondrians, as shown in FIGS. 9 and 10.

## Single Exon Probes Useful For Measuring Gene Expression

The methods and apparatus of the present invention rapidly produce functional information from genomic sequence. Where the function to be identified is protein coding, the methods and apparatus of the present invention rapidly identify and confirm the expression of portions of genomic sequence that function to encode protein. As a direct result, the methods and apparatus of the present invention rapidly yield large numbers of single-exon nucleic acid probes, the majority from previously unknown genes, each of which is useful for measuring and/or surveying expression of a specific gene in one or more tissues or cell types.

It is, therefore, another aspect of the present invention to provide genome-derived single exon nucleic acid probes useful for gene expression analysis, and particularly for gene expression analysis by microarray.

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Using the methods and genome-derived single-exon microarrays of the present invention, we have for example readily identified a large number of unique ORFs from human genomic sequence. Using single exon probes that encompass these ORFs, we have demonstrated, through microarray hybridization analysis, the expression of 13,232 of these ORFs in placenta.

As would immediately be appreciated by one of skill in the art, each single exon probe having demonstrable expression in placenta is currently available for use in measuring the level of its ORF's expression in placenta.

Given the substantial impact on human morbidity and mortality of diseases directly caused by genetic defect, and given the profound influence of genetic factors on the predisposition, onset, and/or aggressiveness of most, if not all human diseases, there has long been

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interest in efficient and safe means for early detection of gene defects and polymorphisms that cause, are associated with, or are implicated in development of disease.

Classically, such antenatal diagnosis was 5 effected during second trimester by metaphase karyotyping of fetal cells that had shed spontaneously into amniotic fluid.

More recently, techniques have been developed that permit direct sampling of placenta earlier in pregnancy.

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One technique in current clinical practice is chorionic villus sampling, which can be used to detect gene defects or polymorphisms in cells from the developing fetus, usually between 10 and 12 weeks of pregnancy. In 15 chorionic villus sampling, a small sample of chorionic villi, which are tiny projections that make up part of the placenta, a fetal-derived tissue, is removed through the mother's cervix or the abdominal wall. Placental chromosomal DNA is then isolated from the chorionic villus 20 cells and analyzed to detect a small number of known genetic defects. Such defects range from gross karyotypic changes, such as triploidy, to discrete point mutations known to cause diseases having significant morbidity or mortality.

Although only a few diseases are at present diagnosed by antenatal analysis of human placenta, a far higher number of human diseases and disorders have been catalogued in which dysfunction or misregulation of one or more genes contributes to the disease phenotype. At one 30 end of the spectrum of genetic diseases are those, such as sickle cell trait, in which a single point mutation is responsible for the disease phenotype. At the other end of the spectrum lie disorders such as Down syndrome wherein the presence of a supernumerary chromosome manifests itself in variety of phenotypic defects that vary in severity

among affected individuals. For most, possibly all genetic diseases, the precise phenotypic manifestation and its severity is a function of a complex interaction between the definable genetic lesion and the action of many other genes and environmental factors.

Although the incidence of many genetic diseases is low, a sufficient number of such genetic diseases affect a sufficiently large population that they impact the national health economy. For example, cystic fibrosis, 10 caused by mutations in a gene encoding a chloride ion channel and resulting in lung and other disorders, occurs at a rate of about 1 in 3000 births among Caucasians and costs over \$1 billion annually for direct medical treatment in the U.S. alone. Furthermore, it is increasingly thought 15 that for many diseases where no clear-cut genetic lesion appears responsible, possession by individuals of particular gene alleles naturally occurring within certain populations places such individuals at increased risk for developing those diseases. Examples include heart disease, neurogenerative disorders, diabetes, cancer and autoimmune disorders. For yet other diseases, especially cancer, the etiology is truly polygenic in that defects in multiple genes must cooincide in the same individual or even the same cell for the disease to develop and/or progress.

A large number of human genetic diseases and disorders are known, as are the gene or genes implicated in the etiology of the disease. Although in some cases single gene defects are known to be responsible for the etiology of a genetic disease, it is believed that for most or all such diseases, penetrance of the disease is affected by interaction with other genes. For other diseases or disorders, is believed that their mechanism is explained by the interaction of multiple genes, or by mutations or other defects in multiple genes. Such diseases and disorders may be detected in placenta.

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The human genome-derived single exon nucleic acid probes and microarrays of the present invention are useful for antenatal diagnosis of human genetic disorders. With each of the single exon probes described herein shown to be 5 expressed at detectable levels in human placenta, and with about 2/3 of the probes identifying novel genes, the single exon microarrays of the present invention provide exceptionally high informational content for such studies.

For example, antenatal diagnosis can be based 10 upon the quantitative relatedness of a placental gene expression profile to one or more reference expression profiles known to be characteristic of a given disease, or to specific grades or stages thereof.

In one embodiment, the gene expression profile is generated by hybridizing nucleic acids obtained directly or indirectly from placenta, typically through chorionic villus sampling, to the genome-derived single exon microarray of the present invention. Reference profiles are obtained similarly by hybridizing nucleic acids from individuals with known disease.

Methods for quantitatively relating gene expression profiles, without regard to the function of the protein encoded by the gene, are disclosed in WO 99/58720, incorporated herein by reference in its entirety.

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In another approach, the genome-derived single exon probes and microarrays of the present invention can be used to interrogate genomic DNA, rather than pools of expressed message; this latter approach permits presence and/or predisposition to disease to be assessed through the 30 massively parallel determination of altered copy number, deletion, or mutation of exons known to be expressed in human placenta. The algorithms set forth in WO 99/58720 can be applied to such genomic profiles without regard to the function of the protein encoded by the interrogated gene.

The utility is specific to the probe; at sufficiently high hybridization stringency, which stringencies are well known in the art — see Ausubel et al. and Maniatis et al. — each probe reports the level of expression of message specifically containing that ORF.

It should be appreciated, however, that the probes of the present invention, for which expression in the placenta has been demonstrated are useful for both measurement in the placenta and for survey of expression in other tissues.

Significant among such advantages is the presence of probes for novel genes.

As mentioned above and further detailed in
Examples 1 and 2, the methods described enable ORFs which
15 are not present in existing expression databases to be
identified. And the fewer the number of tissues in which
the ORF can be shown to be expressed, the more likely the
ORF will prove to be part of a novel gene: as further
discussed in Example 2, ORFs whose expression was
20 measurable in only a single of the tested tissues were
represented in existing expression databases at a rate of
only 11%, whereas 36% of ORFs whose expression was
measurable in 9 tissues were present in existing expression
databases, and fully 45% of those ORFs expressed in all ten
25 tested tissues were present in existing expressed sequence
databases.

Either as tools for measuring gene expression or tools for surveying gene expression, the genome-derived single exon probes of the present invention have significant advantages over the cDNA or EST-based probes that are currently available for achieving these utilities.

The genome-derived single exon probes of the present invention are useful in constructing genome-derived single exon microarrays; the genome-derived single exon

35 microarrays, in turn, are useful devices for measuring and

for surveying gene expression in the human.

Gene expression analysis using microarrays — conventionally using microarrays having probes derived from expressed message — is well-established as useful in the biological research arts (see Lockhart et al. Nature 405, 827-836).

Microarrays have been used to determine gene expression profiles in cells in response to drug treatment (see, for example, Kaminski et al., "Global Analysis of 10 Gene Expression in Pulmonary Fibrosis Reveals Distinct Programs Regulating Lung Inflammation and Fibrosis, " Proc. Natl. Acad. Sci. USA 97(4):1778-83 (2000); Bartosiewicz et al., "Development of a Toxicological Gene Array and Quantitative Assessment of This Technology, " Arch. Biochem. 15 Biophys. 376(1):66-73 (2000)), viral infection (see for example, Geiss et al., "Large-scale Monitoring of Host Cell Gene Expression During HIV-1 Infection Using cDNA Microarrays, " Virology 266(1):8-16 (2000)) and during cell processes such as differentiation, senescence and apoptosis 20 (see, for example, Shelton et al., "Microarray Analysis of Replicative Senescence, "Curr. Biol. 9(17):939-45 (1999); Voehringer et al., "Gene Microarray Identification of Redox and Mitochondrial Elements That Control Resistance or Sensitivity to Apoptosis, " Proc. Natl. Acad. Sci. USA 25 97(6):2680-5 (2000)).

Microarrays have also been used to determine abnormal gene expression in diseased tissues (see, for example, Alon et al., "Broad Patterns of Gene Expression Revealed by Clustering Analysis of Tumor and Normal Colon Tissues Probed by Oligonucleotide Arrays," Proc. Natl. Acad. Sci. USA 96(12):6745-50 (1999); Perou et al., "Distinctive Gene Expression Patterns in Human Mammary Epithelial Cells and Breast Cancers, Proc. Natl. Acad. Sci. USA 96(16):9212-7 (1999); Wang et al., "Identification of Genes Differentially Over-expressed in Lung Squamous Cell

Carcinoma Using Combination of cDNA Subtraction and Microarray Analysis, "Oncogene 19(12):1519-28 (2000); Whitney et al., "Analysis of Gene Expression in Multiple Sclerosis Lesions Using cDNA Microarrays," Ann. Neurol.

5 46(3):425-8 (1999)), in drug discovery screens (see, for example, Scherf et al., "A Gene Expression Database for the Molecular Pharmacology of Cancer," Nat. Genet. 24(3):236-44 (2000)) and in diagnosis to determine appropriate treatment strategies (see, for example, Sgroi et al., "In vivo Gene Expression Profile Analysis of Human Breast Cancer Progression," Cancer Res. 59(22):5656-61 (1999)).

In microarray-based gene expression screens of pharmacological drug candidates upon cells, each probe provides specific useful data. In particular, it should be appreciated that even those probes that show no change in expression are as informative as those that do change, serving, in essence, as negative controls.

For example, where gene expression analysis is used to assess toxicity of chemical agents on cells, the failure of the agent to change a gene's expression level is evidence that the drug likely does not affect the pathway of which the gene's expressed protein is a part.

Analogously, where gene expression analysis is used to assess side effects of pharmacological agents — whether in lead compound discovery or in subsequent screening of lead compound derivatives — the inability of the agent to alter a gene's expression level is evidence that the drug does not affect the pathway of which the gene's expressed protein is a part.

WO 99/58720 provides methods for quantifying the relatedness of a first and second gene expression profile and for ordering the relatedness of a plurality of gene expression profiles. The methods so described permit useful information to be extracted from a greater percentage of the individual gene expression measurements

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from a microarray than methods previously used in the art. Other uses of microarrays are described in Gerhold et al., Trends Biochem. Sci. 24(5):168-173 (1999) and Zweiger, Trends Biotechnol. 17(11):429-436 (1999); 5 Schena et al.

The invention particularly provides genomederived single-exon probes known to be expressed in placenta. The individual single exon probes can be provided in the form of substantially isolated and purified 10 nucleic acid, typically, but not necessarily, in a quantity sufficient to perform a hybridization reaction.

Such nucleic acid can be in any form directly hybridizable to the message that contains the probe's ORF, such as double stranded DNA, single-stranded DNA 15 complementary to the message, single-stranded RNA complementary to the message, or chimeric DNA/RNA molecules so hybridizable. The nucleic acid can alternatively or additionally include either nonnative nucleotides, alternative internucleotide linkages, or both, so long as 20 complementary binding can be obtained. For example, probes can include phosphorothioates, methylphosphonates, morpholino analogs, and peptide nucleic acids (PNA), as are described, for example, in U.S. Patent Nos. 5,142,047; 5,235,033; 5,166,315; 5,217,866; 5,184,444; 5,861,250.

Usefully, however, such probes are provided in a form and quantity suitable for amplification, where the amplified product is thereafter to be used in the hybridization reactions that probe gene expression. Typically, such probes are provided in a form and quantity 30 suitable for amplification by PCR or by other well known amplification technique. One such technique additional to PCR is rolling circle amplification, as is described, inter alia, in U.S. Patent Nos. 5,854,033 and 5,714,320 and international patent publications WO 97/19193 and 35 WO 00/15779. As is well understood, where the probes are

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to be provided in a form suitable for amplification, the range of nucleic acid analogues and/or internucleotide linkages will be constrained by the requirements and nature of the amplification enzyme.

Where the probe is to be provided in form suitable for amplification, the quantity need not be sufficient for direct hybridization for gene expression analysis, and need be sufficient only to function as an amplification template, typically at least about 1, 10 or 100 pg or more.

Each discrete amplifiable probe can also be packaged with amplification primers, either in a single composition that comprises probe template and primers, or in a kit that comprises such primers separately packaged therefrom. As earlier mentioned, the ORF-specific 5' primers used for genomic amplification can have a first common sequence added thereto, and the ORF-specific 3' primers used for genomic amplification can have a second, different, common sequence added thereto, thus permitting, in this embodiment, the use of a single set of 5' and 3' primers to amplify any one of the probes. The probe composition and/or kit can also include buffers, enzyme, etc., required to effect amplification.

As mentioned earlier, when intended for use on a genome-derived single exon microarray of the present invention, the genome-derived single exon probes of the present invention will typically average at least about 100, 200, 300, 400 or 500 bp in length, including (and typically, but not necessarily centered about) the ORF.

Furthermore, when intended for use on a genome-derived single exon microarray of the present invention, the genome-derived single exon probes of the present invention will typically not contain a detectable label.

When intended for use in solution phase hybridization, however — that is, for use in a

hybridization reaction in which the probe is not first bound to a support substrate (although the target may indeed be so bound) — length constraints that are imposed in microarray-based hybridization approaches will be relaxed, and such probes will typically be labeled.

In such case, the only functional constraint that dictates the minimum size of such probe is that each such probe must be capable of specifically identifying in a hybridization reaction the exon from which it is drawn. In theory, a probe of as little as 17 nucleotides is capable of uniquely identifying its cognate sequence in the human genome. For hybridization to expressed message — a subset of target sequence that is much reduced in complexity as compared to genomic sequence — even fewer nucleotides are required for specificity.

Therefore, the probes of the present invention can include as few as 20, 25 or 50 bp or ORF, or more. In particular embodiments, the ORF sequences are given in SEQ ID NOS. 13,233 - 26,232, respectively, for probe SEQ ID NOS. 1 - 13,232. The minimum amount of ORF required to be included in the probe of the present invention in order to provide specific signal in either solution phase or microarray-based hybridizations can readily be determined for each of ORF SEQ ID NOS. 13,233 - 26,232 individually by routine experimentation using standard high stringency conditions.

Such high stringency conditions are described, inter alia, in Ausubel et al. and Maniatis et al. For microarray-based hybridization, standard high stringency conditions can usefully be 50% formamide, 5% SSC, 0.2 µg/µl poly(dA), 0.2 µg/µl human cotl DNA, and 0.5% SDS, in a humid oven at 42°C overnight, followed by successive washes of the microarray in 1% SSC, 0.2% SDS at 55°C for 5 minutes, and then 0.1% SSC, 0.2% SDS, at 55°C for 20 minutes. For solution phase hybridization, standard high

stringency conditions can usefully be aqueous hybridization at 65°C in 6X SSC. Lower stringency conditions, suitable for cross-hybridization to mRNA encoding structurally- and functionally-related proteins, can usefully be the same as the high stringency conditions but with reduction in temperature for hybridization and washing to room temperature (approximately 25°C).

When intended for use in solution phase hybridization, the maximum size of the single exon probes of the present invention is dictated by the proximity of other expressed exons in genomic DNA: although each single exon probe can include intergenic and/or intronic material contiguous to the ORF in the human genome, each probe of the present invention will include portions of only one expressed exon.

Thus, each single exon probe will include no more than about 25 kb of contiguous genomic sequence, more typically no more than about 20 kb of contiguous genomic sequence, more usually no more than about 15 kb, even more usually no more than about 10 kb. Usually, probes that are maximally about 5 kb will be used, more typically no more than about 3 kb.

appended hereto presents, by convention, only that strand
of the probe and ORF sequence that can be directly
translated reading from 5' to 3' end. As would be well
understood by one of skill in the art, single stranded
probes must be complementary in sequence to the ORF as
present in an mRNA; it is well within the skill in the art
to determine such complementary sequence. It will further
be understood that double stranded probes can be used in
both solution-phase hybridization and microarray-based
hybridization if suitably denatured.

Thus, it is an aspect of the present invention to provide single-stranded nucleic acid probes that have

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sequence complementary to those described herein above and below, and double-stranded probes one strand of which has sequence complementary to the probes described herein.

The probes can, but need not, contain intergenic 5 and/or intronic material that flanks the ORF, on one or both sides, in the same linear relationship to the ORF that the intergenic and/or intronic material bears to the ORF in genomic DNA. The probes do not, however, contain nucleic acid derived from more than one expressed ORF.

And when intended for use in solution hybridization, the probes of the present invention can usefully have detectable labels. Nucleic acid labels are well known in the art, and include, inter alia, radioactive labels, such as  $^{3}H$ ,  $^{32}P$ ,  $^{33}P$ ,  $^{35}S$ ,  $^{125}I$ ,  $^{131}I$ ; fluorescent 15 labels, such as Cy3, Cy5, Cy5.5, Cy7, SYBR®

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Green and other labels described in Haugland, Handbook of Fluorescent Probes and Research Chemicals, 7th ed., Molecular Probes Inc., Eugene, OR (2000), or fluorescence resonance energy transfer tandem conjugates 20 thereof; labels suitable for chemiluminescent and/or enhanced chemiluminescent detection; labels suitable for ESR and NMR detection; and labels that include one member of a specific binding pair, such as biotin, digoxigenin, or the like.

The probes, either in quantity sufficient for hybridization or sufficient for amplification, can be provided in individual vials or containers.

Alternatively, such probes can usefully be packaged as a plurality of such individual genome-derived 30 single exon probes.

When provided as a collection of plural individual probes, the probes are typically made available in amplifiable form in a spatially-addressable ordered set, typically one per well of a microtiter dish. Although a 96 35 well microtiter plate can be used, greater efficiency is

obtained using higher density arrays.

If, as earlier mentioned, the ORF-specific 5' primers used for genomic amplification had a first common sequence added thereto, and the ORF-specific 3' 5 primers used for genomic amplification had a second, different, common sequence added thereto, a single set of 5' and 3' primers can be used to amplify all of the probes from the amplifiable ordered set.

Such collections of genome-derived single exon 10 probes can usefully include a plurality of probes chosen for the common attribute of expression in the human placenta.

In such defined subsets, typically at least 50, 60, 75, 80, 85, 90 or 95% or more of the probes will be 15 chosen by their expression in the defined tissue or cell type.

The single exon probes of the present invention, as well as fragments of the single exon probes comprising selectively hybridizable portions of the probe ORF, can be used to obtain the full length cDNA that includes the ORF by (i) screening of cDNA libraries; (ii) rapid amplification of cDNA ends ("RACE"); or (iii) other conventional means, as are described, inter alia, in Ausubel et al. and Maniatis et al.

It is another aspect of the present invention to 25 provide genome-derived single exon nucleic acid microarrays useful for gene expression analysis, where the term "microarray" has the meaning given in the definitional section of this description, supra.

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The invention particularly provides genomederived single-exon nucleic acid microarrays comprising a plurality of probes known to be expressed in human placenta. In preferred embodiments, the present invention provides human genome-derived single exon microarrays 35 comprising a plurality of probes drawn from the group

consisting of SEQ ID NOS.: 1 - 13,232.

When used for gene expression analysis, the genome-derived single exon microarrays provide greater physical informational density than do the genome-derived 5 single exon microarrays that have lower percentages of probes known to be expressed commonly in the tested tissue. At a fixed probe density, for example, a given microarray surface area of the defined subset genome-derived single exon microarray can yield a greater number of expression 10 measurements. Alternatively, at a given probe density, the same number of expression measurements can be obtained from a smaller substrate surface area. Alternatively, at a fixed probe density and fixed surface area, probes can be provided redundantly, providing greater reliability in 15 signal measurement for any given probe. Furthermore, with a higher percentage of probes known to be expressed in the assayed tissue, the dynamic range of the detection means can be adjusted to reveal finer levels discrimination among the levels of expression.

Although particularly described with respect to their utility as probes of gene expression, particularly as probes to be included on a genome-derived single exon microarray, each of the nucleic acids having SEQ ID NOS.: 1 - 13,232 contains an open-reading frame, set forth

25 respectively in SEQ ID NOS.: 13,233 - 26,232, that encodes a protein domain. Thus, each of SEQ ID NOS. 1 - 13,232 can be used, or that portion thereof in SEQ ID NOS. 13,233 - 26,232 used, to express a protein domain by standard in vitro recombinant techniques. See Ausubel et al. and

30 Maniatis et al.

Additionally, kits are available commercially that readily permit such nucleic acids to be expressed as protein in bacterial cells, insect cells, or mammalian cells, as desired (e.g., HAT Protein Expression & Purification System, ClonTech Laboratories, Palo Alto, CA;

Adeno-X™ Expression System, ClonTech Laboratories, Palo Alto, CA; Protein Fusion & Purification (pMAL™) System, New England Biolabs, Beverley, MA)

Furthermore, shorter peptides can be chemically

synthesized using commercial peptide synthesizing equipment and well known techniques. Procedures are described, inter alia, in Chan et al. (eds.), Fmoc Solid Phase Peptide

Synthesis: A Practical Approach (Practical Approach Series, (Paper)), Oxford Univ. Press (March 2000) (ISBN:

10 0199637245); Jones, Amino Acid and Peptide Synthesis
(Oxford Chemistry Primers, No 7), Oxford Univ. Press
(August 1992) (ISBN: 0198556683); and Bodanszky, Principles
of Peptide Synthesis (Springer Laboratory), Springer Verlag
(December 1993) (ISBN: 0387564314).

It is, therefore, another aspect of the invention to provide peptides comprising an amino acid sequence translated from SEQ ID NOS: 13,233 - 26,232. Such amino acid sequences are set out in SEQ ID NOS: 26,233 - 38,837. Any such recombinantly-expressed or synthesized peptide of at least 8, and preferably at least about 15, amino acids, can be conjugated to a carrier protein and used to generate antibody that recognizes the peptide. Thus, it is a further aspect of the invention to provide peptides that have at least 8, preferably at least 15, consecutive amino acids.

The following examples are offered by way of illustration and not by way of limitation.

## 30 EXAMPLE 1

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Preparation of Single Exon Microarrays from ORFs Predicted in Human Genomic Sequence

## Bioinformatics Results

All human BAC sequences in fewer than 10 pieces

that had been accessioned in a five month period immediately preceding this study were downloaded from GenBank. This corresponds to ~2200 clones, totaling ~350 MB of sequence, or approximately 10% of the human genome.

After masking repetitive elements using the program CROSS\_MATCH, the sequence was analyzed for open reading frames using three separate gene finding programs. The three programs predict genes using independent algorithmic methods developed on independent training sets:

GRAIL uses a neural network, GENEFINDER uses a hidden Markoff model, and DICTION, a program proprietary to Genetics Institute, operates according to a different heuristic. The results of all three programs were used to create a prediction matrix across the segment of genomic

DNA.

The three gene finding programs yielded a range of results. GRAIL identified the greatest percentage of genomic sequence as putative coding region, 2% of the data analyzed. GENEFINDER was second, calling 1%, and DICTION yielded the least putative coding region, with 0.8% of genomic sequence called as coding region.

The consensus data were as follows. GRAIL and GENEFINDER agreed on 0.7% of genomic sequence, GRAIL and DICTION agreed on 0.5% of genomic sequence, and the three programs together agreed on 0.25% of the data analyzed. That is, 0.25% of the genomic sequence was identified by all three of the programs as containing putative coding region.

ORFs predicted by any two of the three programs

("consensus ORFs") were assorted into "gene bins" using two criteria: (1) any 7 consecutive exons within a 25 kb window were placed together in a bin as likely contributing to a single gene, and (2) all ORFs within a 25 kb window were placed together in a bin as likely contributing to a single gene if fewer than 7 exons were found within the 25 kb

window.

PCR

The largest ORF from each gene bin that did not span repetitive sequence was then chosen for amplification, as were all consensus ORFs longer than 500 bp. This method approximated one exon per gene; however, a number of genes were found to be represented by multiple elements.

Previously, we had determined that DNA fragments

10 fewer than 250 bp in length do not bind well to the aminomodified glass surface of the slides used as support
substrate for construction of microarrays; therefore,
amplicons were designed in the present experiments to
approximate 500 bp in length.

Accordingly, after selecting the largest ORF per gene bin, a 500 bp fragment of sequence centered on the ORF was passed to the primer picking software, PRIMER3 (available online for use at

http://www-genome.wi.mit.edu/cgi-bin/primer/ ). A first
20 additional sequence was commonly added to each ORF-unique
5' primer, and a second, different, additional sequence was
commonly added to each ORF-unique 3' primer, to permit
subsequent reamplification of the amplicon using a single
set of "universal" 5' and 3' primers, thus immortalizing

the amplicon. The addition of universal priming sequences also facilitates sequence verification, and can be used to add a cloning site should some ORFs be found to warrant further study.

The ORFs were then PCR amplified from genomic

30 DNA, verified on agarose gels, and sequenced using the
universal primers to validate the identity of the amplicon
to be spotted in the microarray.

Primers were supplied by Operon Technologies

(Alameda, CA). PCR amplification was performed by standard

techniques using human genomic DNA (Clontech, Palo Alto,

CA) as template. Each PCR product was verified by  $SYBR^{\oplus}$ green (Molecular Probes, Inc., Eugene, OR) staining of agarose gels, with subsequent imaging by Fluorimager (Molecular Dynamics, Inc., Sunnyvale, CA). PCR 5 amplification was classified as successful if a single band appeared.

The success rate for amplifying ORFs of interest directly from genomic DNA using PCR was approximately 75%. FIG. 5 graphs the distribution of predicted ORF (exon) 10 length and distribution of amplified PCR products, with ORF length shown in red and PCR product length shown in blue (which may appear black in the figure). Although the range of ORF sizes is readily seen to extend to beyond 900 bp, the mean predicted exon size was only 229 bp, with a median 15 size of 150 bp (n=9498). With an average amplicon size of 475  $\pm$  25 bp, approximately 50% of the average PCR amplification product contained predicted coding region, with the remaining 50% of the amplicon containing either intron, intergenic sequence, or both.

Using a strategy predicated on amplifying about 500 bp, it was found that long exons had a higher PCR failure rate. To address this, the bioinformatics process was adjusted to amplify 1000, 1500 or 2000 bp fragments from exons larger than 500 bp. This improved the rate of 25 successful amplification of exons exceeding 500 bp, constituting about 9.2% of the exons predicted by the gene finding algorithms.

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Approximately 75% of the probes disposed on the array (90% of those that successfully PCR amplified) were 30 sequence-verified by sequencing in both the forward and reverse direction using MegaBACE sequencer (Molecular Dynamics, Inc., Sunnyvale, CA), universal primers, and standard protocols.

Some genomic clones (BACs) yielded very poor PCR 35 and sequencing results. The reasons for this are unclear,

but may be related to the quality of early draft sequence or the inclusion of vector and host contamination in some submitted sequence data.

Although the intronic and intergenic material

flanking coding regions could theoretically interfere with
hybridization during microarray experiments, subsequent
empirical results demonstrated that differential expression
ratios were not significantly affected by the presence of
noncoding sequence. The variation in exon size was

similarly found not to affect differential expression
ratios significantly; however, variation in exon size was
observed to affect the absolute signal intensity (data not
shown).

The 350 MB of genomic DNA was, by the abovedescribed process, reduced to 9750 discrete probes, which
were spotted in duplicate onto glass slides using
commercially available instrumentation (MicroArray GenII
Spotter and/or MicroArray GenIII Spotter, Molecular
Dynamics, Inc., Sunnyvale, CA). Each slide additionally
included either 16 or 32 E. coli genes, the average
hybridization signal of which was used as a measure of
background biological noise.

Each of the probe sequences was BLASTed against the human EST data set, the NR data set, and SwissProt GenBank (May 7, 1999 release 2.0.9).

One third of the probe sequences (as amplified) produced an exact match (BLAST Expect ("E") values less than 1 e<sup>-100</sup>) to either an EST (20% of sequences) or a known mRNA (13% of sequences). A further 22% of the probe sequences showed some homology to a known EST or mRNA (BLAST E values from 1 e<sup>-5</sup> to 1 e<sup>-99</sup>). The remaining 45% of the probe sequences showed no significant sequence homology to any expressed, or potentially expressed, sequences present in public databases.

All of the probe sequences (as amplified) were

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then analyzed for protein similarities with the SwissProt database using BLASTX, Gish et al., Nature Genet. 3:266 (1993). The predicted functional breakdowns of the 2/3 of probes identical or homologous to known sequences are presented in Table 1.

Table 1

		•	
Function	of Predic	ted ORFs As	Deduced From Comparative
Sequence	Analysis		
Total	V6 chip	V7 chip	Function Predicted from
			Comparative Sequence
			Analysis
211	96	115	Receptor
120	43	77	Zinc Finger
30	11	19	Homeobox
25	9	16	Transcription Factor
17	11	7	Transcription
118	57	61	Structural
95	39	56	Kinase.
36	18	18	Phosphatase
83	31	52	Ribosomal
45	19	26	Transport
21	17	14	Growth Factor
17	12	5	Cytochrome
50	33	17	Channel
L		<u> </u>	

As can be seen, the two most common types of 10 genes were transcription factors and receptors, making up 2.2% and 1.8% of the arrayed elements, respectively.

#### EXAMPLE 2

15 Gene Expression Measurements From Genome-Derived Single

Exon Microarrays

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The two genome-derived single exon microarrays 5 prepared according to Example 1 were hybridized in a series of simultaneous two-color fluorescence experiments to (1) Cy3-labeled cDNA synthesized from message drawn individually from each of brain, heart, liver, fetal liver, placenta, lung, bone marrow, HeLa, BT 474, or HBL 100 10 cells, and (2) Cy5-labeled cDNA prepared from message pooled from all ten tissues and cell types, as a control in each of the measurements. Hybridization and scanning were carried out using standard protocols and Molecular Dynamics equipment.

Briefly, mRNA samples were bought from commercial sources (Clontech, Palo Alto, CA and Amersham Pharmacia Biotech (APB)). Cy3-dCTP and Cy5-dCTP (both from APB) were incorporated during separate reverse transcriptions of 1  $\mu g$ of polyA $^{+}$  mRNA performed using 1  $\mu g$  oligo(dT)12-18 primer 20 and  $2~\mu g$  random 9 mer primers as follows. After heating to 70°C, the RNA:primer mixture was snap cooled on ice. After snap cooling on ice, added to the RNA to the stated final concentration was: 1X Superscript II buffer, 0.01 M DTT, 100  $\mu M$  dATP, 100  $\mu M$  dGTP, 100  $\mu M$  dTTP, 50  $\mu M$  dCTP, 50  $\mu M$ 25 Cy3-dCTP or Cy5-dCTP 50  $\mu M,$  and 200 U Superscript II The reaction was incubated for 2 hours at 42°C. After 2 hours, the first strand cDNA was isolated by adding 1 U Ribonuclease H, and incubating for 30 minutes at 37°C. The reaction was then purified using a Qiagen PCR cleanup 30 column, increasing the number of ethanol washes to 5. Probe was eluted using 10 mM Tris pH 8.5.

Using a spectrophotometer, probes were measured for dye incorporation. Volumes of both Cy3 and Cy5 cDNA corresponding to 50 pmoles of each dye were then dried in a 35 Speedvac, resuspended in 30 µl hybridization solution

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containing 50% formamide, 5% SSC, 0.2  $\mu g/\mu l$  poly(dA), 0.2  $\mu$ g/ $\mu$ l human cot1 DNA, and 0.5 % SDS.

Hybridizations were carried out under a coverslip, with the array placed in a humid oven at 42°C 5 overnight. Before scanning, slides were washed in 1X SSC, 0.2% SDS at 55°C for 5 minutes, followed by 0.1% SSC, 0.2% SDS, at 55°C for 20 minutes. Slides were briefly dipped in water and dried thoroughly under a gentle stream of nitrogen.

Slides were scanned using a Molecular Dynamics 10 Gen3 scanner, as described. Schena (ed.), Microarray Biochip: Tools and Technology, Eaton Publishing Company/BioTechniques Books Division (2000) (ISBN: 1881299376).

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Although the use of pooled cDNA as a reference permitted the survey of a large number of tissues, it attenuates the measurement of relative gene expression, since every highly expressed gene in the tissue/cell typespecific fluorescence channel will be present to a level of 20 at least 10% in the control channel. Because of this fact, both signal and expression ratios (the latter hereinafter, "expression" or "relative expression") for each probe were normalized using the average ratio or average signal, respectively, as measured across the whole slide.

Data were accepted for further analysis only when signal was at least three times greater than biological noise, the latter defined by the average signal produced by the E. coli control genes.

The relative expression signal for these probes 30 was then plotted as function of tissue or cell type, and is presented in FIG. 6.

FIG. 6 shows the distribution of expression across a panel of ten tissues. The graph shows the number of sequence-verified products that were either not 35 expressed ("0"), expressed in one or more but not all

tested tissues ("1" - "9"), and expressed in all tissues tested ("10").

Of 9999 arrayed elements on the two microarrays (including positive and negative controls and "failed" products), 2353 (51%) were expressed in at least one tissue or cell type. Of the gene elements showing significant signal — where expression was scored as "significant" if the normalized Cy3 signal was greater than 1, representing signal 5-fold over biological noise (0.2) — 39% (991) were expressed in all 10 tissues. The next most common class (15%) consisted of gene elements expressed in only a single tissue.

The genes expressed in a single tissue were further analyzed, and the results of the analyses are compiled in FIG. 7.

FIG. 7A is a matrix presenting the expression of all verified sequences that showed expression greater than 3 in at least one tissue. Each clone is represented by a column in the matrix. Each of the 10 tissues assayed is 20 represented by a separate row in the matrix, and relative expression of a clone in that tissue is indicated at the respective node by intensity of green shading, with the intensity legend shown in panel B. The top row of the matrix ("EST Hit") contains "bioinformatic" rather than 25 "physical" expression data — that is, presents the results returned by query of EST, NR and SwissProt databases using the probe sequence. The legend for "bioinformatic expression" (i.e., degree of homology returned) is presented in panel C. Briefly, white is known, black is 30 novel, with gray depicting nonidentical with significant homology (white: E values < 1e-100; gray: E values from 1e-05 to 1e-99; black: E values > 1e-05).

As FIG. 7 readily shows, heart and brain were demonstrated to have the greatest numbers of genes that were shown to be uniquely expressed in the respective

tissue. In brain, 200 uniquely expressed genes were identified; in heart, 150. The remaining tissues gave the following figures for uniquely expressed genes: liver, 100; lung, 70; fetal liver, 150; bone marrow, 75; placenta, 100; HeLa, 50; HBL, 100; and BT474, 50.

"novel" genes among those that were up-regulated in only one tissue, as compared with those that were down-regulated in only one tissue. In fact, it was found that ORFs whose expression was measurable in only a single of the tested tissues were represented in sequencing databases at a rate of only 11%, whereas 36% of the ORFs whose expression was measurable in 9 of the tissues were present in public databases. As for those ORFs expressed in all ten tissues, fully 45% were present in existing expressed sequence databases. These results are not unexpected, since genes expressed in a greater number of tissues have a higher likelihood of being, and thus of having been, discovered by EST approaches.

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# Comparison of Signal from Known and Unknown Genes

The normalized signal of the genes found to have high homology to genes present in the GenBank human EST database were compared to the normalized signal of those genes not found in the GenBank human EST database. The data are shown in FIG. 8.

for all sequence-verified products with a BLAST Expect
("E") value of greater than 1e-30 (designated "unknown")

upon query of existing EST, NR and SwissProt databases, and shows in blue the normalized Cy3 signal intensity for all sequence-verified products with a BLAST Expect value of less than 1e-30 ("known"). Note that biological background noise has an averaged normalized Cy3 signal intensity of

0.2.

As expected, the most highly expressed of the This is not surprising, since ORFs were "known" genes. very high signal intensity correlates with very commonlyexpressed genes, which have a higher likelihood of being 5 found by EST sequence.

However, a significant point is that a large number of even the high expressers were "unknown". the genomic approach used to identify genes and to confirm their expression does not bias exons toward either the 3' 10 or 5' end of a gene, many of these high expression genes will not have been detected in an end-sequenced cDNA library.

The significant point is that presence of the gene in an EST database is not a prerequisite for 15 incorporation into a genome-derived microarray, and further, that arraying such "unknown" exons can help to assign function to as-yet undiscovered genes.

## Verification of Gene Expression

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To ascertain the validity of the approach 20 described above to identify genes from raw genomic sequence, expression of two of the probes was assayed using reverse transcriptase polymerase chain reaction (RT PCR) and northern blot analysis.

Two microarray probes were selected on the basis of exon size, prior sequencing success, and tissue-specific gene expression patterns as measured by the microarray experiments. The primers originally used to amplify the two respective ORFs from genomic DNA were used in RT PCR 30 against a panel of tissue-specific cDNAs (Rapid-Scan gene expression panel 24 human cDNAs) (OriGene Technologies, Inc., Rockville, MD).

Sequence AL079300\_1 was shown by microarray hybridization to be present in cardiac tissue, and sequence 35 AL031734\_1 was shown by microarray experiment to be present

in placental tissue (data not shown). RT-PCR on these two sequences confirmed the tissue-specific gene expression as measured by microarrays, as ascertained by the presence of a correctly sized PCR product from the respective tissue type cDNAs.

Clearly, all microarray results cannot, and indeed should not, be confirmed by independent assay methods, or the high throughput, highly parallel advantages of microarray hybridization assays will be lost. However, in addition to the two RT-PCR results presented above, the observation that 1/3 of the arrayed genes exist in expression databases provides powerful confirmation of the power of our methodology — which combines bioinformatic prediction with expression confirmation using genome-derived single exon microarrays — to identify novel genes from raw genomic data.

To verify that the approach further provides correct characterization of the expression patterns of the identified genes, a detailed analysis was performed of the microarrayed sequences that showed high signal in brain.

For this latter analysis, sequences that showed high (normalized) signal in brain, but which showed very low (normalized) signal (less than 0.5, determined to be biological noise) in all other tissues, were further studied. There were 82 sequences that fit these criteria, approximately 2% of the arrayed elements. The 10 sequences showing the highest signal in brain in microarray hybridizations are detailed in Table 2, along with assigned function, if known or reasonably predicted.

30

Table 2

Function of the Most Highly
Expressed Genes Expressed Only in Brain

Sequence ized on Ratio to EST as described by Present GenBank  AP000217-1 5.2 +7.7 High S-100 protein, b-chain, Ca <sup>2+</sup> binding protein expressed in central nervous system  AP000047-1 2.3 High Unknown Function  AC006548-9 1.7 High Similar to mouse membrane glyco-protein M6, expressed in central nervous system  AC007245-5 1.5 High Similar to amphiphysin, a synaptic vesicle-associated protein. Ref 21  L44140-4 1.2 +2.0 High Endothelial actin-binding protein found in nonmuscle filamin  AC004689-9 1.2 +3.5 High Protein Phosphatase PP2A, neuronal/downregulates	Microarray	Normal	Expressi	Homology	Gene Function
in GenBank  AP000217-1 5.2 +7.7 High S-100 protein, b-chain, Ca²+ binding protein expressed in central nervous system  AP000047-1 2.3 High Unknown Function  AC006548-9 1.7 High Similar to mouse membrane glyco-protein M6, expressed in central nervous system  AC007245-5 1.5 High Similar to amphiphysin, a synaptic vesicle-associated protein. Ref 21  L44140-4 1.2 +2.0 High Endothelial actin-binding protein found in nonmuscle filamin  AC004689-9 1.2 +3.5 High Protein Phosphatase PP2A, neuronal/	Sequence	ized	on Ratio	to EST	as described by
AP000217-1 5.2 +7.7 High S-100 protein, b-chain, Ca <sup>2+</sup> binding protein expressed in central nervous system  AP000047-1 2.3 High Unknown Function  AC006548-9 1.7 High Similar to mouse membrane glyco-protein M6, expressed in central nervous system  AC007245-5 1.5 High Similar to amphiphysin, a synaptic vesicle-associated protein. Ref 21  L44140-4 1.2 +2.0 High Endothelial actin-binding protein found in nonmuscle filamin  AC004689-9 1.2 +3.5 High Protein Phosphatase PP2A, neuronal/	Name	Signal		present	GenBank
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binding protein expressed in central nervous system  AP000047-1 2.3 High Unknown Function  AC006548-9 1.7 High Similar to mouse membrane glyco-protein M6, expressed in central nervous system  AC007245-5 1.5 High Similar to amphiphysin, a synaptic vesicle-associated protein. Ref 21  L44140-4 1.2 +2.0 High Endothelial actin-binding protein found in nonmuscle filamin  AC004689-9 1.2 +3.5 High Protein Phosphatase PP2A, neuronal/	AP000217-1	5.2	+7.7	High	S-100 protein,
expressed in central nervous system  AP000047-1 2.3 High Unknown Function  AC006548-9 1.7 High Similar to mouse membrane glyco-protein M6, expressed in central nervous system  AC007245-5 1.5 High Similar to amphiphysin, a synaptic vesicle-associated protein. Ref 21  L44140-4 1.2 +2.0 High Endothelial actin-binding protein found in nonmuscle filamin  AC004689-9 1.2 +3.5 High Protein Phosphatase PP2A, neuronal/					b-chain, Ca <sup>2+</sup>
AP000047-1 2.3 High Unknown Function  AC006548-9 1.7 High Similar to mouse membrane glyco-protein M6, expressed in central nervous system  AC007245-5 1.5 High Similar to amphiphysin, a synaptic vesicle- associated protein. Ref 21  L44140-4 1.2 +2.0 High Endothelial actin-binding protein found in nonmuscle filamin  AC004689-9 1.2 +3.5 High Protein Phosphatase PP2A, neuronal/					binding protein
AP000047-1 2.3 High Unknown Function  AC006548-9 1.7 High Similar to mouse membrane glyco-protein M6, expressed in central nervous system  AC007245-5 1.5 High Similar to amphiphysin, a synaptic vesicle- associated protein. Ref 21  L44140-4 1.2 +2.0 High Endothelial actin-binding protein found in nonmuscle filamin  AC004689-9 1.2 +3.5 High Protein Phosphatase PP2A, neuronal/					expressed in
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mouse membrane glyco-protein M6, expressed in central nervous system  AC007245-5 1.5 High Similar to amphiphysin, a synaptic vesicle-associated protein. Ref 21  L44140-4 1.2 +2.0 High Endothelial actin-binding protein found in nonmuscle filamin  AC004689-9 1.2 +3.5 High Protein Phosphatase PP2A, neuronal/				}	Function
glyco-protein M6, expressed in central nervous system  AC007245-5 1.5 High Similar to amphiphysin, a synaptic vesicle- associated protein. Ref 21  L44140-4 1.2 +2.0 High Endothelial actin-binding protein found in nonmuscle filamin  AC004689-9 1.2 +3.5 High Protein Phosphatase PP2A, neuronal/	AC006548-9	1.7		High	Similar to
M6, expressed in central nervous system  AC007245-5 1.5 High Similar to amphiphysin, a synaptic vesicle-associated protein. Ref 21  L44140-4 1.2 +2.0 High Endothelial actin-binding protein found in nonmuscle filamin  AC004689-9 1.2 +3.5 High Protein Phosphatase PP2A, neuronal/					mouse membrane
in central nervous system  AC007245-5 1.5 High Similar to amphiphysin, a synaptic vesicle-associated protein. Ref 21  L44140-4 1.2 +2.0 High Endothelial actin-binding protein found in nonmuscle filamin  AC004689-9 1.2 +3.5 High Protein Phosphatase PP2A, neuronal/					glyco-protein
AC007245-5 1.5 High Similar to amphiphysin, a synaptic vesicle-associated protein. Ref 21  L44140-4 1.2 +2.0 High Endothelial actin-binding protein found in nonmuscle filamin  AC004689-9 1.2 +3.5 High Protein Phosphatase PP2A, neuronal/					M6, expressed
AC007245-5 1.5 High Similar to amphiphysin, a synaptic vesicle-associated protein. Ref 21  L44140-4 1.2 +2.0 High Endothelial actin-binding protein found in nonmuscle filamin  AC004689-9 1.2 +3.5 High Protein Phosphatase PP2A, neuronal/		ļ.		,	in central
amphiphysin, a synaptic vesicle-associated protein. Ref 21  L44140-4 1.2 +2.0 High Endothelial actin-binding protein found in nonmuscle filamin  AC004689-9 1.2 +3.5 High Protein Phosphatase PP2A, neuronal/					nervous system
synaptic vesicle- associated protein. Ref 21  L44140-4 1.2 +2.0 High Endothelial actin-binding protein found in nonmuscle filamin  AC004689-9 1.2 +3.5 High Protein Phosphatase PP2A, neuronal/	AC007245-5	1.5	<b> </b>	High	Similar to
vesicle- associated protein. Ref 21  L44140-4 1.2 +2.0 High Endothelial actin-binding protein found in nonmuscle filamin  AC004689-9 1.2 +3.5 High Protein Phosphatase PP2A, neuronal/					amphiphysin, a
associated protein. Ref 21  L44140-4 1.2 +2.0 High Endothelial actin-binding protein found in nonmuscle filamin  AC004689-9 1.2 +3.5 High Protein Phosphatase PP2A, neuronal/					synaptic
L44140-4 1.2 +2.0 High Endothelial actin-binding protein found in nonmuscle filamin  AC004689-9 1.2 +3.5 High Protein Phosphatase PP2A, neuronal/					vesicle-
L44140-4 1.2 +2.0 High Endothelial actin-binding protein found in nonmuscle filamin  AC004689-9 1.2 +3.5 High Protein Phosphatase PP2A, neuronal/					associated
actin-binding protein found in nonmuscle filamin  AC004689-9 1.2 +3.5 High Protein Phosphatase PP2A, neuronal/					protein. Ref 21
protein found in nonmuscle filamin  AC004689-9 1.2 +3.5 High Protein Phosphatase PP2A, neuronal/	L44140-4	1.2	+2.0	High	Endothelial
in nonmuscle filamin  AC004689-9 1.2 +3.5 High Protein Phosphatase PP2A, neuronal/					actin-binding
AC004689-9 1.2 +3.5 High Protein Phosphatase PP2A, neuronal/			}		protein found
AC004689-9 1.2 +3.5 High Protein Phosphatase PP2A, neuronal/					in nonmuscle
Phosphatase PP2A, neuronal/					filamin
PP2A, neuronal/	AC004689-9	1.2	+3.5	High	Protein
					Phosphatase
downramilates		,		]	PP2A, neuronal/
					downregulates

				activated
				protein kinases
AL031657-1	1.2	+3.0	High	Unknown
				function/
				Contains the
				anhyrin motif,
				a common
				protein
				sequence motif
AC009266-2	1.1	+3.7	Low	Low homology to
				the
				Synaptotagmin I
				protein in
				rat/present at
				low levels
				throughout rat
]				brain
AP000086-1	1.0	+2.7	Low	Unknown, very
				poor homology
				to collagen
AC004689-3	1.0	<del>                                     </del>	High	Protein
				Phosphatase
	ļ			PP2A, neuronal/
				downregulates
				activated
				protein kinases

Of the ten sequences studied by these latter confirmatory approaches, eight were previously known. Of these eight, six had previously been reported to be important in the central nervous system or brain. The exon giving the highest signal (AP00217-1) was found to be the gene encoding an S100B Ca<sup>2+</sup> binding protein, reported in the literature to be highly and uniquely expressed in the central nervous system. Heizmann, Neurochem. Res. 9:1097

(1997).

A number of the brain-specific probe sequences (including AC006548-9, AC009266-2) did not have homology to any known human cDNAs in GenBank but did show homology to rat and mouse cDNAs. Sequences AC004689-9 and AC004689-3 were both found to be phosphatases present in neurons (Millward et al., Trends Biochem. Sci. 24(5):186-191 (1999)). Two microarray sequences, AP000047-1 and AP000086-1 have unknown function, with AP000086-1 being absent from GenBank. Functionality can now be narrowed down to a role in the central nervous system for both of these genes, showing the power of designing microarrays in this fashion.

Next, the function of the chip sequences with the

15 highest (normalized) signal intensity in brain, regardless
of expression in other tissues, was assessed. In this
latter analysis, we found expression of many more common
genes, since the sequences were not limited to those
expressed only in brain. For example, looking at the 20

20 highest signal intensity spots in brain, 4 were similar to
tubulin (AC00807905; AF146191-2; AC007664-4; AF14191-2), 2
were similar to actin (AL035701-2; AL034402-1), and 6 were
found to be homologous to glyceraldehyde-3-phosphate
dehydrogenase (GAPDH) (AL035604-1; Z86090-1; AC006064-L,

25 AC006064-K; AC035604-3; AC006064-L). These genes are often
used as controls or housekeeping genes in microarray
experiments of all types.

Other interesting genes highly expressed in brain were a ferritin heavy chain protein, which is reported in the literature to be found in brain and liver (Joshi et al., J. Neurol. Sci. 134(Suppl):52-56 (1995)), a result duplicated with the array. Other highly expressed chip sequences included a translation elongation factor 10 (AC007564-4), a DEAD-box homolog (AL023804-4), and a Y-chromosome RNA-binding motif (Chai et al., Genomics

49(2):283-89 (1998)) (AC007320-3). A low homology analog (AP00123-1/2) to a gene, DSCR1, thought to be involved in trisomy 21 (Down's syndrome), showed high expression in both brain and heart, in agreement with the literature (Fuentes et al., Mol. Genet. 4(10):1935-44 (1995)).

As a further validation of the approach, we selected the BAC AC006064 to be included on the array. This BAC was known to contain the GAPDH gene, and thus could be used as a control for the ORF selection process.

The gene finding and exon selection algorithms resulted in choosing 25 exons from BAC AC006064 for spotting onto the array, of which four were drawn from the GAPDH gene. Table 3 shows the comparison of the average expression ratio for the 4 exons from BAC006064 compared with the average expression ratio for 5 different dilutions of a commercially available GAPDH cDNA (Clontech).

Table 3

	C. T	stio for each
Compari	son of Expression Ra	acio, for each
tissue, of GAPDH		• •
	•	•
	AC006064 (n = 4)	
Bone Marrow	-1.81 ± 0.11	-1.85 ± 0.08
Brain	-1.41 ± 0.11	-1.17 ± 0.05
BT474	1.85 ± 0.09	1.66 ± 0.12
Fetal Liver	-1.62 ± 0.07	$-1.41 \pm 0.05$
HBL100	1.32 ± 0.05	2.64 ± 0.12
Heart	1.16 ± 0.09	1.56 ± 0.10
HeLa	1.11 ±0.06	1.30 ± 0.15
Liver	-1.62 ± 0.22	-2.07 ±
Lung	-4.95 ± 0.93	$-3.75 \pm 0.21$
Placenta	$-3.56 \pm 0.25$	$-3.52 \pm 0.43$

Each tissue shows excellent agreement between the experimentally chosen exons and the control, again demonstrating the validity of the present exon mining approach. In addition, the data also show the variability of expression of GAPDH within tissues, calling into question its classification as a housekeeping gene and utility as a housekeeping control in microarray experiments.

#### 10 EXAMPLE 3

Representation of Sequence and Expression Data as a "Mondrian"

For each genomic clone processed for microarray

as above-described, a plethora of information was
accumulated, including full clone sequence, probe sequence
within the clone, results of each of the three gene finding
programs, EST information associated with the probe
sequences, and microarray signal and expression for
multiple tissues, challenging our ability to display the
information.

Accordingly, we devised a new tool for visual display of the sequence with its attendant annotation which, in deference to its visual similarity to the paintings of Piet Mondrian, is hereinafter termed a "Mondrian". FIGS. 3 and 4 present the key to the information presented on a Mondrian.

FIG. 9 presents a Mondrian of BAC AC008172 (bases 25,000 to 130,000 shown), containing the carbamyl phosphate synthetase gene (AF154830.1). Purple background within the region shown as field 81 in FIG. 3 indicates all 37 known exons for this gene.

As can be seen, GRAIL II successfully identified 27 of the known exons (73%), GENEFINDER successfully identified 37 of the known exons (100%), while DICTION

identified 7 of the known exons (19%).

Seven of the predicted exons were selected for physical assay, of which 5 successfully amplified by PCR and were sequenced. These five exons were all found to be from the same gene, the carbamyl phosphate synthetase gene (AF154830.1).

The five exons were arrayed, and gene expression measured across 10 tissues. As is readily seen in the Mondrian, the five chip sequences on the array show identical expression patterns, elegantly demonstrating the reproducibility of the system.

FIG. 10 is a Mondrian of BAC AL049839. We selected 12 exons from this BAC, of which 10 successfully sequenced, which were found to form between 5 and 6 genes. 15 Interestingly, 4 of the genes on this BAC are protease inhibitors. Again, these data elegantly show that exons selected from the same gene show the same expression patterns, depicted below the red line. From this figure, it is clear that our ability to find known genes is very 20 'good. A novel gene is also found from 86.6 kb to 88.6 kb, upon which all the exon finding programs agree. We are confident we have two exons from a single gene since they show the same expression patterns and the exons are proximal to each other. Backgrounds in the following 25 colors indicate a known gene (top to bottom): red = kallistatin protease inhibitor (P29622); purple = plasma serine protease inhibitor (P05154); turquoise =  $\alpha$ 1 anti-chymotrypsin (P01011); mauve = 40S ribosomal protein (P08865). Note that chip sequence 8 and 30 12 did not sequence verify.

#### EXAMPLE 4

Genome-Derived Single Exon Probes Useful For Measuring
35 Human Gene Expression

The protocols set forth in Examples 1 and 2, supra, were applied to additional human genomic sequence as it became newly available in GenBank to identify unique 5 exons in the human genome that could be shown to be expressed at significant levels in placenta tissue.

These unique exons are within longer probe sequences. Each probe was completely sequenced on both strands prior to its use on a genome-derived single exon 10 microarray; sequencing confirms the exact chemical structure of each probe. An added benefit of sequencing is that it placed us in possession of a set of single baseincremented fragments of the sequenced nucleic acid, starting from the sequencing primer 3' OH. (Since the 15 single exon probes were first obtained by PCR amplification from genomic DNA, we were of course additionally in possession of an even larger set of single base incremented fragments of each of the 13,232 single exon probes, each fragment corresponding to an extension product from one of 20 the two amplification primers.)

The structures of the 13,232 unique single exon probes are clearly presented in the Sequence Listing as SEQ ID Nos.: 1 - 13,232 . The 16 nt 5' primer sequence and 16 nt 3' primer sequence present on the amplicon are not 25 included in the sequence listing. The sequences of the exons present within each of these probes is presented in the Sequence Listing as SEQ ID Nos.: 13,233 - 26,232, respectively. It will be noted that some amplicons have more than one exon, some exons are contained in more than one amplicon.

As detailed in Example 2, expression was demonstrated by disposing the amplicons as single exon probes on nucleic acid microarrays and then performing twocolor fluorescent hybridization analysis; significant 35 expression is based on a statistical confidence that the

30

signal is significantly greater than negative biological control spots. The negative biological control is formed from spotted DNA sequences from a different species. Here, 32 sequences from E.Coli were spotted in duplicate to give a total of 64 spots.

For each hybridisation (each slide, each colour) the median value of the signal from all of the spots is determined. The normalised signal value is the arithmetic mean of the signal from duplicate spots divided by the population median.

Control spots are eliminated if there is more that a five-fold difference between each one of the duplicate spots raw signals.

The median of the signal from the remaining

15 control spots is calculated and all subsequent calculations are done with normalised signals.

Control spots having a signal of greater than median + 2.4 (the value 2.4 is roughly 12 times the observed standard deviation of control spot populations)

20 are eliminated. Spots with such high signals are considered to be "outliers".

The mean and standard deviation of the modified control spot populations are calculated.

The mean + 3x the standard deviation (mean + 25 (3\*SD)) is used as the signal threshold qualifier for that particular hybridisation. Thus, individual thresholds are determined for each channel and each hybridisation.

This means that, assuming that the data is distributed normally, there is a 99% confidence that any signal exceeding the threshold is significant.

The probes and their expression data are presented in Table 4, set forth respectively in Example 5. Example 5 presents the subset of probes that is significantly expressed in the human placenta and thus presents the subset of probes that was recognized to be

useful for measuring expression of their cognate genes in human placenta tissue.

The sequence of each of the exon probes
identified by SEQ ID NOS.: 13,233 - 26,232 was individually
used as a BLAST (or, for SWISSPROT, BLASTX) query to
identify the most similar sequence in each of dbEST,
SwissProt (BLASTX), and NR divisions of GenBank. Because
the query sequences are themselves derived from genomic
sequence in GenBank, only nongenomic hits from NR were
scored.

The smallest in value of the BLAST (or BLASTX) expect ("E") scores for each query sequence across the three database divisions was used as a measure of the "expression novelty" of the probe's ORF. Table 4 is sorted in descending order based on this measure, reported as "Most Similar (top) Hit BLAST E Value". Those sequences for which no "Hit E Value" is listed are those exons which were found to have no similar sequences.

As sorted, Table 4 thus lists its respective

20 probes (by "AMPLICON SEQ ID NO.:" and additionally by the

SEQ ID NO:. of the exon contained within the probe: "EXON

SEQ ID NO.:") from least similar to sequences known to be

expressed (i.e., highest BLAST E value), at the beginning

of the table, to most similar to sequences known to be

expressed (i.e., lowest BLAST E value), at the bottom of

the table.

Table 4 further provides, for each listed probe, the accession number of the database sequence that yielded the "Most Similar (top) Hit BLAST E Value", along with the name of the database in which the database sequence is found ("Top Hit Database Source").

Table 4 further provides SEQ ID NOS.

corresponding to the predicted amino acid sequences where
they have been determined for the probe and exon nucleotide
sequences. These are set out as PEPTIDE SEQ ID NOS.:. The

peptide sequences for a given exon are predicted as follows: Since each chip exon is a consensus sequence drawn from predictions from various exon finding programs (i.e. Grail, GeneFinder and GenScan), the multiple initial ORFs are first determined in a uniform way according to each prediction. In particular, the reading frame for predicting the first amino acid in the peptide sequence always starts with the first base of any codon and ends with the last base of non-termination codon. Next, for each strand of the exon, initial ORFs are merged into one or more final ORFs in an exhaustive process based on the following criteria:

1) the merging ORFs must be overlapping, and 2) the merging ORFs must be in the same frame.

The Sequence Listing, which is a superset of all

of the data presented in Table 4, further includes, for
each probe, the most similar hit, with accession number and
BLAST E value, from the each of the three queried
databases.

Table 4 further lists, for each probe, a portion

of the descriptor for the top hit ("Top Hit Descriptor") as provided in the sequence database. For those ORFs that are similar in sequence, but nonidentical to known sequences (e.g., those with BLAST E values between about 1e-05 and 1e-100), the descriptor reveals the likely function of the protein encoded by the probe's ORF.

Using BLAST E value cutoffs of 1e-05 (i.e., 1 x  $10^{-5}$ ) and 1e-100 (i.e., 1 x  $10^{-100}$ ) as evidence of similarity to sequences known to be expressed is of course arbitrary: in Example 2, supra, a BLAST E value of 1e-30 was used as the boundary when only two classes were to be defined for analysis (unknown, >1e-30; known <1e-30) (see also FIG. 8). Furthermore, even when the "Most Similar (Top) Hit BLAST E Value" is low, e.g., less than about 1e-100 — which is probative evidence that the query sequence has previously been shown to be expressed — the top hit is highly unlikely

exactly to match the probe sequence.

First, such expression entries typically will not have the intronic and/or intergenic sequence present within the single exon probes listed in the Table. Second, even the ORF itself is unlikely in such cases to be present identically in the databases, since most of the EST and mRNA clones in existing databases include multiple exons, without any indication of the location of exon boundaries.

As noted, the data presented in Table 4 represent a proper subset of the data present within the attached sequence listing. For each amplicon probe (SEQ ID NOs.: 1 - 13,232) and probe exon (SEQ ID NOs.: 13,233 - 26,232, respectively), the sequence listing further provides, through iterated annotation fields <220> and <223>:

- (a) the accession number of the BAC from which the sequence was derived ("MAP TO"), thus providing a link to the chromosomal map location and other information about the genomic milieu of the probe sequence;
- (b) the most similar sequence provided by BLAST 20 query of the EST database, with accession number and BLAST E value for the "hit";
  - (c) the most similar sequence provided by BLAST query of the GenBank NR database, with accession number and BLAST E value for the "hit"; and
  - (d) the most similar sequence provided by BLASTX query of the SWISSPROT database, with accession number and BLAST E value for the "hit".

### 30 EXAMPLE 5

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Genome-Derived Single Exon Probes Useful For Measuring Expression of Genes in Human Placenta

Table 4 (550 pages) presents expression, homology, and functional information for the genome-derived single exon

probes that are expressed significantly in human placenta.

Page 1 of 550 Table 4 Single Exon Probes Expressed in Placenta

ביינון וויסססק דיליון ססססק ווין וויסססק	Most Similar Top Hit Acession (Top) Hit Top Hit Acession Signal BLASTE No. Source Source	Tu u	896	3.01	10.9	1.92	4.94	1.03	1.67	8.63	1.57	2.66	9.39	2.63	3.76	1.48	10.5	1980	86'0	0.94	1.65	6.88	0.87	0.87	1,69	0.61	1.86	90	5.14	1.24	1.78	1.76	4.12	20.2	1 107.7
	Most Similar (Top) Hit BLAST E Value	160	8	-	6	2	4	3			1	9	6	6	2	8	9	4	8	4	2	8			[ ]6		9	9	4	4	9	9	2		-
	ORF SEQ Expression Signal		27152 9.6														29783 10.		29912 0.9				30519 0.8	30520 0.8		30639 0.6		o			31442 1.7		4.1		
	Exon SEQ ID NO:	13658	14087	14236	14487	14797	14818	14913	14937	14943	15082	15175	15368	15484	16429	16702	16768	16814	16908	17213	17457	17520	17539	17539	17597	17851	18088		18279	18290	18574	18574		18007	
	Probe SEQ ID NO:	463	912	1070	1330	1645	1666	1764	1788	1794	1939	2034	234	2353	3255	3537	3604	3651	3747	4057	4314	4377	4396	4396	4457	4512	4958	6002	5157	5168	6371	5371	5538	K 1.4.2	<u>+</u>

Page 2 of 550 Table 4

					Buis	Exon Probe	Single Exon Probes Expressed in Placenta
Probe SEQ ID NO:	Exan SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
5858	19048	32354	4.22				
6146							
6174	19350		1.92				
6540	19708		1.01				
6299			1.25				
6879			1.25				
7275	ľ		1.42				
7275	ı	33813	1.42				
7569		34117	1.18				
7569		34118	1.18				
8251	li	34851	1.44				
8682	21762	35296	1.14				
9061		35684					
9061	22140	35685	92'0				
9734	22799	36373					
8966		36602	99'0				
10086	23124	36725					
10229	H						
10643		37286	0.74				
10643	23677	37287	0.74				
10922			2.32				
11280							
11348			2.79				
11641	_		1.73				
11749	_ 1						
11749		37562					
11792							
12057		38746	1.56				
12623			2.06				
12967		31980	1.5				
6177		32700	19	9.9E+00	9.9E+00 AJ239028.1	NT	Homo sapiens LSS gene, partial, exons 15, 16, 17 and 18
8195	- 1	1		9.8E+00	9.8E+00 U32716.1	뉟	Haemophlius Influenzae Rd section 31 of 163 of the complete genome
9844	22383			9.8E+00	9.8E+00 Y18930.1	F	Sulfolobus solfataricus 281 kb genomic DNA fragment, strain P2
9944	ii	36576	0.48	9.8E+00	9.8E+00 Y18930.1	NT,	Sulfolobus solfataricus 281 kb genomic DNA fragment, strain P2

Page 3 of 550 Table 4 Single Exon Probes Expressed In Placenta

Page 4 of 550 Table 4 Single Exon Probes Expressed in Placenta

		_		_	_	_	_	_	_	-	_	_	_		_			_	_	_		_	_	_	_	_	_	÷	_	_	_			1
Top Hit Descriptor	Lycopersicon esculentum Mill. GTPase (SAR2) mRNA, complete cds	Lycopersicon esculentum Mill. G l Pase (SAR2) mRNA, complete cds	RC0-HT0613-200300-031-a07 HT0613 Homo sapiens cDNA	ZINC-FINGER PROTEIN 1 (ZINC-FINGER HOMEODOMAIN PROTEIN 1)	ZINC-FINGER PROTEIN 1 (ZINC-FINGER HOMEODOMAIN PROTEIN 1)	Arabidopsis thallana DNA chromosome 4, contig fragment No. 91	HYPOTHETICAL 17.3 KDA PROTEIN IN MRDA-PHPB INTERGENIC REGION	ARGININE KINASE (AK)	WD-40 REPEAT PROTEIN MSI3	60S RIBOSOMAL PROTEIN L4 (L2)	DNA MISMATCH REPAIR PROTEIN MUTS	SKT5 PROTEIN	za07c11.r1 Scares melanocyte 2NbHM Homo sapiens cDNA clone IMAGE:291860 5'	za07c11.r1 Soares melanocyte ZNbHM Homo sapiens cDNA clone IMAGE:291860 51	OUTER CAPSID PROTEIN VP4 (HEMAGGLUTININ) (OUTER LAYER PROTEIN VP4) [CONTAINS:	OUTER CAPSID PROTEINS VP5 AND VP8]	HYPOTHETICAL 157.0 KDA PROTEIN C38C10.5 IN CHROMOSOME III	CATECHOL-O-METHYLTRANSFERASE, SOLUBLE FORM (S-COMT)	602152573F1 NIH_MGC_81 Homo sepiens cDNA clone IMAGE:4293427 5'	AF-4 PROTEIN (FEL PROTEIN)	URIDYLATE KINASE (UK) (URIDINE MONOPHOSPHATE KINASE) (UMP KINASE)	URIDYLATE KINASE (UK) (URIDINE MONOPHOSPHATE KINASE) (UMP KINASE)	ym60f06.s1 Soares infant brain 1NIB Homo sapiens cDNA done IWAGE:52737 3'	PROBABLE CATION-TRANSPORTING ATPASE C6C3.05C	ENV POLYPROTEIN [CONTAINS: COAT PROTEIN GPS2; COAT PROTEIN GP36]	601678435F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3960969 5'	Schizophylum commune unknown mRNA	Mus musculus mannosidase 2, alpha B1 (Man2b1), mRNA	601468031F1 NIH_MGC_67 Homo saplens cDNA clone IMAGE:3871303 5	Pyrococcus horikoshii OT3 genamie DNA, 1168001-1485000 nt. position (6/7)	Deinococcus radiodurans R1 section 1 of 2 of the complete chromosome 2	Dehococcus radiodurans R1 section 1 of 2 of the complete chromosome 2	Mus musculus mixed lineage kinase 3 (MIk3) and two pore domain K+ channel subunit (Kcnk6) genes, complete cds	
Top Hit Database Source	E		EST_HUMAN	SWISSPROT	SWISSPROT	TN	SWISSPROT	SWISSPROT	SWISSPROT	SWISSPROT	SWISSPROT	SWISSPROT	EST HUMAN	EST HUMAN		SWISSPROT	SWISSPROT	SWISSPROT	EST_HUMAN	SWISSPROT	SWISSPROT	SWISSPROT	EST_HUMAN	SWISSPROT	SWISSPROT	EST_HUMAN	٦	N.	EST_HUMAN	뉟	뉟	IN	Ņ	
Top Hit Acessian No.	L12051.1	12051.1	7.2E+00 BE179090.1	P28166	P28166	7.1E+00 AL161595.2	P05850	P48610	022469	P35679	P44834	P34226	6.8E+00 W03412.1	6.8E+00 W03412.1		P3630 <b>7</b>	203570	Q99028	6.6E+00 BF672121.1	P51825	G9ZE07	Q9ZE07	H29330.1	Q10309	P03374	6.5E+00 BE866001.1	6.2E+00 AY010901.1	6754621 NT	6.0E+00 BE780163.1	6.0E+00 AP000006.1	6.0E+00 AE001862.1	6.0E+00 AE001862.1	5.9E+00 AF155142.1	
Most Similar (Top) Hit BLAST E Value	7.2E+00 L12051.1	7.2E+00 L12051.1	7.2E+00	7.1E+00 P28166	7.1E+00 P28166	7.1E+00	7.1E+00 P05850	7.0E+00 P48610	7.0E+00 O22469	6.9E+00 P35679	6.9E+00 P44834	6.9E+00 P34226	6.8E+00	6.8E+00		6.8E+00 P36307	6.8E+00 Q03570	6.6E+00 Q99028	6.6E+00	6.6E+00 P51825	6.6E+00 Q9ZE07	6.6E+00 Q9ZE07	6.6E+00 H29330.1	6.6E+00 Q10309	6.5E+00 P03374	6.5E+00	6.2E+00	6.2E+00	6.0E+00	6.0E+00	6.0E+00	6.0E+00	5.9E+00	
Expression Signal	3.41	3.41	1.07	1.22	1.22	9.23	2.44	2.76	1.52	3.17	1.12	9.0	1.64	1.64		1.62	3.6	0.65	0.86	0.55	2.14	2:14	0.47	1.48	7	0.52	1.34	7.0	1.6	0.49	0.82	0.82	7.14	
ORF SEQ ID NO:			33750	33838	33839		38437		38261		37200	37219	34688	34689			37053		33223	<u> </u>	36912		37496		36020	37158	36574			36655	37373	37374	33197	l
Exon SEQ ID NO:	16218	16218	20307	20381	20381	22838	24745	23224	24584	21559	23594	<u> </u>	21174	21174		22409	23448		19834	26226	23314			24454	22457	23547	22982	23820	20313	23059	23765	23765	19809	l
Probe SEQ ID NO:	3042	3042	7174	7299	7299	9626	11668	10187	11528	8478	10559	10579	8092	8092	[•	5333	10413	5398	6675	9234	10279	10279	10843	11393	9382	10512	9943	10787	7181	10021	10732	10732	0999	

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																	(PP1)																	$\top$	
Strigte Extri Fronce Expressed in Fracetta	Top Hit Descriptor	601645279F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:3930451 5'	Homo sapiens DESC1 protein (DESC1), mRNA	Mus musculus immunoglobulin scavenger receptor IgSR mRNA, complete cds	Mus musculus immunoglobulin scavenger receptor IgSR mRNA, complete cds	DNA POLYMERASE III, ALPHA CHAIN POLC-TYPE (POLIII)	Cyprinus carpto mRNA for lysozyme C, complete cds	Opprinus carpio mRNA for lysozyme C, complete cds	LYCOPENE BETA CYCLASE	HEAT-INDUCIBLE TRANSCRIPTION REPRESSOR HRCA	EXTENSIN PRECURSOR (CELL WALL HYDROXYPROLINE-RICH GLYCOPROTEIN)	Mus musculus DNA methyltransferase (Dnmt1) gene, exons 30, 31, and 32	PNEUMOLYSIN (THIOL-ACTIVATED CYTOLYSIN)	Chicken alpha-cardiac actin gene	Chicken alpha-cardiac actin gene	NEL PROTEIN PRECURSOR (NEL-RELATED PROTEIN 2)	NEUROPEPTIDE Y RECEPTOR TYPE 4 (NPY4-R) (PANCREATIC POLYPEPTIDE RECEPTOR 1) (PP1)	VITELLOGENIN PRECURSOR (VTG) [CONTAINS: LIPOVITELLIN LV-1N; LIPOVITELLIN LV-1C;	LIPOVITELLIN LV-2]	REP1 PROTEIN	REP1 PROTEIN	RHODOPSIN	RHODOPSIN	Bovine Immunodeficiency-like virus surface envelope gene, 5' end of cds	HOMEOBOX PROTEIN CEH-20	DNA POLYMERASE GAMMA (MITOCHONDRIAL DNA POLYMERASE CATALYTIC SUBUNIT)	Homo sapiens HERPUD1 gene for stress protein Herp, complete cds	PROBABLE ANTIBACTERIAL PEPTIDE POLYPROTEIN PRECURSOR	QV4-HT0691-270400-186-f09 HT0691 Homo sapiens cDNA.	Droscohila orientacea R1B retrotransposable element reverse transcriptase gene, partial cds	HYPOTHETICAL 61.1 KD PROTEIN C23E2.03C IN CHROMOSOME I	RHODOPSIN	COLICIN N IMMUNITY PROTEIN (MICROCIN N IMMUNITY PROTEIN)	601894910F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:41241145	601890420F1 NIH_MGC_17 Homo sepiens cDNA clone IMAGE:4131509 5
	Top Hit Database Source	EST HUMAN	된	뒫	M	SWISSPROT	NT	N	SWISSPROT	SWISSPROT	SWISSPROT	NT.	SWISSPROT	NT	뉟	SWISSPROT	SWISSPROT		SWISSPROT	SWISSPROT	SWISSPROT	SWISSPROT	SWISSPROT	NT	SWISSPROT	SWISSPROT	TN	SWISSPROT	EST_HUMAN	N	SWISSPROT	SWISSPROT	SWISSPROT	EST_HUMAN	EST_HUMAN
lgiilo.	Top Hit Acession No.	5.9E+00 BE958630.1	7661557 NT	5.7E+00 AF302046.1	5.7E+00 AF302046.1	P75080	5.6E+00 AB027305.1	5.6E+00 AB027305.1			P13983	5.5E+00 AF175425.1	P11990	X02212.1	X02212.1	Q99435	P50391		Q91062	P40379	P40379	Q17094 .	Q17094	L43126.1	P41779	P54098	5.3E+00 AB034990.1	Q27905	5.2E+00 BE184840.1	5.2E+00 AF248070.1	Q10136	016005	P09182	5.0E+00 BF310443.1	5.0E+00 BF308561.1
	Most Similar (Top) Hit BLAST E Value	5.9E+00	5.8E+00	5.7E+00	5.7E+00	5.6E+00 P75080	5.6E+00	5.6E+00	5.6E+00 Q55278	5.5E+00 P47447	5.5E+00 P13983	5.5E+00	5.5E+00 P11990	5.4E+00 X02212.1	5.4E+00 X02212.1	5.4E+00 Q39435	5,4E+00 P50391		5.4E+00 Q91062	5.4E+00 P40379	5.4E+00 P40379	5.4E+00 Q17094	5.4E+00 Q17094	5.3E+00 L43126.1	5.3E+00 P41779	5.3E+00 P54098	5.3E+00	5.3E+00\Q27905	5.2E+00	5.2E+00	6.2E+00 Q10136	5.1E+00 O16005	5.1E+00 P09182	5.0E+00	5.0E+00
-	Expression Signal	3.02	1,15	0.74	0.74	1.34	2.03	2.03	2.52	0.74	0.56	1.46	2.32	1.11	1.11	1.04	0.74		1.62	0.93	0.93	1,45	1.45	1.47	0.7	3.39	0.72	1.51	1.16	96.0	1.93	96.0	1.33	0.74	0.7
	ORF SEQ ID NO:			33865	33856		37996	26628		32906			87578				34575			35618	35619	36870	36871	31024				38616				35784	36667	32946	
	Exon SEQ ID NO:	24919	16777	20394	20394	20803	24355	24355	23951	19550	23021	24097	23949	·	20122	20559	21063		21137	22078	22078	23277	23277	18036	1.	21352	22262	24914	18775	23618	24529	22240	23068	)	23432
	Probe SEQ ID NO:	11933	3613	7312	7312	7742	11289	11289	11765	6381	8982	11018	11763	7069	2069	7484	8013		8054	6668	8999	10242	10242	4906	6617	8270	9184	11928	5580	10583	11470	9162	10030	6415	10397

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Top Hit Descriptor	Canis familiaris skeletal muscle chloride channel CIC-1 (CLCN1) mRNA, complete cds	Mycobacterium tuberculosis H37Rv complete genome; segment 103/162	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (Histana Danas and explirms phenchete transporter (NDT3) and complete de-	(11-4-1) gale, nover gene, and south prospine naispone (n. 10) gane, comprete cas	Eunice australis historie H3 (H3) gene, partial cds	KCS-GNOO42-100500-011-610 GN0042 HOMO SEPRETS CLOVA IDAM-BT0547-310100-002-004 BT0547 Homo seprems CDNA	GARATERSET NIE MGC 55 Home content of the characters of the charac	6018756684F1 NIH MGC 55 Hamo saplens cDNA clone IMAGE:4099716 5'	Homo sapiens chromosome 21 cegment HS21C080	Methanococcus jannaschii section 111 of 150 of the complete genome	7e88g10.x1 NCI_CGAP_CLL1 Homo sapiens cDNA clone IMAGE:3292098 3' strullar to TR:075140 075140 KIAA0645 PROTEIN.; contains element PTRS repetitive element;	7e88g10.x1 NCI_CGAP_CLL1 Homo sepiens cDNA clone IMAGE:3292098 3' similar to TR:075140 075140 KIAA0645 PROTEIN. ;contains element PTRS repetitive element;	Homo sepiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds	Issatchenkia orientalis inositolphosphorylceramide synthase (IPC1) gene, complete cds	Archaeoglobus fulgidus section 63 of 172 of the complete genome	602123238F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4280216 5'	602072585F1 NCI_CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4215284 5	602072585F1 NCI_CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4215284 5'	Murine I gene for MHC class II(Ia) associated invariant chain	Homo capiens neutrophil collagenase (CLGNA) gene, promoter region and 5"UTR	Plasmodium faiciparum R29R+var1 gene, exon 1	Treponema pallidum section 38 of 87 of the complete genome	Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1)	MICROSOMAL TIPEDTIDASE PRECI IRSOR (MIDP) (DEHYDROPEPTIDASE-I) (RENAL DIPEPTIDASE)	(RDP)	LAF-4 PROTEIN (LYMPHOID NUCLEAR PROTEIN)	PUTATIVE ATP-DEPENDENT HELICASE MTH1802	EXTENSIN PRECURSOR (CELL WALL HYDROXYPROLINE-RICH GLYCOPROTEIN)
Top Hit Database Source	Z.	NT		2	⊢Z I	EST HUMAN	EST DI MANI	EST HUMAN	L'N	Z	EST_HUMAN	EST_HUMAN	Į,	F	Z	EST HUMAN	EST_HUMAN	EST_HUMAN	NT	TN	TN	NT	Ę	2	SWISSPROT	SWISSPROT	SWISSPROT	SWISSPROT
Top Hit Acession. No.	5.0E+00 AF162445.2	5.0E+00 Z83860.1		.9E+00 091326.1	1.8E+00 AF185255.1	4.8E+00 BF36/909.1	7E+00 BE940EE9 4	4.7E+00 BF240552.1	4.7E+00 AL163280.2	1.6E+00 U67569.1	.6E+00 BE646437.1	.6E+00 BE646437.1	1.6E+00 AF240786.1	1.5E+00 AF126177.1	4.5E+00 AE001044.1	.5E+00 BF668841.1	1.4E+00 BF530893.1	1.4E+00 BF530893.1	.4E+00 X13414.1	4.3E+00 AF059679.1	4.3E+00 Y13402.1	.3E+00 AE0012221	25.00 AC240706.4	AL 240700.1.	P16444	P51826	027830	P13983
Most Similar (Top) Hit BLAST E Value	5.0E+00	5.0E+00	o i	4.95+00	4.8E+00	4.8E+00	75.00	4.7E+00	4.7E+00	4.6E+00	4.6E+00	4.6E+00	4.6E+00	4.5E+00	4.5E+00	4.5E+00	4.4E+00	4.4E+00	4.4E+00	4.3E+00	4.3E+00	4.3E+00	`	1	4.2E+00 P16444	4.2E+00 P51826	4.2E+00 O27830	4.2E+00 P13983
Expression Signal	289	7.24	. G	0.76	12.39	0.6	100	1.85	1.02	0.59	1.1	1.7	0.63	0.7	1.87	1.53	0.84	0.84	1.58	22.0	2.53	89:0	77.77	14.74	4.1	1.07	0.71	1.67
ORF SEQ ID NO:	37289					34953	03380	28550		L		38037			38593	38747		29297			34142	34341		1	-	32199		33657
Exen SEQ ID NO:	23679					21429	Т		L		<u>i</u>	<u> </u>	23635	20997		٠.			19502	19419	20686			7/177	18828	18904		20228
Probe SEQ ID NO:	10645	11569	7	10437	4172	8348	0000	30.	3347	7962	9397	9397	10600	7947	11904	12058	3105	3105	6331	6245	7596	7792	,		5634	5711	5880	6911

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Only E LAUL FLODES LAPIESSED III Flagelia	Top Hit Database Source	Ι.											THUMAN   602247838F1 NIH_MGC_62 Hano sapiens cDNA clone IMAGE:4335209 5		CYCLIN-DEPENDENT KINASE INHIBITOR 18 (CYCLIN-DEPENDENT KINASE INHIBITOR P27)											VISSPROT NITRIC-OXIDE SYNTHASE (NOS, TYPE I) (NEURONAL NOS) (N-NOS) (NNOS)		Ureaplasma urealyticum section 33 of 59 of the complete genome	VISSPROT (URICASE (URATE OXIDASE)	VISSPROT   URICASE (URATE OXIDASE)	VISSPROT CYTOCHROME C OXIDASE POLYPEPTIDE III	NITA A CAMPANA (NITATA A PARAMANA PARAMANA PARAMANA PARAMANA A PARAMANA PARAMANA PARAMANA PARAMANA PARAMANA PARAMANA PARA
Aproposa III I Isoonisa		EXTENSIN PRECURSOR (CELL WALL HY	wf67g03.x1 Soares_NFL_T_GBC_S1 Homo:	<b>NUBBIN PROTEIN (TWAIN PROTEIN) (PO</b>	HEXOSE TRANSPORTER HXT8	301110727F1 NIH_MGC_16 Homo sapiens o	771 PROTEIN PRECURSOR	Patinopecten yessoensis mRNA for calcineuri	GENE 68 PROTEIN	SENE 68 PROTEIN	an troglodytes novel repetitive solo LTR elem	50S RIBOSOMAL PROTEIN L4	302247938F1 NIH_MGC_62 Homo sapiens o	Rickettsia prowazekii strain Madrid E, complet	SYCLIN-DEPENDENT KINASE INHIBITOR	P27KIP1)	HYPOTHETICAL PROTEIN HVLF1	301507510F1 NIH_MGC_71 Hamo sapiens c	3LC7-INTERACTING PROTEIN 1	SUCRASE-ISOMALTASE, INTESTINAL [CC	SUCRASE-ISOMALTASE, INTESTINAL [CC	SUCRASE-ISOMALTASE, INTESTINAL [OC	SUCRASE-ISOMALTASE, INTESTINAL [CC	<b>JELL DIVISION PROTEIN FTSY HOMOLO</b> (	HYPOTHETICAL PROTEIN KIAA0144	NITRIC-OXIDE SYNTHASE (NOS, TYPE I)	VITRIC-OXIDE SYNTHASE (NOS, TYPE I)	Jreaplasma urealyticum section 33 of 59 of th	JRICASE (URATE OXIDASE)	JRICASE (URATE OXIDASE)	SYTOCHROME COXIDASE POLYPEPTIDI	SENOME POLYPROTEIN (CONTAINS: CA
2000	Top Hit Database Source	SWISSPROT	EST_HUMAN M		SWISSPROT H	EST_HUMAN 6	SWISSPROT Y	_		ISSPROT		SWISSPROT 5	EST_HUMAN 6	LN TN			SWISSPROT	•	SWISSPROT		SWISSPROT	SWISSPROT	SWISSPROT S	SWISSPROT	SWISSPROT	Ι.	SWISSPROT	F	SWISSPROT	Ι.		
a Build	Top Hit Acesslon No.					4.1E+00 BE253668.1		23.1					4.1E+00 BF692425.1	4.1E+00 AJ235273.1				80.1										4.0E+00 AE002132.1				
	Most Similar (Top) Hit BLAST E Value	4.2E+00 P13983	4.2E+00 AI809013.1	4.2E+00 P31368	4.2E+00 P40886	4.1E+00 E	4.1E+00 O23810	4.1E+00	4.1E+00 P28964	4.1E+00 P28964	4.1E+00 U57503.1	4.1E+00 P11253	4.1E+00	4.1E+00/		4.1E+00 P46414	4.1E+00 P09716	4.1E+00	4.0E+00 P38229	4.0E+00 O62653	4.0E+00 O62653	4.0E+00 O62653	4.0E+00 O62653	4.0E+00 033010	4.0E+00 Q14157	4.0E+00 O61309	4.0E+00	4.0E+00 /	4.0E+00 Q00511	4.0E+00 Q00511	4.0E+00 P14546	
	Expression Signal	1.67	5.3	1.03	0.47	86.0	7.66	0.64	3.8	3.8	2.88	0.61	2.25	0.55		0.52	2.15	12.25	0.72	0.93	0.93	66'0	0.99		0.49	0.65	0.65	9.0	0.45	0.45	1.59	
	ORF SEQ ID NO:	33658	35783	36759		33796	34396		34523	34524	34703	36381	36498	l					-	33546	33547	33546	33547	33881	35697	36783	36783	37014	37111			
	SEQ ID NO:	20226	22238	23160	23387	20344		21010		21013	21183	22805	L	23405		23549	24196	24283	16799	20130	20130	20130	20130	20419	22153		23186	23403	L	L	L	
	Probe SEQ ID NO:	<u>8</u>	9160	10122	10352	7261	7839	7960	7983	7963	8101	9740	9873	10370		10514	11124	11214	3635	5275	5225	7077	7707	7339	9074	10148	10148	10368	10464	10464	11762	

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No.   ID NO: Signal   BLASTE   No.   Source	Probe SEO ID	Econ SEO ID	ORF SEQ	Expression	Most Similar (Top) Hit	Top Hit Acession	Top Hit	Top Hit Descriptor
24832         39625         2.98         4.0E+00         P07564         SWISSPROT           16765         29770         6         3.9E+00         P365611         SWISSPROT           16765         29770         6         3.9E+00         P36511         NT           17581         0.87         3.9E+00         AF055468.1         NT           18967         3.2271         2.92         3.9E+00         BE814357.1         EST_HUMAN           18967         3.2271         2.92         3.9E+00         BE814357.1         EST_HUMAN           19627         33322         0.87         3.9E+00         BE814357.1         EST_HUMAN           20449         33570         4.43         3.9E+00         B73280.1         NT           20527         3.2E+00         B73280.1         NT         NT           21583         3.5128         2.44         3.9E+00         B73280.1         NT           21583         3.3E+00         B73280.1         NT         NT           21681         3.3E+00         B74726.1         B71HUMAN           23027         1.05         3.8E+00         B74726.1         B71HUMAN           23037         1.05         3.8E+00			ID NO:	Signal	BLASTE · Value	OO.	Source	
25113         38817         1.34         4.0E+00         P35611         SWISSPROT           16755         29770         6         3.9E+00         K64518.1         NT           17581         0.87         3.9E+00         MF055468.1         NT           18967         32270         2.92         3.9E+00         BE814357.1         EST_HUMAN           18967         32271         2.92         3.9E+00         BE814357.1         EST_HUMAN           19968         33322         0.83         3.9E+00         BE814357.1         EST_HUMAN           20149         33570         4.43         3.9E+00         BE814357.1         EST_HUMAN           20522         3.9E+00         BE814357.1         EST_HUMAN           21503         3.9E+00         MF03907.1         NT           20149         33570         4.43         3.9E+00         MF03907.1         NT           21908         3.7E4         2.77         3.9E+00         ME017562.1         NT           21908         3.7E4         3.9E+00         ME017562.1         NT           21007         3.7E4         3.9E+00         ME017562.1         NT           2107         3.9E+00         ME0017562.1	- ~	24B32			4.0E+00		SWISSPROT	GENOME POLYPROTEIN [CONTAINS: CAPSID PROTEIN C (CORE PROTEIN); MATRIX PROTEIN (ENVELOPE GLYCOPROTEIN M); MAJOR ENVELOPE PROTEIN E; NONSTRUCTURAL PROTEINS NS1, NS2A, NS2B, NS4A AND NS4B; HELICASE (NS3); RNA-DIRECTED RNA POLYMERASE (NS5)]
16755         29770         6         3.9E+00         X64518.1         NT           17861         0.87         3.9E+00         AF055468.1         NT           18967         32270         2.92         3.9E+00         BE814357.1         EST_HUMAN           18967         32271         2.92         3.9E+00         BE814357.1         EST_HUMAN           199687         33322         0.83         3.9E+00         BE814357.1         EST_HUMAN           20149         33570         4.43         3.9E+00         BE814357.1         NT           20149         33570         4.43         3.9E+00         P39299         SWISSPROT           20149         33570         4.43         3.9E+00         M23907.1         NT           21503         35128         2.44         3.9E+00         M23907.1         NT           21503         33057         1.05         3.8E+00         M23907.1         NT           21707         35244         3.9E+00         M27829.5         SWISSPROT           21707         35244         1.12         3.8E+00         M27829.1         NT           23057         1.05         3.8E+00         M47250.1         NT	m	25113	L		ľ		SWISSPROT	ERYTHROCYTE ADDUCIN ALPHA SUBUNIT
17881         0.87         3.9E+00         AF055466.1         NT           18967         3.2270         2.92         3.9E+00         BE814357.1         EST_HUMAN           18967         3.2271         2.92         3.9E+00         BE814357.1         EST_HUMAN           19627         33322         0.93         3.9E+00         BE814357.1         EST_HUMAN           19682         33329         0.7         3.9E+00         BE814357.1         EST_HUMAN           20149         33570         4.43         3.9E+00         PR32299         SWISSPROT           20562         34086         4.26         3.9E+00         M23907.1         NT           21503         37524         2.77         3.9E+00         M23907.1         NT           23057         1.05         3.9E+00         M23907.1         NT           21707         35244         1.12         3.8E+00         M27829         SWISSPROT           21707         35244         1.12         3.8E+00         M27826         NT           21707         35244         1.12         3.8E+00         M472505.1         NT           21707         35244         1.65         3.8E+00         M47250.1         NT <td><del>1-</del></td> <td>16755</td> <td></td> <td>9</td> <td>ľ</td> <td></td> <td>F</td> <td>N tabacum chitinase gene 50 for class I chitinase C</td>	<del>1-</del>	16755		9	ľ		F	N tabacum chitinase gene 50 for class I chitinase C
18967         32270         2.92         3.9E+00         BE814357.1         EST_HUMAN           18967         32271         2.92         3.9E+00         BE814357.1         EST_HUMAN           19682         33322         0.93         3.9E+00         AF298209.1         NT           20149         33570         4.43         3.9E+00         P91328.1         NT           20562         34066         4.26         3.9E+00         M23907.1         NT           21983         35128         2.44         3.9E+00         M23907.1         NT           21983         35128         2.44         3.9E+00         M23907.1         NT           21902         3754         2.77         3.9E+00         M23907.1         NT           2107         3524         1.05         3.9E+00         M23907.1         NT           2107         3524         1.12         3.9E+00         M27250         SWISSPROT           2107         3524         1.12         3.8E+00         M27250         NT           2107         3.0E+00         M27266.1         NT         SWISSPROT           2107         1.165         3.8E+00         M24726.1         NT	t=	17581		0.87	3.9E+00			Mus musculus seminal vesicle secretory protein 99 (MSVSP99) gene, promoter region
18967         32271         2.92         3.9E+00         BE814357.1         EST_HUMAN           19682         33322         0.83         3.9E+00         AF288209.1         NT           20149         33570         4.43         3.9E+00         D91328.1         NT           20149         33570         4.43         3.9E+00         M23907.1         NT           21593         35128         2.44         3.9E+00         M23907.1         NT           21593         35128         2.44         3.9E+00         M23907.1         NT           1583         3.9E+00         M23907.1         NT         NT           21502         3.7E+0         AF400         M23907.1         NT           1583         3.9E+0         M23907.1         NT         NT           23027         1.05         3.8E+0         M24725.1         NT           23037         1.12         3.8E+0         M4725.1         NT           24754         1.16         3.8E+0         M4725.1         NT           25100         1.16         3.8E+0         M4725.1         NT           25100         1.16         3.8E+0         M4725.1         NT	100	18967	32270					MR0-BN0070-300500-028-h05 BN0070 Homo sapiens cDNA
19982         33322         0.83         3.9E+00         AF288209.1         NT           19982         33389         0.7         3.9E+00         U91328.1         NT           20149         33570         4.43         3.9E+00         M23807.1         NT           20149         33570         4.26         3.9E+00         M23807.1         NT           21583         35128         2.44         3.9E+00         M23807.1         NT           23902         37524         2.77         3.9E+00         M23807.1         NT           15843         33057         1.05         3.8E+00         M2725.1         NT           21707         35244         1.12         3.8E+00         M2725.1         EST_HUMAN           22403         30377         1.165         3.8E+00         M2725.1         EST_HUMAN           22454         3.16+00         A145066.1         NT           22454         3.16+00         A145066.1         NT           22454         3.16+00         A1445066.1         NT           24755         38450         2.11         3.7E+00         A145066.1         NT           24756         38451         1.04         3.7E+00	īΩ	ı	32271	2.92	ိ			MR0-BN0070-300500-028-h05 BN0070 Homo sapiens cDNA
1998Z         33389         0.7         3.9E+00         D91328.1         NT           20149         33570         4.43         3.9E+00         P39299         SWISSPROT           2056Z         34068         4.26         3.9E+00         M23907.1         NT           21563         3512B         2.44         3.9E+00         K58665.1         NT           2390Z         37524         2.77         3.9E+00         K58665.1         NT           16813         3.8E+00         K58665.1         NT         NT           21707         35244         1.12         3.8E+00         Q57830         SWISSPROT           21707         35244         1.12         3.8E+00         Q57830         SWISSPROT           23037         0.6         3.8E+00         Q57830         SWISSPROT           23037         1.166         3.8E+00         Q4726.1         EST_HUMAN           24765         38450         1.78         3.7E+00         Q42656.1         NT           24756         38450         2.11         3.7E+00         Q42650.2         NT           24756         38451         2.11         3.7E+00         Q4569279.1         EST_HUMAN           24756<	12				3.9E+00		TN	Dictyostelium discoldeum non-LTR retrotransposon TRE5-B, polyprotein (gag) and group-specific antigen (pol) genes, complete cds
20149         33570         4,43         3.9E+00         P39289         SWISSPROT           20562         34066         4.26         3.9E+00         MZ3907.1         NT           21593         35128         2.44         3.9E+00         MZ3907.1         NT           15813         3.7524         2.77         3.9E+00         AE001562.1         NT           19685         33057         1.05         3.8E+00         AE001562.1         NT           21707         35244         1.12         3.8E+00         AG04756.1         NT           23037         1.05         3.8E+00         A47256.1         BT-MMAN           25100         11.65         3.8E+00         A47259.4         NT           20396         1.165         3.8E+00         AL481539.2         NT           20396         0.83         3.7E+00         AL45065.1         NT           24756         38450         2.11         3.7E+00         AL45065.1         NT           24756         38451         2.11         3.7E+00         BAS9379.1         EST_HUMAN           24756         38451         2.11         3.7E+00         BAS9379.1         EST_HUMAN           21828	- Ω	19982					L Z	H <sup>i</sup> rman hereditary haemochtomatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RoRet gene, and sodium phosphate transporter (NPT3) gene, complete cds
20562         34086         4.26         3.9E+00         M23907.1         NT           21563         35128         2.44         3.9E+00         X65865.1         NT           23902         37524         2.77         3.9E+00         X65865.1         NT           16813         3.8E+00         AE001562.1         NT         NT           21707         3524         1.05         3.8E+00         G57830         SWISSPROT           23037         1.05         3.8E+00         G47250.1         NT           25100         11.65         3.8E+00         A1390561.1         NT           20398         30277         12.79         3.7E+00         AL1491639.2         NT           20399         0.83         3.7E+00         AL45065.1         NT           24754         3.0017         1.04         3.7E+00         AL45065.1         NT           24755         38450         2.11         3.7E+00         BF689279.1         EST_HUMAN           24756         38451         2.11         3.7E+00         BA13448.3         NT           13765         26814         3.7E+00         BA20474.3         EST_HUMAN           21828         35364         0.86<	60	20149	Ĺ		3.9E+00		SWISSPROT	HYPOTHETICAL TRANSCRIPTIONAL REGULATOR IN AIDB-RPSF INTERGENIC REGION
21563         35128         2.44         3.9E+00         K65865.1         NT           23902         37524         2.77         3.9E+00         PK18000.1         NT           16813         3.3E+00         GAR01562.1         NT         NT           19685         33057         1.05         3.8E+00         GA7230.         NI           23037         0.6         3.8E+00         GA7250.1         NT           25100         11.65         3.8E+00         A47256.1         NT           25100         11.65         3.8E+00         A47256.1         NT           20398         3.0277         12.79         3.7E+00         AL181539.2         NT           20398         3.0277         12.79         3.7E+00         AL181539.2         NT           22454         3.0017         1.04         3.7E+00         AL181539.2         NT           24755         38450         2.11         3.7E+00         BE69279.1         EST HUMAN           24756         38451         2.11         3.7E+00         BA13448.3         RST HUMAN           18572         31440         0.78         3.6E+00         BA70410531.1         EST HUMAN           21828 <td< td=""><td>6</td><td>20592</td><td>34066</td><td></td><td></td><td></td><td>LN</td><td>Human MHC class II lymphocyte antigen (DPw4-beta-1) ger.e, exon 2</td></td<>	6	20592	34066				LN	Human MHC class II lymphocyte antigen (DPw4-beta-1) ger.e, exon 2
23902         37524         2.77         3.9E+00         V18000.1         NT           16813         1.63         3.8E+00         AE001562.1         NT           19685         33057         1.05         3.8E+00         D4725.1         EST_HUMAN           23037         0.6         3.8E+00         AJ30961.         NT           25100         11.65         3.8E+00         AJ30961.         NT           25100         11.65         3.8E+00         AJ30961.         NT           25100         11.65         3.8E+00         AL45065.1         NT           20369         30277         12.79         3.7E+00         AL415065.1         NT           22454         36017         1.04         3.7E+00         AL445065.1         NT           24755         38450         2.11         3.7E+00         BF695279.1         EST_HUMAN           24756         38451         1.04         3.7E+00         BF695279.1         EST_HUMAN           18572         31440         0.78         3.6E+00         BF31448.3         RT           18572         31440         0.78         3.6E+00         BF31449.1         EST_HUMAN           21828         35364	N	L			3.9E+00		LN	X. laevis mRNA for M4 muscarinic receptor
15813         1.63         3.8E+00         AE001502.1         NT           19625         33057         1.05         3.8E+00         D54725.1         EST_HUMAN           21707         36244         1.12         3.8E+00         D94725.1         EST_HUMAN           23037         0.6         3.8E+00         A136966.1         NT           22100         11.66         3.8E+00         A136966.1         NT           22454         30277         12.78         3.7E+00         AL445066.1         NT           22454         38450         2.11         3.7E+00         BF689278.1         EST_HUMAN           24756         38451         2.11         3.7E+00         BF689278.1         EST_HUMAN           25196         1.37         3.7E+00         AB013746.3         NT           1867         2.11         3.7E+00         AB013746.3         EST_HUMAN           1872         3.6E+00         BF386371.1         EST_HUMAN           21828         35364         0.86         3.6E+00         BF386136.1         EST_HUMAN           21828         35365         0.86         3.6E+00         BF3867.1         EST_HUMAN           21828         35366         0.86	4	i_			3.9E+00		LN	Homo saplens NF2 gene
19685         33057         1.05         3.8E+00         G57830         SWISSPROT           21707         35244         1.12         3.8E+00         D44725.1         EST_HUMAN           23037         0.6         3.8E+00         P631294         NT           17282         30277         12.79         3.7E+00         AL161539.2         NT           20368         30277         12.79         3.7E+00         AL45065.1         NT           24756         38450         2.11         3.7E+00         BF69279.1         EST_HUMAN           24756         38451         3.7E+00         BF69279.1         EST_HUMAN           13795         22814         3.7E+00         BAD033746.3         NT           13786         3.6E+00         BF316316.1         EST_HUMAN           21828         35364         0.86         3.6E+00         BF31637.1         EST_HUMAN           21828<	0			1.53	3.8E+00		LNT	Helicobacter pylori, strain J99 section 123 of 132 of the complete genome
21707         35244         1.12         3.8E+00         D44725.1         EST_HUMAN           23037         0.6         3.8E+00         AJ390961.1         NT           25100         11.65         3.8E+00         9631294         NT           17282         30277         12.79         3.7E+00         AL45065.1         NT           20368         3.7E+00         L445065.1         NT         NT           22454         38450         2.11         3.7E+00         L43541.1         NT           24755         38450         2.11         3.7E+00         BF695279.1         EST_HUMAN           24756         38450         2.11         3.7E+00         BF695279.1         EST_HUMAN           24756         28914         3.7E+00         BF695279.1         EST_HUMAN           13795         22814         3.7E+00         BF316316.3         EST_HUMAN           18572         31440         0.78         3.6E+00         BY761055.1         EST_HUMAN           21828         35364         0.86         3.6E+00         D12367.1         EST_HUMAN           21828         35464         3.6F+00         D12367.1         EST_HUMAN           21926         35640	0	1		1.05			SWISSPROT	HYPOTHETICAL PROTEIN MJ0385
23037         0.6         3.8E+00         AJ390961.1         NT           25100         11.66         3.8E+00         9631294         NT           17282         30277         12.79         3.7E+00         AL450565.1         NT           20368         0.83         3.7E+00         AL450565.1         NT           22454         36017         1.04         3.7E+00         IA450565.1         NT           24755         38450         2.11         3.7E+00         BF69279.1         EST HUMAN           24755         38451         2.11         3.7E+00         BF69279.1         EST HUMAN           25196         1.87         3.7E+00         BF692779.1         EST HUMAN           13795         26814         3.7E+00         AR013746.3         NT           13796         26814         3.7E+00         AP061055.1         EST HUMAN           21828         35364         0.86         3.6E+00         D12367.1         EST HUMAN           21828         35365         0.86         3.6E+00         D12367.1         EST HUMAN           21926         35640         3.6E+00         D12367.1         EST HUMAN	$\overline{}$		L				EST_HUMAN	HUMSUPY135 Human brain cDNA Homo sapiens cDNA clone 148
25100         11.66         3.8E+00         9631294 NT           17282         30277         12.79         3.7E+00         AL761539.2         NT           20368         0.83         3.7E+00         AL45055.1         NT           22454         36017         1.04         3.7E+00         U43541.1         NT           24755         38450         2.11         3.7E+00         BF69279.1         EST_HUMAN           24755         38451         2.11         3.7E+00         BF69279.1         EST_HUMAN           25196         1.87         3.7E+00         BF69279.1         EST_HUMAN           13795         26814         3.7E+00         AM013746.3         NT           13795         26814         3.7E+00         AM013746.3         NT           18572         31440         0.78         3.6E+00         BF316316.1         EST_HUMAN           21828         35364         0.86         3.6E+00         D12367.1         EST_HUMAN           21828         35464         3.6E+00         D12367.1         EST_HUMAN           21926         35640         3.6E+00         D12367.1         EST_HUMAN	6	l_					NT	Streptococcus oralis partial xpt gene for xanthine phosphoribosyltransferase, strain NCTC7864
17282         30277         12.78         3.7E+00         AL161639.2         NT           20369         0.83         3.7E+00         AL445065.1         NT           22454         36017         1.04         3.7E+00         U43541.1         NT           24755         38450         2.11         3.7E+00         BF89279.1         EST_HUMAN           24756         38451         2.11         3.7E+00         BF69279.1         EST_HUMAN           13795         2649         1.87         3.7E+00         AB013746.3         NT           13795         26814         3.7E+00         AV761055.1         EST_HUMAN           18572         31440         0.78         3.6E+00         BY361055.1         EST_HUMAN           21828         35364         0.86         3.6E+00         D12367.1         EST_HUMAN           21828         35660         3.6E+00         D12367.1         EST_HUMAN           21828         35464         3.6F+00         D12367.1         EST_HUMAN	O.			11.65			TN	Melanoplus sanguinipes entomopoxvirus, complete genome
2039B         0.83         3.7E+00         AL445065.1         NT           22454         36017         1.04         3.7E+00         U43541,1         NT           24755         38450         2.11         3.7E+00         BF699278.1         EST_HUMAN           24756         38451         2.11         3.7E+00         BF699279.1         EST_HUMAN           13796         28814         3.7E+00         AB031446.3         NT           13796         3.6E+00         AV761055.1         EST_HUMAN           21828         35364         0.36         3.6E+00         BF346316.1         EST_HUMAN           21828         35365         0.86         3.6E+00         D12367.1         EST_HUMAN           21828         35464         3.6F+00         D12367.1         EST_HUMAN           21926         35464         3.6F+00         D12367.1         EST_HUMAN	g,	<u> </u>		12.79			۲	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 39
22454         36017         1.04         3.7E+00         U43541,1         NT           24755         38450         2.11         3.7E+00         BF696279.1         EST_HUMAN           24755         38451         2.11         3.7E+00         BF09279.1         EST_HUMAN           15795         2.0814         3.7E         3.E+00         AV761056.1         EST_HUMAN           18572         31440         0.78         3.6E+00         BF346316.1         EST_HUMAN           21828         35364         0.86         3.6E+00         D12367.1         EST_HUMAN           21828         35464         3.6E+00         D12367.1         EST_HUMAN           21926         35464         3.6F+00         D12367.1         EST_HUMAN	ø	l		0.83			LN	Thermoplasma acidophilum complete genome; segment 3/5
24756         38450         2.11         3.7E+00         BF695279.1         EST_HUMAN           24756         38451         2.11         3.7E+00         BF699279.1         EST_HUMAN           25156         1.87         3.7E+00         AB013746.3         EST_HUMAN           18572         31440         0.78         3.6E+00         BF316316.1         EST_HUMAN           21828         35364         0.86         3.6E+00         D12367.1         EST_HUMAN           21926         35464         3.6E+00         D12367.1         EST_HUMAN           21926         35464         3.6E+00         D12367.1         EST_HUMAN	Ð			·			NT	Mus musculus laminin beta 2 gene, exons 17-33, and complete cds
24755         38451         2.11         3.7E+00         BF699Z79.1         EST_HUMAN           25136         1.87         3.7E+00         AB013746.3         NT           13795         2.6814         3.76         3.6E+00         AV761055.1         EST_HUMAN           18572         31440         0.78         3.6E+00         BF316316.1         EST_HUMAN           21828         35364         0.86         3.6E+00         D12367.1         EST_HUMAN           21826         35365         0.86         3.6E+00         D12367.1         EST_HUMAN           21926         35464         3.67         3.6E+00         AE00447.1         NT	3				3.7E+00		EST_HUMAN	602120551F1 NIH_MGC_56 Homo saplens cDNA clone II/AGE:4277748 5'
26196         1.87         3.7E+00 AB013746.3         NT           13795         26814         3.76         3.6E+00 AV761055.1         EST_HUMAN           18572         31440         0.78         3.6E+00 BF316316.1         EST_HUMAN           21828         35364         0.86         3.6E+00 D12367.1         EST_HUMAN           21826         35365         0.86         3.6E+00 D12367.1         EST_HUMAN           21926         35464         3.67         3.6E+00 AE00447.1         NT	2	Ŀ	_		3.7E+00		EST_HUMAN	602120551F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4277748 5'
13796         28814         3.76         3.6E+00 AV761055.1         EST HUMAN           18572         31440         0.78         3.6E+00 BF316316.1         EST HUMAN           21828         35364         0.86         3.6E+00 D12367.1         EST HUMAN           21828         35365         0.86         3.6E+00 D12367.1         EST HUMAN           21926         35464         3.67         3.6E+00 AE004447.1         NT	Ö			1.87			LN	Gallus gallus mRNA for hypoxia-Inducible factor-1 alpha, complete cds
18572         31440         0.78         3.6E+00 BF316316.1         EST HUMAN           21828         35364         0.86         3.6E+00 D12367.1         EST HUMAN           21828         35365         0.86         3.6E+00 D12367.1         EST HUMAN           21926         35464         3.67         3.6E+00 AE004447.1         NT	Ø					·	<b>EST_HUMAN</b>	AV761055 MDS Homo capiens cDNA clone MDSBUE10 5'
21828         35364         0.86         3.6E+00 D12367.1         EST_HUMAN           21828         35365         0.86         3.6E+00 D12367.1         EST_HUMAN           21926         35464         3.67         3.6E+00 AE00447.1         NT	Q						EST_HUMAN	601901866F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4131016 5'
21828 35365 0.86 3.6E+00 D12367.1 EST_HUMAN 21926 35464 3.67 3.6E+00 AE00447.1 NT	Ø.	l I					EST_HUMAN	HUM000TB08 Liver Hep/G2 cell line, Homo sapiens cDNA done tb08
21926 35464 3.67 3.6E+00 AE004447.1 NT	ō	ΙĮ					EST_HUMAN	HUM000TB08 Liver HepG2 cell line. Homo saplens cDNA clone tb08
	17	_					LZ	Pseudomonas aeruginosa PA01, section 8 of 529 of the complete genome

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Single Exon Probes Expressed in Placenta	Acession Top Hit Top Hit Descriptor Top Hit Descriptor Source	NT Pseudomonas aeruginosa PA01, section 8 of 529 of the complete genome	NT Ciconia episcopus cytochrome b gene, mitochondrial gene encoding mitochondrial protein, partial cds	Olconia episcopus cytochrome b gene, mitochondrial gene encoding mitochondrial protein, partial ods	Escherichia coli glycerophosphale dehydrogenase (glpD) gene, partial cds; and the translation start site has been verified (glpC), and repressor protein (glpR) genes, omplete cds	18.1 NT Cryptosporidium felis heat shock protein 70 (HSP70) gene, partial cds	F	1 EST_HUMAN yg40:c08.r1 Soares infant brein 1NIB Homd septens cDNA clone IMAGE:34940 5'	SWISSPROT	2986004.s1 Stratagene HeLa cell s3 937216 Homo sapiens cDNA clone IMAGE:627055 3' similar to EST HUMAN contains Alu repetitive element, contains element, contains element, contains element.	HOL	NAMOR I SE	5.2. N. Arabudopsis traitara DNA critomosome 4, corrug iragment ino. 55. N.T. Bos burus mRNA for Par-binding protein 2, partial	ΙN	L		SWISSPROT DNA-DIRECTED RNA POLYMERASE II LARGEST SUBUNIT	Human atternatively spliced potassium channels ROM-K1, ROM-K2, ROM-K4, ROM-K5, and ROM-K6 (KCNJ1) gene, complete cds	LN.	-N	Γ	Γ	SWISSPROT PUTATIVE IRON ALCOHOL DEHYDROGENASE		LN	. TN	FN	
\[\sigma\]	Top Hit Acession No.	6E+00 AE004447.1	6E+00 U72775.1	6E+00 U72775.1	3.6E+00 M96795.1	3.5E+00 AF221538.1	L42898.1	R19745.1	P24557	6E+00 AA190998.1	1 00000	3.3E+UU AA 190995.1	3.5E+00[AL163523.2	AF254577.1	AL163278.2	P04052	P04052	4E+00 U65406.1	AJ229042.1	3.4E+00 AJ250567.1	AF013167.1	L77570.1	009669	209669	AF111168.2	3.3E+00 AP001511.1	3.3E+00 AP001511.1	2E+00 X96422.1
	Most Similar (Top) Hit BLAST E Value	3.6E+00	3.6E+00	3.6E+00	3.6E+00	3.5E+00	3.5E+00 L42898.1	3.5E+00	3.5E+00 P24557	3.6E+00	L	3.35+00	3.5F+00	3.4E+00	3.4E+00	3.4E+00	3.4E+00	3.4E+00	3.4E+00	3.4E+00	3.4E+00	3.4E+00	3.3E+00	3.3E+00	3.3E+00	3.3E+00	3.3E+00	3.2E+00
	Expression Signal	3.67	0.51	0.51	3.24	9.	٦	0.93	0.56	66.0	8	S	L 850	3.81	1.07	2.33	0.76	0.77	0.77	0.54	3.35	2.06	26.0	76.0	1.03	1.04	1.04	1.79
	ORF SEQ ID NO:	35465	36488	36489		29509		32868		35851	02000	70000	37383	27773	28882	34065			35901	35939		38506	32719	32720				26735
	Exan SEQ ID NO:	21928	22904	22904	24167	16492	19302	19511	21761	22310	2000	01.077	23772	14694	15767		20932	21955		22388	L	24811	19369	19369	21159	23715	23715	
	Probe SEQ ID NO:	8847	9864	9864	11093	3319	6123	6341	8681	9232	000	9232	10739	1542	2844	7518	7880	. 8876	9274	9312	10471	11822	6193	6193	8077	10681	10681	513

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Single Exon Proces Expressed in Placefita	Top Hit Descriptor	D.rerlo zp-50 POU gene	Homo sapiens carcinoembryonic antigen-related cell adhesion molecule 1 (biliary glycoprotein) (CEACAM1).	mRNA	SQUALENE-HOPENE CYCLASE	SQUALENE-HOPENE CYCLASE	PHOSPHOGLYCERATE KINASE, CYTOSOLIC	PHOSPHOGLYCERATE KINASE, CYTOSOLIC	NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 4	NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 4	VON WILLEBRAND FACTOR PRECURSOR (VWF)	Chlamydomonas reinhardti chloroplast DNA for rps9, yof4, yof3, rps18 genes	Chiamydomonas reinhardtii chloroplast DNA for rps9, ycf4, ycf3, rps18 genes	PERIPLASMIC [NIFE] HYDROGENASE SMALL SUBUNIT (NIFE HYDROGENLYASE SMALL CHAIN)	S.cerevisiae threonine deaminase (ILV1) gene, complete ods	Oryzias latipes OIGC6 gane for guanylyl cyclase C, complete cds	Sus scrofa choline acetyltransferase gene, promoter region	HYPOTHETICAL 1425 KD PROTEIN C23E2.02 IN CHROMOSOME I	TRIOSE PHOSPHATE/PHOSPHATE TRANSLOCATOR, NON-GREEN PLASTID PRECURSOR (CTPT)	Bacillus alcalophilus pectate lyase (pelE) gene, complete cds	PROBABLE UBIQUITIN-PROTEIN LIGASE HUL4	TYPE I IODOTHYRONINE DEIODINASE (TYPE-I & DEIODINASE) (DIOI) (TYPE 1 DI) (5DI)	TYPE I IODOTHYRONINE DEIODINASE (TYPE-I 5'DEIODINASE) (DIOI) (TYPE 1 DI) (5DI)	GLUTAMATE [NMDA] RECEPTOR SUBUNIT EPSILON 3 PRECURSOR (N-METHYL D-ASPARTATE RECEPTOR SUBTYPE 2C) (NR2C) (NMDAR2C)	COLLAGEN ALPHA 2(1) CHAIN PRECURSOR	Chlorella vulgaris chloroplast, complete genome	HYPOTHETICAL 56.3 KD PROTEIN F52C9.5 IN CHROMOSOME III	DEOXYHYPUSINE SYNTHASE (DHS)	GENOME POLYPROTEIN (CONTAINS: CAPSID PROTEIN C (CORE PROTEIN), MATRIX PROTEIN (ENVELOPE PROTEIN M); MAJOR ENVELOPE PROTEIN E; NONSTRUCTURAL PROTEINS NS1, NS2A, NS2B, NS4A, AND NS4B; HELICASE (NS3); RNA-DIRECTED RNA POLYMERASE (NS5))	refindic acid nuclear recentor isotorm heta 2 fmice embrumal cardinoma cell line PCC7.M71 mRNA 2971	יוסי בייני	Brassica rapa pollen coat protein homolog (BAN103) gene, complete cds
Exon Propes	Top Hit Database Source	NT			SWISSPROT		SWISSPROT P	SWISSPROT P	Г	Г	_	NT	D IN	ISSPROT		O IN	NT	SWISSPROT H	SWISSPROT	Г	SWISSPROT P	SWISSPROT T	SWISSPROT T	SWISSPROT R	SWISSPROT		ISSPROT	SWISSPROT D	G (E SWISSPROT	T		N B
Single	Top Hit Acession No.	.2E+00 X96422.1		4502404								.2E+00 Y13655.1	.2E+00 Y13655.1			3.2E+00 AB016081.2		Γ		25.1						7524769 NT						
	Most Similar (Top) Hit BLAST E Value	3.2E+00		3.2E+00	3.2E+00 P54924	3.2E+00 P54924	3.2E+00 P12783	3.2E+00 P12783	3.2E+00 P18931	3.2E+00 P18931	3.2E+00 P04275	3.2E+00	3.2E+00	3.2E+00 P13061	3.2E+00	3.2E+00	3.2E+00	3.1E+00	3.1E+00 P52178	3.1E+00/	3.1E+00 P40985	3.1E+00	3.1E+00 P49894	3.1E+00 Q14957	3.1E+00	3.1E+00	3.1E+00	3.1E+00 P49365	3.1E+00 P33515		3.1E+00 S56660.1	3.1E+00 U77666.1
	Expression Signal	0.78		0.95	1.16	1.16	2.49	2.49	1.91	1.91	0.86	2.41	2.41	5.26	1.31	2.06	2.95	2.29	0.91	1.09	0.51	5.14	5.14	3.7	0.55	0.76	0.56	4.09	2.45		2.49	1.17
	ORF SEQ ID NO:	26735		30971	32170	32171	32207	32208	32966	32967	34330	34513	34514		36369	36991		32503	34095		34880	35417	35418		36162	36739		37187			_	
	Exon SEQ ID NO:	13707			18880		18912	18912	١.			21002				23380		19181		١.,			21880	22575	١.	J !	,	23578	23937			
	Probe SEQ ID NO:	4136	61.07	4820	2686	5686	5719	5719	6436	6436	7781	7952	7952	9230	9730	10345	12219	9669	7547	7904	8279	8807	8801	9459	9256	10100	10193	10543	11751		11771	13019

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Top Hit Descriptor	Homo sapiens hypothetical protein PRO0889 (PRO0889), mRNA	S.aureus genes encoding Sau96i DNA methyfransferase and Sau96i restriction endonuclease	Connebacterium glutamicum thrC gene for threonine synthase (EC 4.2.99.2)	Corynebacterium glutamicum thrC gene for threonine synthase (EC 4.2.99.2)	CYR61 PROTEIN PRECURSOR (3CH61)	ENDOTHELIAL CELL MULTIMERIN PRECURSOR	B.napus DNA for myrosinase	S-ADENOSYLMETHIONINE SYNTHETASE (METHIONINE ADENOSYLTRANSFERASE) (ADOMET SYNTHETASE)	RETINAL GUANYLYL CYCLASE 2 PRECURSOR (GUANYLATE CYCLASE 2F, RETINAL) (RETGC-2)	(ROD OUTER SEGMENT MEMBRANE GUANYLATE CYCLASE 2) (ROS-GC2) (GUANYLATE CYCLASE)		RETINAL GUANYLYL CYCLASE 2 PRECURSOR (GUANYLATE CYCLASE 2F, RETINAL) (RETGC-2) (ROD OUTER SEGMENT MEMBRANE GUANYLATE CYCLASE 2) (ROS-GC2) (GUANYLATE CYCLASE 7.00 OUTER SEGMENT MEMBRANE GUANYLATE CYCLASE 2) (ROS-GC2) (GUANYLATE CYCLASE	r) (GC-F)	NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 4	Chlemydophila pneumoniae AR39, section 53 of 94 of the complete genome	F.pringlel gdcsPA gene for P-protein of the glycine cleavage system	BRAIN-SPECIFIC ANGIOGENESIS INHIBITOR 1 PRECURSOR	BRAIN-SPECIFIC ANGIOGENESIS INHIBITOR 1 PRECURSOR	ADHERENCE FACTOR (ADHESION AND AGGREGATION MEDIATING SURFACE ANTIGEN)	STRUCTURAL POLYPROTEIN [CONTAINS: MAJOR STRUCTURAL PROTEIN VP2; NONSTRUCTURAL PROTEIN VP4; MINOR STRUCTURAL PROTEIN VP3]	STRUCTURAL POLYPROTEIN (CONTAINS: MAJOR STRUCTURAL PROTEIN VP2; NONSTRUCTURAL PROTEIN VP4; MINOR STRUCTURAL PROTEIN VP3]	602017413F1 NCI CGAP Brn64 Homo sapiens cDNA clone IMAGE:4153059 5	Saguinus oedipus gene for seminal vesicle secreted protein semenogelin l	Buxus harlandii maturase K (matk) gene, partial cds; chloroplast gene for chloroplast product	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 52	Mus musculus endomucin (LOC53423), mRNA	601342758F1 NII I_MGC_53 Hamo sapiens cDNA clone IMAGE:3684807 5	Mus musculus endomucin (LOC53423), mRNA	Mus musculus per-hexamer repeat gene 3 (Phxr3), mRNA	Mus musculus per-hexamer repeat gene 3 (Phxr3), mRNA
Top Hit Database Source		LN	TN	Ł	SWISSPROT	SWISSPROT		SWISSPROT		TOGGGGWG			1	SWISSPROT		LN	SWISSPROT	SWISSPROT	Г	SWISSPROT	SWISSPROT	T	Т		Į.		EST_HUMAN			
Top Hit Acession No.	R923984 NT	(53096.1	(56037.1	X56037.1	218406	213201	(67838.1	258605		25,040	-51042		251842	3.0E+00 P34194	4E002225.2	236879.1	214514	J14514	246589	205844	205844	3F344171 1	4J002153.2	2.8E+00 AF186398.1	4L161552.2	E393724 NT	BE565182.1	8393724 NT	6679306 NT	6679306 NT
Most Similar (Top) Hit BLAST E Value	3.0E+00	3.0E+00	3.0E+00	3.0E+00	3.0E+00	3.0E+00	3.0E+00 X67838.1	3.0E+00 Q58605		00.00	3.05+00	i d	3.0E+00 P51842	3.0E+00	2.9E+00	2.9E+00	2.9E+00	2.9E+00	2.9E+00	2.9E+00 P05844	2 9F+00	2 9F +00	2.9E+00	2.8E+00	2.8E+00	2.8E+00	2.8E+00	2.8E+00	2.7E+00	2.7E+00
Expression Signal	0.95	1.29	0.82	0.82	11.21	0.7	1.62	0.56		90 5	4.90		4.96	1.37	2.69	1.65	4.66	4.66	6.19	0.57	0.57	0.84	0.82	4.77	3.14	5.05	9.0	1.53	13.96	13.96
ORF SEQ ID NO:	29095	31633	33234	33235				37146		23062	20876		37968	38570	28324	ŀ		33900		34655		34892		27722		34010			26490	26491
Exan SEQ (D NO:	16078			19844	1	ı	1	23536		0,000	24320		- 1	24873		ı	l	l	20684	21135	ı						22853			Ш
Probe SEQ ID NO:	2899	5454	9899	9899	7306	7346	9108	10501		74.050	607		11259	11885	2067	7049	7380	7360	7614	8052	8052	8289	9438	1486	1662	7460	9813	10928	240	240

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					1		
Probe SEQ ID NO:	Exan SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Sœurce	Top Hit Descriptor
6134	19313	32652	4.09	2.4E+00 P02843		SWISSPROT	VITELLOGENIN I PRECURSOR (YOLK PROTEIN 1)
7538				2.4E+00	02.1	Г	602120856F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4278012 5'
7538		34086	0.71	2.4E+00	2.4E+00 BF667502.1	П	602120858F1 NIH_MGC_56 Homo saplens cDNA clone IMAGE:4278012 5
8334	L.	L		2.4E+00 P26842			CD27L RECEPTOR PRECURSOR (T-CELL ACTIVATION ANTIGEN CD27) (T14)
8334	L			2.4E+00 P26842		SWISSPROT	CD27L RECEPTOR PRECURSOR (T-CELL ACTIVATION ANTIGEN CD27) (T14)
8406			2.8	2.4E+00	86.1	FZ	Helicobacter pylori, strain J99 section 47 of 132 of the complete genome
8852	21931		1.72	2.4E+00	2.4E+00 AW875126.1	EST_HUMAN	RC2-PT0004-031299-011-d05 PT0004 Homo sapiens cDNA
8206	l	35648		2.4E+00 P24091		SWISSPROT	ENDOCHITINASE B PRECURSOR (CHN-B)
10244	ı		2.26	2.4E+00 P13673		SWISSPROT	SKIN GRANULE PROTEIN PRECURSOR
10244	23279	ļ		2.4E+00 P13673		SWISSPROT	SKIN GRANULE PROTEIN PRECURSOR
10313	1	Ľ		2.4E+00	1	N	H.sepiens CTGF gene and promoter region
10449	ı		7.28	2.4E+00 P09099		SWISSPROT	XYLULOSE KINASE (XYLULOKINASE)
10528	l	37169	1.64	2.4E+00	2.4E+00 BE326702.1	EST_HUMAN	hre3f06.x1 NCI_CGAP_Kld11 Homo sapiens cDNA clone IMAGE:31331873'
10528	l			2.4E+00		EST_HUMAN	hre3f06.x1 NCI_CGAP_Kid11 Homo sepiens cDNA clone IMAGE:3133187 3'
10818	Ι.	L		2.4E+00 Q51481		SWISSPROT	DENITRIFICATION REGULATORY PROTEIN NIRQ
11335	i I	38047	1.36	2.4E+00	2.4E+00 Y14079.1	NT	Bacillus subtilis chromosomal DNA, region 75 degrees: glpPFKD operon and downstream
11640	24720		2.44	2.4E+00	2.4E+00 AF158652.2	N	Fregaria x ananassa cytosolic ascorbate peroxidase (ApxSC) gene, ApxSC-c allele, complete cds
1282	1	27507		2.3E+00		ZL	G.domesticus artificial single chain antibody gene (L3)
4237				2.3E+00	-	N	Bos faurus partial cytb gene for cytochrome b
				L		, 14 5 14 15 1	J7340F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA clone J7340 5' similar to
5957	19143	24450	0.91		N86245.1	ES I HOMAIN	Refuse consectors ATPase Ca++ transporting ubbuildurs (Atp2s3) mRNA
7777		$oldsymbol{\perp}$			P07199	SWISSPROT	MAJOR CENTROMERE AUTOANTIGEN B (CENTROMERE PROTEIN B) (CENP.B)
7958		34518		2.3E+00		NT	M.mazei dnak and dnaJ genes homologues coding for Dnak and DnaJ
9310	<u>l_</u>				5835317 NT	F	Polypterus amatipinnis mitochondrion, complete genome
2007					044427	TOGGSSIVIS	ALPHA-(1,3)-FUCOSYLTRANSFERASE (GALACTOSIDE 3-L-FUCOSYLTRANSFERASE) FUCOSY TRANSFERASE 4) (FUCT-IV)
	П					TOGGGGWG	ANNIEYIN VII (SYNEYIN)
11041	-			2.35-700	,,,	TOUR TOUR	602060124E1 NIH MCC 58 Hrms sariens CDNA clane IMAGE 4068173 5
0/021	-					TOT TOWN	CONSCIONATE A NIET MCC. CO Diamo combine CINIA almo IMAGE: MCRA72 E'
12075	-1				Ī	EST_HUMAN	90205912171 NINT MICE OF UTION SEPTEMBER CONTRIBUTION OF THE PROPERTY OF THE P
12445						EST_HUMAN	601433673F1 NIH MGC 72 Hcmo sapiens cDNA clone IMACE:3918643 5
4126	ı	1			-	Ę	Magnaporthe grisea Class IV chitin synthase (chs4) gene, complete cos
4432	17572	30553	4.12		2.2E+00 D67071.1	Z	Rat gene for regucalcin, exon1 (non-coding exon)

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Most Similar (Top) Hit Top Hit Acession Database BLAST E No. Source
2.2E+00 D67071.1 NT
2.2E+00 O88307  SWISSPROT
TOBRESON SWISSED TO THE STATE OF THE STATE O
20.1
2.2E+00 BE250383.1 EST_HUMAN
2,2E+00 Q00335 SWISSPROT
2.2E+00 P51459 SWISSPROT
2.2E+00 AA594574.1 EST_HUMAN
2.2E+00 AA449012.1 EST_HUMAN
2.2E+00 P54918  SWISSPROT
2.2E+00 BE301560.1 EST HUMAN
2.2E+00 Q04706 SWISSPROT
2.2E+00 A1290373.1 EST HUMAN
2.2E+00 BF246782.1 EST_HUMAN
2.2E+00 AF183416.1 NT
2.2E+00 P07911 SWISSPROT
2.1E+00 AW449366.1   EST_HUMAN

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	-						
Probe E SEQ ID SE NO:	SEQ ID	ORF SEQ ID NO:	Expression Signal	Most Stmilar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
	19434		76.0	2.1E+00 P75357	P75357	SWISSPROT	HYPOTHETICAL PROTEIN MG302 HOMOLOG
6947	20260	33698	3.51	2.1E+00	.1E+00 O70159	SWISSPROT	ALPHA-2-HS-GLYCOPROTEIN PRECURSOR (FETUIN-A)
L	20302	33745	0.77	2.1€+00	4503430 NT	ΤN	Homo sapiens dysferlin, ilmb girdle muscular dystrophy 2B (autosomal recessive) (DYSF) mRNA, and translated products
	20056	33466	5.88	· 2.1E+00	2.1E+00 N28575.1	EST HUMAN	yy08a10.s1 Soares melanocyte 2NbHM Homo sapiens cDNA clone IMAGE.270618 3' similar to gb:M55654 TRANSCRIPTION INITIATION FACTOR TFIID (HUMAN);
上	21774		2.43	2.1E+00	2.1E+00 AU123630.1	EST_HUMAN	AU123630 NT2RM2 Homo sapiens cDNA clane NT2RM2000671 5'
	14383	27444	1.32	2.0E+00		۲	Homo sapiens p22Dokdel (DOKDEL) mRNA, complete cds
	14383	27445	1.32	2.0E+00	2.0E+00 AF180527.1	LN	Homo sapiens p22Dokdei (DOKDEL) mRNA, complete cds
1366	14520	27595	1.37	2.0E+00		NT	Oryctolagus cuniculus Na+,K+-ATPase beta 1 subunit mRNA, complete cds
	14759		3.09	2.0E+00	2.0E+00 P25582	SWISSPROT	PUTATIVE RRNA METHYLTRANSFERASE SPB1
2216	16350	28480	7.2	2.0E+00		LN	R.norvegicus mRNA for collagen alphaf type i
l	15350	28481	7.2	2.0E+00	.0E+00 Z78279.1	₽N	R.norvegicus mRNA for collagen alpha1 type l
	17365	30353	1.71	2.0E+00	2.0E+00 AW664496.1	EST_HUMAN	hi13c05.x1 NCL_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2972168 3' similar to gb:X01677 GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, LIVER (HUMAN);
	17365	30354	1.71	2.0E+00	2.0E+00 AW664496.1	EST_HUMAN	hi13c05.x1 NCI_CGAP_GU1 Homo sepiens cDNA clone IMAGE:2972168 3' similar to gb.X01677 GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, LIVER (HUMAN);
	20786		0.96	2.0E+00 P07588	P07588	SWISSPROT	STRUCTURAL POLYPROTEIN [CONTAINS: NUCLEOCAPSID PROTEIN C; MEMBRANE GLYCOPROTEINS E1 AND E2]
1	21236	34815	4	2.0E+00		۲N	Escherichia coli 0157 DNA, map position at 46 min., complete cds
8214	21296	34816	4	2.0E+00		. LN	Escherichia coli 0157 DNA, map position at 46 min., complete cds
	21296	34817	4	2.0E+00	2	TN	Eschertchia coli 0157 DNA, map position at 46 mln., complete cds
9122	22201	35743	3.04	2.0E+00 F31500.1	F31500.1	EST_HUMAN	HSPD22703 HM3 Homo sapiens cDNA clone s4000117B08
1	26022	31670	6.76	2.0E+00	5834843 NT	LN	Gallus gallus mitochondrion, complete genome
	18908	32202	4.28	1.9E+00	6754389 NT	LN	Mus musculus inosital 1,4,5-triphosphate receptor 1 (Itpr1), mRNA
l	18908	32203	428	1.9E+00	6754389 NT	N	Mus musculus Inositol 1,4,5-triphosphate receptor 1 (ltpr1), mRNA
	19400	32750	1.2	1.9E+00	9E+00 BE969695.1	EST_HUMAN	601679636F1 NIH_MGC_78 Homo sapiens cDNA done IMAGE:3949881 5'
6792	19947		0.92	1.9E+00	.9E+00 AW845689.1	EST_HUMAN	MR0-CT0063-071099-002-g02 CT0063 Homo sapiens cDNA
	20040		1.91	1.9E+00	.9E+00 Q63627	SWISSPROT	CTD-BINDING SR-LIKE PROTEIN RA4
l	21733	35272	2.21	1.9E+00	.9E+00 P02467	SWISSPROT	COLLAGEN ALPHA 2(I) CHAIN PRECURSOR
, ,	21733	35273	. 2.21	1	.9E+00 P02467	SWISSPROT	COLLAGEN ALPHA 2(I) CHAIN PRECURSOR
8859	21938		3.32	,	08.1	EST_HUMAN	CM3-MT0114-010900-323-h12 MT0114 Homo sapiens cDNA
	22174		1.86	1.9E+00  051781	·	SWISSPROT	ARGININE DEIMINASE (ADI) (ARGININE DIHYDROLASE) (AD)

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_			_	_			-	_	_	$\overline{}$		_		_	$\overline{}$		$\overline{}$	T	_	_	$\overline{}$	_		_		т.	•		
	Top Hit Descriptor	ab94a04.s.1 Stratagene lung (#937210) Homo sapiens cDNA clone IMAGE:854574.3' similar to contains Alu repetitive element, contains element L1 L1 repetitive element;	Homo sapiens gag-pro-pol precursor protein gene, partial cds	PROTEIN B8 PRECURSOR	Synechococcus sp. PCC7942 copper transporting P-ATPase (ctaA) and ATP synthase epsilon subunit (atpE) genes, complete cds	Synechococcus sp. PCC7942 copper transporting P-ATPase (ctaA) and ATP synthase epsilon subunit	(atpE) genes, complete cds	HEDGEHOG RECEPTOR (PATCHED PROTEIN)	601897854F1 NIH_MGC_19 Homo sapiens cDNA done IMAGE:4127364 5'	602139470F1 NIH_MGC_46 Homo sapiens cDNA done IMAGE:4298272 5'	601893489F1 NIH_MGC_17 Homo saplens cDNA done IMAGE:4139038 5'	MAJOR ANTIGEN	LIPOPOLYSACCHARIDE 1,6-GALACTOSYLTRANSFERASE (UDP-D-GALACTOSE  (GLUCOSYL)LIPOPOLYSACCHARIDE-ALPHA-1,3-D-GALACTOSYLTRANSFERASE)	RETROVIRUS-RELATED POL POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE;	ENDONUCLEASE	RETROVIRUS-RELATED POL POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE; JENDONI ICI EARET	EMBRYONAL FYN, ASSOCIATED SLIBSTRATE (HEES)	472-208 Chartes planents Nh7HP Homo saniens CDNA done IMAGE 135/278 5	QV0-OT0030-070300-148-e03 OT0030 Homo saplens cDNA	FUSION GLYCOPROTEIN PRECURSOR (CONTAINS: FUSION GLYCOPROTEIN F2; FUSION	GLYCOPROTEIN F1]	CHITINASE D PRECURSOR	Homo sapiens PRO0530 mRNA, complete cds	CYTIDINE DEAMINASE (CYTIDINE AMINOHYDROLASE) (CDA)	Chiamwdomones reinhardii alternative oxdasse 1 (AOX1) gene, nuclear gene encoding mitochondrial protein	Rattus norvegicus Actin-related protein complex 1b (Arpc1b), mRNA	601813714F1 NIH MGC 54 Homo sapiens cDNA clone IMAGE:4048251 5	LEVANSUCRASE (BETA-D-FRUCTOFURANOSYL TRANSFERASE) (SUCROSE 6-FRUCTOSYL TRANSFERASE)	Homo sapiens chromosome 21 segment HS21C080
	Top Hit Defabase Source	EST_HUMAN	N	SWISSPROT	NT		NT	SWISSPROT	EST_HUMAN	EST_HUMAN	EST_HUMAN	SWISSPROT	SWISSPROT		SWISSPROT	TOGGGGIAIG	SWISSPACE	EST LINAN	EST HUMAN		SWISSPROT	SWISSPROT	<u>N</u>	SWISSPROT	LΝ	Į.	EST HUMAN	SWISSPROT	TN
,	Top Hit Acesslon No.	1.9E+00  AA669125.1	1.9E+00 AF248269.1	P21004	U04356.1		1.8E+00 U04356.1	P18502	1.8E+00 BF311999.1	1.8E+00 BF683327.1	1.8E+00 BF305652.1	P21249	P27127		P11369	044960	711308	4 PE 400 D24042 4	1.8E+00 AW880004.1		P06828	P27050	1.8E+00 AF111849.1	P44325	1 8F+00 AF314254 1	9506404 NT	1.8E+00.BF212412.1	Q60114	1.7E+00 AL163280.2
	Most Similar (Top) Hit BLAST E Value	1.9E+00	1.9E+00	1.8E+00 P21004	1.8E+00 U04356.1		1.8E+00	1.8E+00 P18502	1.8E+00	1.8E+00	1.8E+00	1.8E+00 P21249	1.8E+00 P27127		1.8E+00 P11369	000100	1.0E-100 F 11308	1.01	1.8E+00		1.8E+00 P06828	1.8E+00 P27050	1.8E+00	1.8E+00 P44325	1.85+00	1.8E+00	1.8E+00	1.7E+00 Q60114	1.7E+00
	Expression Signal	89:0	0.67	1.89	2.15		2.15	1.63	2.02	1.28	1.15	1.22	0.8		. 0.98	6	000	07.0	0.82		0.47	0.94	4.71	0.75	497	6.01	1.45	1.68	4.9
	ORF SEQ ID NO:	36452			28370		29371		32755		33441				34913			26013			36626						31854		Ш
	Exan SEQ ID NO:	22870	23823	16337	16365	1	16365	19173	19405	1	l	20069			21390	1	1	22,64	1	1			ı	23810	25994	1	1		15476
	Probe SEQ ID NO:	9830	10790	3162	3190		3190	2988	6230	6528	6878	7204	7411		8308	0000	0000	92.00	9462		9666	10054	10490	10777	12575	12667	13005	1132	2345

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6787 Human retina cDNA Tsp509I-cleaved sublibrary Homo sapiens cDNA not directional tu82407.x1 NCI\_CGAP\_Gas4 Homo sapiens cDNA clone IMAGE:2257549 3' similar to contains MSR1.t1 IPYRUVATE DEHYDROGENASE (LIPOAMIDEI).PHOSPHATASE, MITOCHONDRIAL PRECURSOR (PDP) (PYRUVATE DEHYDROGENASE PHOSPHATASE, CATALYTIC SUBUNIT) (PDPC) oz43h05.x1 Soares\_NhHMPu\_S1 Homo sapiens cDNA clone IMAGE:1678137 3' LEVANSUCRASE (BETA-D-FRUCTOFURANOSYL TRANSFERASE) (SUCROSE 6.FRUCTOSYL zd25f01.r1 Scenes\_fetal\_heart\_NbHH19W Homo sapiens cDNA clone IMAGE:341689 5' similer to gb:D29806 N-ACETYLLACTOSAMINE SYNTHASE (HUMAN); Homo saplens small proline-rich protein (SPRR3) gene, exons 1, 2, and 3 and complete cds.
Mus musculus STGGalNAcill gene, exon 2.
B.napuc gene encoding endo-pdygalacturonase Homo sapiens lens epithelium-derived growth factor gene, alternatively spliced, complete cds Mus musculus T cell receptor gamma locus, TCR gamma 2 and gamma 4 gene clusters Mus musculus T-cell acute brinchocytic leukemia 1 (Tal1), mRNA 602071917F1 NCI\_CGAP\_Bin67 Homo saplens cDNA clone IMAQE:4214669 5 Hippoglossus hippoglossus interferon inducible Mx protein (Mx) mRNA, complete ods HYPOTHETICAL 38.0 KD PROTEIN IN CAT2-AMD1 INTERGENIC REGION HYPOTHETICAL 38.0 KD PROTEIN IN CAT2-AMD1 INTERGENIC REGION EST365791 MAGE resequences, MAGC Homo sapiens cDNA 601488170F1 NIH\_MGC\_69 Homo sapiens cDNA clone IMAGE:3890464 5' 601488170F1 NIH MGC 69 Homo sapiens cDNA clone IMAGE:3890464 5 601894255F1 NIH\_MGC\_17 Homo sapiens cDNA clone IMAGE:4140084 5 GM0-BT0282-171299-127-905 BT0282 Homo sapiens cDNA COUP TRANSCRIPTION FACTOR 1 (COUP-TF1) (COUP-TF1) Top Hit Descriptor CM0-BT0282-171299-127-e05 BT0282 Homo sapiens cDNA M.musculus Ank-1 mRNA for erythroid ankyrin M.musculus Ank-1 mRNA for erythroid ankyrin Rattus norvegicus SA gene, partial cds HOMEOBOX PROTEIN DLX-3 Homo sapiens HSPC262 mRNA, partial ods HOMEOBOX PROTEIN DLX-3 MSR1 repetitive element; TRANSFERASE EST HUMAN EST HUMAN EST\_HUMAN NT EST HUMAN EST HUMAN EST\_HUMAN EST HUMAN EST\_HUMAN SWISSPROT EST\_HUMAN SWISSPROT HUMAN SWISSPROT EST\_HUMAN SWISSPROT Top Hit Database Source SWISSPROT SWISSPROT Top Hit Acession 1.7E+00 BE063546.1 1.7E+00 BE063546.1 1.7E+00 BF308000.1 .8E+00 AF199339.1 1.7E+00 AF021335.1 1.7E+00|AI678443.1 ġ 1.7E+00 AF245513. BE878260. 1.7E+00 AF161380. 1.7E+00 AW953681 1.6E+00 W 58426.1 1.7E+00 AI141067. 1.7E+00 O60479 1.7E+00 O60479 W22424. 1.7E+00 Q60114 1.7E+00 Q9TTR8 1.7E+00 Q03703 1.6E+00 1.7E+00 1.7E+00 .7E+00 1.7E+00 1.7E+00 .7E+00 1.7E+00 1.6E+00 1.6E+00 (Top) Hit BLAST E Value 2 1.73 1.03 19.53 1.49 1.18 1.18 1.63 4.4 Expression Signal 3.02 ORF SEQ ID NO: 32216 32217 32661 33230 34641 34825 34852 35519 35520 35633 35981 37510 38582 29225 28702 33909 35352 35982 28352 32066 28362 16202 19840 20446 15241 15246 16573 17718 18923 19319 25859 25356 SEQ ID 18923 21907 15230 20446 ö Probe SEQ ID 5730 6141 7367 7367 8038 8222 8252 8828 8901 8901 9014 9350 9806 10375 10857 11896 12523 2090 3028 4581 5730 10857 2445 9350 2357 ö

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Top Hit Descriptor	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)	60218609571 NIH_MGC_45 Homo saplens cDNA clone IMAGE:4310591 3'	Homo sapiens proliferation associated SNF2-like protein (SMARCA6) mRNA, complete cds	Homo sapiens proliferation associated SNF2-like protein (SMARCA6) mRNA, complete cds	Salmiri bollwensis offactory receptor (SBO27) gene, partial cds	Mus musculus ST6GalNAcill gene, exon 2	Mus musculus ST6GalNAcill gene, exon 2	Brachydanio rerio MHC class II DA-bela-2*01 gene, 3' end	Homo sapiens transglutaminase type I (Tgasel) gene, promoter region	IL2-UT0073-060900-145-E02 UT0073 Homo capiens cDNA	UI-H-BI2-ahr-b-04-0-UI,s1 NCI_CGAP_Sub4 Homo sapiens cDNA clone IMAGE:27275113'	RC0-CT0415-200700-032-c10 CT0415 Homo sapiens cDNA	VIRULENCE FACTOR MVIN HOMOLOG	Mus musculus SII, MAP_17, CYP_a, SCL & CYP_b genes	Homo sapiens hypothetical protein PRO0971 (PRO0971), mRNA	Homo sapiens hypothetical protein PR00971 (PR00971), mRNA	601283925F1 NIH_MGC_44 Horno sapiens cDNA clone IMAGE:3605647 5'	M.musculus COL3A1 gene for collagen alpha-l	M.musculus COL3A1 gene for collagen alpha-l	Thermoanaerobacter ethanolicus D-xylose-binding protein (xylF) gene, complete cds	ph6b6_19/1TV Outward Alty-primed hncDNA library Homo sapiens cDNA clone ph6b6_19/1TV	QV4-LT0016-090200-100-d07 LT0016 Homo sapiens cDNA	QV4-LT0016-090200-100-d07 LT0016 Homo sapiens cDNA	Mus musculus T cell receptor gamma locus, TCR gamma 1 and gamma 3 gene clusters	CAPSID PROTEIN P40 [CONTAINS: ASSEMBLIN (PROTEASE); CAPSID ASSEMBLY PROTEIN]	Homo sapiens transglutaminase type I (Tgasel) gene, promoter region	Homo sapiens unknown mRNA	Rattus norvegicus Jun dimenzation protein 2 (Jdp-2) mRNA, complete cds	Chlamydophila pneumoniao AR38, section 32 of 94 of the complete genome	Mus musculus a disintegrin and metalloproteinase domain (ADAM) 15 (metargidin) (Adam15), mRNA	Potato virus A RNA complete genome, isolate U	Mus musculus T-cell lymphoma invasion and metastasis 1 (Tiam1), mRNA
Top Hit Database Source	Ę	EST_HUMAN	F	۲	N	Þ	님	₽	ᅜ	EST_HUMAN	EST_HUMAN	EST_HUMAN	SWISSPROT	Ę	۲	۶	EST_HUMAN	Ŋ	Ł	F	EST_HUMAN	EST_HUMAN	EST_HUMAN	TN	SWISSPROT	F	۲N	LN.	LN	IN.	Z	NT
Top Hit Acession No.	.6E+00 AB026898.1	.6E+00 BF570077.1	.6E+00 AF155827.1	.6E+00 AF155827.1	.6E+00 AF127897.1	.6E+00 Y11344.1	.6E+00 Y11344.1	.6E+00 L04808.1	.6E+00 AF005631.1	.6E+00 BF380703.1	.6E+00 AW 294881.1	.6E+00 BE697267.1	.6E+00 Q46378	.6E+00 AJ297131.1	11437222 NT	11437222 NT	1.1	.6E+00 X52046.1	.6E+00 X52046.1	.6E+00 AF043466.1	.6E+00 T41290.1	.6E+00 AW835644.1	.6E+00 AW835644.1	.6E+00 AF037352.1	P54817	.6E+00 AF005631.1	.6E+00 AF104313.1	.5E+00 U53449.1	5E+00 AE002201.2	6752961 NT	.5E+00 AJ131402.1	6678350 NT
Most Similar (Top) Hit BLAST E Value	1.6E+00	1.6E+00	1.6E+00	1.6E+00	1.6E+00	1.6E+00	1.6E+00	1.6E+00	1.6E+00	1.6E+00	ľ	٦	-	1.8E+00	1.6E+00	1.6E+00	1.6E+00	1.6E+00	1.6E+00	· 1.6E+00	1.6E+00	1.6E+00	1.6E+00	1.6E+00	1.6E+00 P54817	1.6E+00	1.6E+00	1.5E+00	1.5E+00	1.5E+00	1.5E+00	1.5E+00
Expression Signal	1.06	6.05	1.25	1.25	0.59	2.83	2.83	2.38	0.78	16:0	1.05	2.37	1.3	3.3	1.07	1.07	0.49	1.05	1.05	0.7	1.49	1.09	1.09	0.52	1.77	4.8	3.68	2.95	244	1.81	1.56	2.02
ORF SEQ ID NO:			30590	30591		31284		32447	ŀ					35196		35725	35898	34615	34616		ŀ		37030	37195				5/292	26492			28828
Exan SEQ ID NO:	17017	17294	17612	17612		18316	18316		19218			ŀ	1			ł			25857				23423	23587	24089	19218		13271	13463	13821	1	15709
Probe SEQ ID NO:	3857	4142	4472	4472	5184	5194	5194	5948	6035	6293	6849	7394	8219	8574	9101	9101	9272	698	9659	92.6	9935	10388	10388	10552	11010	11082	12008	33	241	636	2481	2584

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					0		
Probe SEQ ID (	Exan SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
				0			
3208	15608	28732		1.5E+00	.5E+00 AJ131402.1	NT	Potato virus A RNA complete genome, isolate U
.3462	16629		72.0	1.5E+00	.5E+00 AE001945.1	NT	DeInococcus radiodurans R1 section 82 of 229 of the complete chromosome 1
							#12/10.x1 NCI_CGAP_GC6 Hamo sepiens cDNA clone IMAGE:2240587 3' similar to TR:000237 000237
5846	19036	32342	0.71	1.5E+00	.5E+00 Al655301.1	EST HUMAN	HK-1.;
2787	10036	20243	2	4 50.00	EC.100 Aleseana a	TOT LINAN	It1210.x1 NCI_CGAP_GC6 Homo saptens cDNA clone IMAGE:2240587.3' similar to TR:000237 000237 HKE-1.
8536	1080	93072		2	5E 100 D17879 1	EST LIMAN	with 0-0.7 Sparse infant brain 1NIB Homo sanians cDNA clone IMAGE:31893 5
7278	20361	1000	1.68	1.5E+00	5E+00 BE785356.1	EST HUMAN	601478745F1 NIH MGC 68 Homo saplens cDNA clone IMAGE:3881555 5'
7311	20393	33853	16.24	1.5E+00	5E+00 P47179	SWISSPROT	HYPOTHETICAL 118.4 KD PROTEIN IN BAT2-DAL5 INTERGENIC REGION PRECURSOR
7311	20393	33854		1.5E+00	SE+00 P47179	SWISSPROT	HYPOTHETICAL 118.4 KD PROTEIN IN BAT2-DAL5 INTERGENIC REGION PRECURSOR
7500	20575	34048		1.5E+00	5E+00 AA889259.1	EST_HUMAN	ak26f10.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1407115 3'
7768	20826	34317	77.0	1.55+00	5E+00 A 1003254 1	EST HUMAN	an07b11.s1 Stratagene schizo brain S11 Homo sapiens cDNA clone IMAGE:1684893 3' similar to do:S95936 SEROTRANSFERRIN PRECURSOR (HUMAN):
8313	21395	34920	6.0	1.5E+00	.5E+00 BE887446.1	EST HUMAN	601509586F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3911181 5'
8367	21448	34971	0.5	1.5E+00	5E+00 AB040887.1	NT	Homo sapiens mRNA for KIAA1454 protein, partial cds
8846	21925	35463	1.09	1.5E+00	.5E+00 K02138.1	LN⊤	Mouse germline IgM chain gene, mu-delta region
9218	22296		0.48	1.5E+00	.5E+00[AB038516.1	NT	Homo sapiens hGPIb alpha gene for platelet glycoprotein Ib alpha, complete cds
9334	22410		0.51	1.5E+00	.5E+00 BF217818.1	EST_HUMAN	601882662F1 NIH_MGC_57 Homo sapiens cDNA done IN/AGE:4095135 5'
9684	22733	36303	0.85	1.5E+00	.5E+00 R81928.1	EST_HUMAN	yi03h01.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:147697 5'
9835	22875	36459	1.6	1.5E+00	5E+00 AW375697.1	EST_HUMAN .	QV3-CT0192-261089-008-d09 CT0192 Homo saplens cDNA
10064	23102	36705		1.5E+00	.5E+00 BF376754.1	EST_HUMAN	RC0-TN0078-150900-034-g05 TN0078 Homo sapiens cDNA
10258	23293		1.85	1.5E+00	.5E+00 BF337944.1	EST_HUMAN	602035771F1 NCI_CGAP_Brn64 Homo saplens cDNA clone IMAGE:4183865 5'
10399	23434	37040	2.26	1.5E+00	.5E+00 AA017689.1	EST_HUMAN	ze38g06.r1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:361306 5'
10399	23434	37041	2.26	1.5E+00	.5E+00 AA017689.1	EST_HUMAN	ze38g06.r1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:361306 5
11684	24683	38373	3.4	1.5E+00	.5E+00 AL134197.1	EST_HUMAN	DKFZp547P243_s1 547 (synonym: hfbr1) Homo sapiens cDNA clone DKFZp547P243 3'
11834	24823		7.68	1.5E+00	.5E+00 X07380.1	NT	Maize mitochondrial tRNA-Ser gene and tRNA-Phe pseudogene
11929	24915		1.39	1.5E+00		EST_HUMAN	tg94d09.x1 NG_CGAP_CLL1 Hamo sapiens cDNA clone IMAGE:2116433 3'
11929	24915			1.5E+00	٠٢.	EST_HUMAN	tg94d09,x1 NCI_CGAP_CLL1 Homo saplens cDNA clone IMAGE:2116433 3'
12515	26095	31662	1.61	1.5E+00	.5E+00 D63480.1	NT	Human mRNA for KIAA0146 gene, partial cds
12785	25508		3.92	1.5E+00	.5E+00 AL445065.1	NT	Thermoplasma actdophilum complete genome; segment 3/5
12888	25589		2.17	1.5E+00	6978492 NT	NT	Rettus norvegicus 5 - Lipoxygenase (Alax5), mRNA
13220	25794	31888	1.31	1.5E+00	BF22393	EST_HUMAN	7q82b06.x1 NCI_CGAP_Lu24 Homo sapiens cDNA done IMAGE: 3'
30	13268			1.4E+00	7661685 NT	LΝ	Homo sapiens DKFZP586M0122 protein (DKFZP586M0122), mRNA
30	13268	26272	2.27	1.4E+00	7661685 NT	NT	Homo sapiens DKFZP586M0122 protein (DKFZP586M0122), mRNA

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	Top Hit Descriptor	Helicobacter pylori glutamine synthetase (glnA) gene, complete cds	Ovis aries prion protein gene, complete cds	Human papillomavirus type 7 genomic DNA	Fugu rubripes neurofibromatosis type 1 (NF1), A-kinase anchor protein (AKAP84), BAW protein (BAW), end W381 protein (W381) genes, complete cds	Fugu rubripes neurofibromatosis type 1 (NF1), A-kinase anchor protein (AKAP84), BAW protein (BAW), and	WSB1 protein (WSB1) genes, complete cás	Homo sapiens Mad4 homolog (MAD4) mRNA	CM0-NN1005-140300-286-h06 NN1005 Homo saplens cDNA	CM0-NN1005-140300-286-h06 NN1005 Homo sapiens cDNA	602156687F1 NIH_MGC_83 Homo sapiens cDNA clone IWAGE:4297556 5'	PEROXISOME PROLIFERATOR ACTIVATED RECEPTOR ALPHA (PPAR-ALPHA)	wt45g07.x1 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2510460 3'	Homo sapiens mRNA for KIAA1157 protein, partial cds	DNA TOPOISOMERASE III ALPHA	Homo sapiens mRNA for KIAA0905 protein, complete cds	SYNAPSIN II	SYNAPSIN II	CM3-NN0006-300300-132-b12 NN0006 Homo sapiens cDNA	Homo sepiens ceveolin-1/-2 locus, Contig1, D7S522, genes CAV2 (exons 1, 2e, and 2b), CAV1 (exons 1 and 2)	he23f05.x1 NCI_CGAP_CML1 Homo sapiens cDNA clone IMAGE:2919873 3' similar to contains Alu	repatitive element;	LAMININ BETA-2 CHAIN PRECURSOR (S-LAMININ)	LAMININ BETA-2 CHAIN PRECURSOR (S-LAMININ)	GLUCOAMYLASE PRECURSOR (GLUCAN 1,4-ALPHA-GLUCOSIDASE) (1,4-ALPHA-D-GLUCAN	GLUCOHYDROLASE)	Homo sapiens Xq pseudoautosomal region; segment 1/2	yg33f12.r1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:34345 5'	RC1-BT0313-301299-012-105 BT0313 Homo sapiens cDNA	Sceloporus undulatus ornithine transcarbamylase (OTC) mRNA, complete cds	602/33/35F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4288137 5'	IL5-HT0198-291099-008-C04 HT0198 Homo sapiens cDNA	IL5-HT0198-291099-008-034 HT0198 Homo sapiens cDNA
	Top Hit Database Source	TN TN	₩	TN TN	F				EST_HUMAN (C	EST_HUMAN C	EST HUMAN	Г	EST_HUMAN V		SWISSPROT	Т	SWISSPROT	SWISSPROT	EST HUMAN				SWISSPROT 1	SWISSPROT		SWISSPROT	i IN	EST_HUMAN	EST_HUMAN F	TN	EST_HUMAN (		EST_HUMAN
)	Top Hit Acession No.	4E+00 AF053357.1	4E+00 U67922.1	4E+00 X74463.1	4E+00 AF064564.2		.4E+00 AF064564.2	5453733 NT	.4E+00 AW900455.1	.4E+00 AW900455.1	4E+00 BF681547.1	4E+00 Q07869	.4E+00 AW054976.1	.4E+00 AB032983.1	4E+00 Q13472	.4E+00 AB020712.1	292777	292777	4E+00 AW893057.1	4E+00 AJ133269.1		.4E+00 AW467760.1	P55268	4E+00 P55268		P07683	.4E+00 AJ271735.1	.4E+00 R20459.1	.4E+00 BE064687.1	.4E+00 AF134844.1	.4E+00 BF575545.1	.4E+00 BE145374.1	.4E+00 BE145374.1
	Most Similar (Top) Hit BLAST E Value	1.4E+00	1.4E+00	1.4E+00	1.4E+00		1.4E+00	1.4E+00	1.4E+00	1.4E+00	1.4E+00	1.4E+00	1.4E+00	1.4E+00	1.4E+00	1.4E+00	1.4E+00 Q92777	1.4E+00 Q92777	1.4E+00	1.4E+00		1.4E+00	1.4E+00 P55268	1.4E+00		1.4E+00 P07683	1.4E+00	1.4E+00	1.4E+00	1.4E+00	1.4E+00	1.4E+00	1.4E+00
	Expression Signal	76.0	9.39	1.7	3.22		3.22	67.0	1.13	1.13	1.51	0.94	1.73	6.04	3.07	3.83	2.8	2.8	8.0	86		1.14	2.0	0.7		0.72	5.4	1.65	3.83	0.65	0.88	88.0	98.0
	ORF SEQ ID NO:			28964	29055		29056		30493				31705		32939		33078		33614				34062	34063				35920	36038	36072			37103
	Exan SEQ ID NO:	15482	15541	15851	15947	1	15947	16583	17513	17513	17843	18434	18887	18839	19578	26214	19705	19705	20189	l	i			20588			22073	22371	22472	22506			23492
	Probe SEQ ID NO:	2351	2411	2734	2833		2833	3414	4370	4370	4708	5317	5488	5645	6403	6424	6542	6542	6961	7438		7454	7514	7514		8530	8994	9295	9398	9432	10412	10457	10457

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Fugu rubripes gamma-aminobutyric acid receptor beta subunit gene, partial cds; 55kd erythrocyte membrane protein (P55), synaptic vesicle-associated integral membrane protein (VAMP-1), procollagen C-proteinase Pneumocystis carinii f. sp. ratti guanine nucleotide binding protein alpha subunit (pcg1) gene, complete cds Pneumocystis cartnii f. sp. ratti guanine nucleotide binding protein alpha subunit (pog1) gene, complete cds Cyprinus carpio MRPb and MASPb genes for mannose-binding lectin-associated serine protease (MASP) PHENOL HYDROXYLASE P3 PROTEIN (PHENOL 2-MONOOXYGENASE P3 COMPONENT) Pandorina cotemaniae chloropiast roct, gene for ribulose bisphosphate carboxylase, partial cds Pandorina cotemaniae chloropiast roct, gene for ribulose bisphosphate carboxylase, partial cds SPORE GERMINATION PROTEIN KB Homo sapiens fibronectin receptor alpha-subunit precursor (ITGA5) mRNA, partial cds Homo sapiens cutaneous T-cell lymphoma tumor antigen se70-2 (SE70-2), mRNA 601661233R1 NIH\_MGC\_72 Homo sapiens cDNA done IMAGE:3915945 3 801855184R1 NIH\_MGC\_85 Hamo sapiens cDNA clone IMAGE:3845805 3' 801655184R1 NIH\_MGC\_65 Homo sapiens cDNA clone IMAGE:3845805 3' Cox lacryma-jobi dihydrodipicolinate synthase (dapA) gene, complete ods forno sapiens putative psihHbA pseudogene for hair keratin, exons 2 to 7 M.m.cedo gene encoding 4-Dinydromethyl-trisporate dehydrogenase Arabidopsis thaliana DNA chromosome 4, contig fragment No. 12 domo sapiens zinc finger protein 157 (HZF22) (ZNF157) mRNA Chlamydia murtdarum, section 66 of 85 of the complete genome Top Hit Descriptor melanogaster no-on-transient A gene product, complete cds Homo sapiens zinc finger protein 157 (HZF22) (ZNF157) mRi Human estradiol 17 beta-dehydrogenase gene, complete cds MO-CT0289-291199-004-f08 CT0289 Homo seplens cDNA Mus musculus alpha-spectrin 1, erythroid (Spna1), mRNA Cantherellus sp. partial 25S rRNA gene, isolate Tibet enhancer protein (PCOLCE) genes, complete c> domo sepiens APECED mRNA for AIRE-1, and MASP-related protein, complete cds TYPOTHETICAL GENE 84 PROTEIN **IRICHOHYALIN** EST\_HUMAN EST\_HUMAN EST\_HUMAN EST\_HUMAN SWISSPROT SWISSPROT Top Hit Dattabase SWISSPROT Source 툳 Ę 눌 눌 6755621 NT 4507998 4507998 Top Hit Acession 1.3E+00 Z73640.1 1.3E+00 AJ271192.1 1.3E+00 Y19213.1 1.3E+00 4507 AW362834.1 1.4E+00 BE962107.2 AE002338.2 AB030447.1 BE966735.2 1.3E+00 AF016494.1 1.4E+00 Q07283 1.4E+00 AB006682.1 1.4E+00 BE962107.2 AL181500.2 ġ 1.3E+00 U61730.2 1.3E+00 M13918.2 .3E+00 M33496.1 1.4E+00 U30790.1 1.4E+00 U30790.1 1.4E+00 D63441.1 D63441.1 1.3E+00 / 1.3E+00 E 1.3E+00 P 1.3E+00 / 1.4E+00 / 1.4E+00 1.3E+00 Aost Similar (Top) Hit BLAST E 23.81 96.0 0.96 4.52 3.46 2.3 14.36 2.38 <u>4</u> 14.36 1.84 98.0 Expression Signal ORF SEQ ID NO: 37390 37397 37504 38232 38379 38380 38444 38445 27549 29857 32322 32662 32663 33634 27164 27550 29201 20243 20206 SEG ID 15448 16849 14100 24751 24751 13775 14482 14482 14542 14793 15739 16180 932 19709 Probe SEQ ID 11711 925 1325 2316 2615 3005 3686 5631 5827 6142 6142 6547 6890 6928 8269 10744 11499 11711 11691 11691 1325 1387 584 1641 ë

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	Top Hit Descriptor	601061420F1 NIH_MGC_10 Hamo sepiens cDNA clone IMAGE:3447965 5'	TCBAP1D0959 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project⊏TCBA Homo saniens cDNA ctone TCBAP0959	ACYLPHOSPHATASE, ORGAN-COMMON TYPE ISOZYMES A AND B (ACYLPHOSPHATE	PHOSPHOHYDROLASE)	Sus scrafa plp gene	601657145R1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3866195 3'	601680250R2 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:3950532 3'	Homo sapiens GL004 protein (GL004), mRNA	wo85a07.x1 NCL_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2462100 3'	yo88c03.s1 Soares breast 3NbHBst Homo saplens cDNA clone IMAGE:183076 3'	yo88c03.s1 Sogres breast 3NbHBst Hamo saplens cDNA clane IMAGE:183076 3'	Homo sapiens heparan glucosaminyl N-deacetylase/N-sulfotransferase-2 gene, complete cds	S.alba phr-1 mRNA for photolyase	S.alba phr-1 mRNA for photolyase	Homo sapiens lipoxygenase (ALOX12B) mRNA, complete cds	ww3f03.x1 NCI_CGAP_Kld3 Homo saplens cDNA clone IMAGE:2628477 3' similar to gb:M31522 TRANSCRIPTION FACTOR ITF-1 (HUMAN);	LYSOSOMAL ALPHA-MANNOSIDASE PRECURSOR (MANNOSIDASE, ALPHA B) (LYSOSOMAL ACID AI PHA MANNOSIDASE) (I AMAN)	WESTERN AND COMP KIND Samiens CDNA close IMAGE:2462100 3'	Lactococcus lactis cremoris NCDO-fivor chromosomal inversion junction DNA	Lactococcus lactis cremoris NCDO-inv1 chromosomal inversion junction DNA	601657145R1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3866195 3'	tq77a12x1 NO_CGAP_Ut1 Homo sepiens cDNA clone IMAGE:2214814 3' similar to gb:X14723 CLUSTERIN PRECURSOR (HUMAN);	Eschericia coli serotype O157:H7 O antigen gene cluster	Eschericia coli serotype O157:H7 O antigen gene cluster	Vibrio cholerae chromosome II, section 49 of 93 of the complete chromosome	Cempylobacter jejuni kanamycin phosphotrancfarace (aphA-7) gene, complete cds	Homo sapiens chromosome 21 segment HS21C102	ws32e10.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2498922 3' similar to SW:TRXB_HUMAN Q16881 THIOREDOXIN REDUCTASE ;	Homo sapiens hypothetical protein FLJ20707 (FLJ20707), mRNA
	Top Hit Database Source	EST_HUMAN 6	T HIMAN		SWISSPROT F	П	EST_HUMAN 6	EST_HUMAN 6		Г	Г	EST_HUMAN				TN PN	EST_HUMAN		Т	Т		EST_HUMAN	EST HUMAN	T	. LN			TN	EST_HUMAN C	
S S S S S S S S S S S S S S S S S S S	Top Hit Acessian No.	1.3E+00 BE538819.1	1 3E+00 BE 243571 1	1.1	P24540	1.3E+00 AJ009912.1	1.3E+00 BE963379.2	1.3E+00 BE974280.1	9910247 NT	1.3E+00 AI927629.1	H42881.1	H42881.1	1.3E+00 AF042084.1	X72019.1	X72019.1	1.3E+00 AF059250.1	1.3E+00 AW024390.1	2000	1.3E+00 000/34	1.3E+00 A J 223962.1	1.3E+00 AJ223962.1	1.3E+00 BE963379.2	1.3E+00 AI559944.1	1.3E+00 AF061251.1	1.3E+00 AF061251.1	1.3E+00 AE004392.1	1.3E+00 M29953.1	1.3E+00 AL163302.2	1.3E+00 Al990846.1	8923637 NT
	Most Similar (Top) Hit BLAST E Value	1.3E+00	4 2E +00	20.	1.3E+00 P24540	1.3E+00	1.3E+00	1.3E+00	1.3E+00	1.3E+00	1.3E+00 H42881.1	1.3E+00 H42881.1	1.3E+00	1.3E+00 X72019.1	1.3E+00 X72019.1	1.3E+00	1.3E+00	4 01 00 000364	1.35-100	135+00	1.3E+00	1.3E+00	1.3E+00	1.3E+00	1.3E+00	1.3E+00	1.3E+00	1.3E+00	1.3E+00	1.3E+00
	Expression Signal	1.16	80.0	26.5	0.78	1.78	2.28	1.05	1.87	68.0	0.51	0.51	5.02	2.47	2.47	1.21	0.47	0	8 2	99.0	0.68	3.93	0.57	0.5	0.5	1.68	1.59	0.99	0.47	0.53
	ORF SEQ ID NO:	33610	92770	8175	34162	35112	35259	35378		35609	35976	35977		36359	38360			9000	30490	36688				36996	L				37493	
	SEQ ID NO:	20186	2000	20002	20686	1	21722	21837	21986	1	l	1	l	22789	22789	22863	22887	7,000	1877		1	ı	ı	23388	1	ı		23844	1	23884
	Probe SEQ ID NO:	7092	2240	2477	7616	8494	8642	8758	8907	8990	9347	9347	9715	9724	9724	8823	9847	200	700	10031	10031	10070	10130	10353	10353	10418	10435	10811	10838	10851

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					`		
Probe SEQ ID NO: .	Ø	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acessian Na	Top Hit Database Source	Top Hit Descriptor
10854		37506		1.3E+00	7949159 NT	LN	Mus musculus vesicle-associated membrane protein 4 (Vamp4), mRNA
10854	L.	37507	97.0	1.3E+00	LN 651676L	TN	Mus musculus vesicle-associated membrane protein 4 (Vamp4), mRNA
10861	23894	37515	0.45	1.3E+00	.3E+00 H42881.1	EST_HUMAN	yo68c03.s1 Seares breast 3NbHBst Homo sapiens cDNA clone IMAGE:183076 3'
10861	23894	37516	0.45	1.3E+00	.3E+00 H42881.1	EST_HUMAN	yo88c03.s1 Seares breact 3NbHBct Homo capiens cDNA clone IMAGE:183076 3'
10932	24014		4.05	1.3E+00	3E+00 Q14117	SWISSPROT	DIHYDROPYRIMIDINASE (DHPASE) (HYDANTOINASE) (DHP)
11145	24217	37844	2.4	1.3E+00	.3E+00 P25299	SWISSPROT	MRNA 3'-END PROCESSING PROTEIN RNA15
11169	24240	37872	1.77	1.3E+00	.3E+00 Z18892.2	N	Mus musculus desmin gene
11619	24670		1.43	1.3E+00	.3E+00 AW274791.1	EST_HUMAN	xp09e03.x1 NCI_CGAP_HN9 Homo sapiens cDNA clone IMAGE:2739868 3'
11831	24820	38511	. 2.73	1.3E+00	.3E+00 D42042.1	ΙN	Human mRNA for KIAA0085 gene, partial cds
11923	24909	38610	2.28	1.3E+00	.3E+00 Z98682.1	LΝ	Bacillus subtilis genomic DNA 23.9kB fragment
11894	24979		1.35	1.3E+00	.3E+00 L31891.1	TN	Arabidopsis thaliana 3-ketoacyl-acyl carrier protein synthase III (KAS III) mRNA, complete cds
12504	25347		3.81	1.3E+00	.3E+00 AF187873.1	. IN	Cavia porcellus inwardiy-rectifying potassium channel Kir2.2 (KCNJ12) gene, complete cds
12698		32022	2.76	1.3E+00	.3E+00 BF348043.1	EST_HUMAN	602023185F1 NCI_CGAP_Bm67 Homo sapiens cDNA clone IMACE:4158452 5
12707			1.98	1.3E+00		SWISSPROT	E1 GLYCOPROTEIN PRECURSOR (MATRIX GLYCOPROTEIN) (MEMBRANE GLYCOPROTEIN)
12822	25549		1.53	1.3E+00	.3E+00 AF187035.1	. LN	Sturnira lilium cytochrome b gene, complete cds; mitochondrial gene for mitochondrial product
							Naphthalanesulfonate-degrading bacterium BN6 2,3-dihydroxybiphenyl dloxygenase (bphCII) gene, complete
13200	25783		1.34	1.3E+00	.3E+00 U38978.1	NT	cds
13231			1.63	1.3E+00	.3E+00 AL163283.2	NT	Hamo sepiens chromosome 21 segment HS21C083
667	13853	26881	8.73	1.2E+00	2E+00 AA676246.1	EST_HUMAN	zi22d08.s1 Scares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:4315353'
846	14024	27082	1.52	1.2E+00	2E+00 P05228	SWISSPROT	HISTIDINE-RICH PROTEIN PRECURSOR (CLONE PFHRP-111)
. 846	14024	27083	1.52	1.2E+00	.2E+00 P05228	SWISSPROT	HISTIDINE-RICH PROTEIN PRECURSOR (CLONE PFHRP-III)
846		27084		1.2E+00	P05228	SWISSPROT	HISTIDINE-RICH PROTEIN PRECURSOR (CLONE PFHRP-III)
901			1.21	1.2E+00	8924234 NT	LN	Homo sepiens hypothetical protein PRO3077 (PRO3077), mRNA
1187		27407	7.6	1.2E+00	2E+00 AF080245.2	NT	Elaeis oleifera sesquiterpene synthase mRNA, complete cds
1232	14391	27453	1.71	1.2E+00	ZE+00 AJ252242.1	NT	pea seed-borne mosaic virus complete genome
1232	14391	27454	1.7.1	1.2E+00		LN.	pea seed-borne mosaic virus complete genome
2066		28323	1.02	1.2E+00	2E+00 AF140631.1	ΙN	Homo saplens G-protein coupled receptor 14 (GPR14) gene, complete cds
3179	16354	29359	1.06	1.2E+00	.2E+00 AB020681.1	LN	Homo sapiens mRNA for KIAA0874 protein, partial cds
3234			10.7	1.2E+00	ZE+00 AL161553.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 63
3234	16408	29422	7.01	1.2E+00	.2E+00 AL161563.2	NT .	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 63
3358				1.2E+00	.2E+00 P54910	SWISSPROT	CONJUGAL TRANSFER PROTEIN TRBE PRECURSOR
3437				1.2E+00	.2E+00 AF188740.1	NT	Homo sapiens L.HX3 gene, intron 2
3804			9.16	1.2E+00	2E+00 U75902.1	NT	Mus musculus subtilisin-like serine protease LPC (PC7) gene, exons 1 to 9, partial cds
4094	17249	30254	1.87	1.2E+00	.2E+00 BF373570.1	EST_HUMAN	MR0-FT0175-050900-203-g06_1 FT0175 Homo sapiens cDNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
4413	16605	29625	1.06	1.2E+00	2E+00 AF188740.1	N <sub>T</sub>	Homo sapiens LHX3 gene, intron 2
4594	17731		19.1	1.2E+00		۲	Rattus rattus cardiac AE3 gene, exons 1-23
4645	17781	30763		1.2E+00	2E+00 AL161509.2	LN LN	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 21
4682	17817	30805		1.2E+00	2E+00 AF156495.1	N	Homo saplens post-synaptic density 95 (DLG4) gene, complete cds
4712	17847		9.9	1	2E+00 Y09200.1	IN	T.phnatum chloroplast rbcL gene, partial
5554	1	31788	1.13	1	2E+00 U20760.1		Human extracellular calcium-sensing receptor mRNA, complete cds
5672				1	2E+00 AW813276.1	T_HUMAN	MR3-ST0191-140200-013-c05 ST0191 Homo sapiens cDNA
5917	19105		0.65	_	.2E+00 X81879.1	Ę	Calicivirus cDNA for orf1, orf2 and orf3
5895	19180	32502	22.0	<u>.                                    </u>	2E+00 AF016052.1	TN	Homo sapiens zinc finger protein ZNF191 (ZNF191) gene, complete cds
9280			2.45	7	2E+00 X74885.1	IN	D.hydei ay/ repeat cluster DNA, fragment D
6342			3.81	1.2E+00	2E+00 BE003113.1	EST_HUMAN	QV4-BN0090-270400-190-a03 BN0090 Homo sapiens cDNA
6420	19589	32953	1.28	1.2E+00	2E+00 X89084.1	NT	C glutamicum pta gene and ackA gene
6420	19589		1.28	1.2E+00	2E+00 X89084.1	N	C.glutamicum pta gene and ackA gene
6463	19630	32991	36.06	-	2E+00 AA759254.1	EST_HUMAN	ah84g12.s1 Soares_testis_NHT Homo saplens cDNA clone 1322374 3'
							yy39b12.s1 Soares melanocyte 2NbHM Homo sapiens cDNA clone IMAGE:273599 3' similar to.
						1	gb M87935 HUMAALU472 Human carcinoma cell-derived Alu RNA transcript, (rRNA); gb:J04970
9999					.ZE+00 N33Z95.1	ES! HOMAN	CARBOXYPET ILASE M PRECURSOR (HUMAN);
9630	1				2E+00 P17671	SWISSPROT	ECDYSONE-INDUCIBLE PROTEIN E78-A
6634			<u>ş</u> .	_	2E+00 AW813276.1	EST_HUMAN	MR3-ST0191-140200-013-c05 ST0191 Home capiens cDNA
7055	20108	33524	1.72		2E+00 AB029010.1	NT	Homo sapiens mRNA for KIAA1087 protein, partial cds
7067	20120	33534	2.81	1.2E+00	2E+00 AJ002141.1	NT	Mus musculus DSPP gene
-	0,000			'		140 m. ±02	zq38f05.r1 Stratagene hNT neuron (#937233) Homo sapiens cDNA done IMAGE 632001 5' similar to
100	2000	99/99	0.00	\	25-00 AA 107010.1	NEW TOWNS	good 10322 Human Illiny of the good property of the contract o
3 5	П		100		1	Т	AVITO SERVICE AND PROGRAMMOUTHER TO SERVICE THE AVITOR SERVICE THE AVI
7542	25847		1.85		-	ESI_HUMAN	AV 734583 can Homo sepiens culva cione calvartius 3
7828			2.91	1.2E+00	.2E+00 X74207.1	NT	L. lactis pyrD and pyrF genes
7897	21047	34580	0.8	1	2E+00 BE787646.1	EST_HUMAN	601481761F1 NIH_MGC_68 Homo septens cDNA clone IMAGE:3884270 5'
8767	21846	35387	3.19	1	.2E+00 AB033030.1	TN	Homo sapiens mRNA for KIAA1204 protein, partial cds
							ALPHA, ALPHA-TREHALOSE-PHOSPHATE SYNTHASE (UDP.FORMING) 123 KD SUBUNIT
0000	2,0	08/77	6	•	00-100 100-000	TOGGGGIA	(TREHALOSE-6-PHOSPHATE SYNTHASE) (UDP-GLUCOSE-GLUCOSEPHOSPHATE GLICOSM TRANSERASE)
3	ı		V.02		1	201.00	
20077		ı		1.25+00	7706271 NT	Į,	Homo sapiens CGI-30 protein (LOC51611), mRNA
9226	22304	35847			.2E+00 AW377210.1	- 1	MR2-CT0222-201099-001-e07 CT0222 Homo sapiens cDNA
9440			0.51		H48599.1	EST_HUMAN	yq80a06.r1 Soares fetal liver spleen 1NFLS Homo saplens cDNA clone IMAGE:202066 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
9598		36224	3.79	1.2E+00	.2E+00 Z32850.1	TN	R. communis gene for pyrophosphate-dependent phosphofructokinase beta subunit
9805	22845		2.13	1.2E+00	2E+00 D11745.1	EST_HUMAN	HUMHM01A01 Liver HepG2 cell line. Homo saplens cDNA clone hm01a01
10135	23173	36771	3.6	1.2E+00	2E+00 X56832.1	LN	H. sapiens ENO3 gene for muscle specific enolase
10532	23567		0.82	1.2E+00	2E+00 AB009666.1	FZ	Homo sapiens klotho gene, expn 1
11432	24493		1.69	1.2E+00	.2E+00 M38686.1	LN L	Mus musculus Id gene, exon 1
11627	24707	38400	1.51	1.2E+00	2E+00 AW817817.1	EST_HUMAN	PMO-ST0264-161199-001-d01 ST0264 Homo sapiens cDNA
11666			69'2	1.2E+00	2E+00 BE160761.1	EST_HUMAN	PM1-HT0422-160200-007-g10 HT0422 Homo sapiens cDNA
11744				· 1.2E+00		NT	Raitus norvegicus synapse-associated protein 102 mRNA, complete cds
12101	25081	38788	1.68	1.2E+00	.2E+00 M10408.1	LN	Maize mitochondrial F-0-A-T Pase proteolipid (subunit 9) gene
12471	25984	31768	17.76		.2E+00 AL163203.2	FN	Homo sapiens chromosome 21 segment HS21C003
12491	25339		1.74	1.2E+00		LN	Bacillus halodurans genomic DNA, section 9/14
13218	L		2.66	1.2E+00	2E+00 AA077909.1	EST_HUMAN	7H11A08 Chromosome 7 HeLa cDNA Library Homo sapiens cDNA clone 7H11A06
476	13671	26703	1111	1.1E+00	.1E+00 D86980.1	LΝ	Human mRNA for KIAA0227 gene, partial cds
1802	14951	28045		1.1E+00	.1E+00 AW995393.1	EST_HUMAN	QV0-BN0042-170300-163-g12 BN0042 Homo saplens cDNA
1948	15091	28192		1.1E+00	.1E+00 AW575889.1	EST HUMAN	UI-HF-BR0p-ajk-f-02-0-UI.s1 NIH_MGC_52 Homo saplens cDNA clone IMAGE:3074834 3'
2017	l '	[ ]	2.74	1.1E+00	.1E+00 AF137273.1	NT	Gallus gallus alpha 1 (V) collagen mRNA, complete cds
3409	16579		98'8'	1.1E+00	.1E+00 AL163213.2	\	Homo sepiens chromosome 21 segment HS21C013
3409	16579	29595		٢	.1E+00 AL163213.2	ΤN	Homo sapiens chromosome 21 segment HS21C013
3575		ĺ	١.	1.1E+00	8922641 NT	ΕN	Homo sapiens hypothetical protein FLJ10749 (FLJ10749), mRNA
3670	16833		0.99	1.1E+00	.1E+00 AI808360.1	EST HUMAN	wf34h11.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2359461 3' similar to SW:P531_HUMAN Q12888 P53-BINDING PROTEIN 53BP1
3812	L	ĺ		1.1E+00		LN	Xylella fastidiosa, section 32 of 229 of the complete genome
3812	16972		1.16	1.1E+00	.1E+00 AE003886.1	K	Xylella fastidiosa, section 32 of 229 of the complete genome
3920			0.92	1.1E+00	.1E+00 X85374.1	TN	H.parahaemolyticus hphlM(A), hphlM(C), hphlR and menB genes
4024	17210			1.1E+00	8922641 NT	NT	Homo sepiens hypothetical protein FLJ10749 (FLJ10749), mRNA.
4130	17283	_	0.72	1.1E+00	6755205 NT	L	Mus musculus proteasome (prosome, macropain) subunit, beta type 7 (Psmb7), mRNA
4331	17474		6.82	1.1E+00	5835331 NT	NT	R. unicornis complete mitochandrial gename
5107	18235	31204	3.45		.1E+00 U18466.1	LN	African swine fever virus, complete genome
5180			2.06	1.1E+00	.1E+00 X78425.1	LN	E.faecalls pbp5 gene
5422	18623	31599	1.49	1.1E+00	E978530 NT	NT	Rattus nervegicus Aquaporin 4 (Aqp4), mRNA
5731	18924	32218	14.33	1.1E+00	.1E+00 BE960184.1	EST_HUMAN	601652776R1 NIH_MGC_58 Homo saplens cDNA clone IMAGE:3825835 3'
5750	18942		1.32	1.1E+00	.1E+00 AI138582.1	EST_HUMAN	qd85c03.x1 Soares_testis_NHT Homo sapiens cDNA clone !MAGE:1736260 3'
6217	19392	32740	6.0	1.1E+00	11419739 NT	L	Homo sapiens solute carrier family 6 (neurotransmitter transporter), member 14 (SLC6A14), mRNA

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Probe SEQ ID	0	ORF SEQ ID NO:	Expression	Most Similar (Top) Hit BLAST E	Top Hit Acessian No.	Top Hit Database	Top Hit Descriptor
ö	NO:			Value		Source	
6404	19573	32935	0.59		1E+00 AF197861.1	LΝ	Macgregoria pulchra cytochrome b gene, complete cds; mitochondrial gene for mitochondrial product
6537	19700	33073	0.72	4	1E+00 R06037.1	EST_HUMAN	ye89e03.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:124924 5'
9899	20008	33419	0.78	1	1E+00 AJ404004.1	NT	Mus musculus mRNA for ER protein 58 (EP68 gene)
7447	20524	33997	85.0	1	.1E+00 X55981.1	NT	Maize mRNA for endase (2-chospho-D-glycerate hydrolase)
7632	20701	34179	0.67	1.1E+00	1E+00 BF683714.1	EST_HUMAN	602139978F1 NIH_MGC_46 Hamo sapiens cDNA clone IMAGE:4301322 5'
7659			2.23	1	1E+00 Z72338.1	LN	Herpes simplex virus type 1 (strain KOS) UL41 gene
7659				1	.1E+00 Z72338.1	NT	Herpes simplex virus type 1 (strain KOS) UL41 gene
7680	20745	34226		4	1E+00 AL161588.2	NT	Arabidopsis thaltana DNA chromosome 4, contig fragment No. 84
7754	25853	34305	1.04	1.1E+00	11967980 NT	Ę	Mus musculus silent mating type Information regulation 2, (S.cerevislae, homolog)-like (SIr2), mRNA
8326	l			[	1E+00 BF693996.1	EST_HUMAN	602082582F1 NIH_MGC_81 Horno sapiens cDNA clone IMAGE:4246628 5'
9416				-	.1E+00 Al478339.1	EST_HUMAN	m39h11.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:21605493'
8935	22014	35554	0.86	٦.	1E+00 AB003088.1	NT	Acetabularia caliculus mitochondrial COXI-like gene
	l			L			VH=anti-cytomegalov/rus glycoprotein B antibody 4D4 heavy chain variable region (human, mRNA Partial, 375
9015				-	1E+00 S80750.1	NT	ut
9126		35748	69.0	1	.1E+00 AI079946.1	EST_HUMAN	oz34f05.x1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:1677249 31
8837	21080		0.75	l l	.1E+00 BE384876.1	EST_HUMAN	601276278F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3617418 5'
888	22868	36450	0.51	1.1E+00	.1E+00 AJ245772.1	LN	Mus musculus mRNA for stretch responsive muscle (X-chromosome) protein (Smx gene)
9883	22923		0.81	-	.1E+00 Y12227.1	LN	Arabidopsis thaliana DNA, 24 kb surrounding PFL locus
	1						Yersinia pseudotuberculosis psaE, psaE, adhesin (psaA), chaperone (psaB), and usher (psaC) genes,
9974	23013	-			.1E+00 L76301.1	- N	complexe cas
10038	23076	١			.1E+00 AB023151.1	LN	Homo sapiens mKNA for KIAAU934 protein, partial cds
10141	23179			1	.1E+00 AL161515.2	LN L	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 27
10202	23239	36829		1.1E+00	6754021 NT	LN	Mus musculus guanine nucleotide binding protein (G protein), gamma 3 subunit (Gng3), mRNA
10719	23752		1.21	1.1E+00	1E+00 P73769	SWISSPROT	DNA MISMATCH REPAIR PROTEIN MUTS
	L_						au51c11.y1 Schneider felal brain 00004 Homo sapiens cDNA clone IMAGE:2518292 5' similar to gb:D10522
10831			0.56	_	.1E+00 AI878921.1	EST_HUMAN	Human mRNA for 80K-L protein, complete cds. (HUMAN);
10886	23970	37600	1.97	1.1E+00	11067364 NT	TN	Homo sapiens KIAA0626 gene product (KIAA0626), mRNA
							Klebsormidium fluftans cytochrome o oxidase subunit 2 (cox2) gene, mitochondrial gene encoding
10947	- 1			-	1E+00 AF088942.1	Ä	mitochondrial protein, partial cds
11343	ll	38055			L16877.1	NT	Home saplens cytochrome P4502C9 (CYP2C9) gene, 5' flank and exon 1
11361	18489		2.74	1.1E+00	TN 8922973 NT	IN	Homo sapiens hypothetical protein FLJ11280 (FLJ11280), mRNA

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Probe SEQ ID NO:	SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
11368	24427	38083	2.93		.1E+00 AF012862.1	NT	Petroselinum crispum cytosolic glucosa-6-phosphate dehydrogenase 1 (cG6PDH1) mRNA, complete cds
11368	24427	38084	2.03		.1E+00 AF012862.1	NT	Petroselinum crispum cytosolic glucose-6-phosphate dehydrogenase 1 (cG6PDH1) mRNA, completo cdc
11637	L		3.99		.1E+00 Al809699.1	EST_HUMAN	wf76e11.xf Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2361548 3'
11870	L.,		1.38	1	.1E+00 D89501.1	NT	Human PBI gene, complete cds
11870	24858		1.38	1	.1E+00 D89501.1	NT	Human PBI gene, complete cds
12441		į	1.82	٦	.1E+00 P07866	SWISSPROT	LOW TEMPERATURE ESSENTIAL PROTEIN
12547	25371	32070	3.56	ļ	.1E+00 AF216696.1	NT	Taenia solium immunogenic protein Ts76 mRNA, partial cds
12689	25980		1.86		.1E+00 AF234169.1	NT	Dictyostellum discoldeum Isopentenyi pyrophosphate isomerase (Dipi) mRNA, complete cds
5	L		48.L	٦	.0E+00 U23808.1	NT	Xenopus laevis rhodopsin gene, complete cds
116		26374	2.1	7	.0E+00 D88425.1	L	Cavia cobaya mRNA for serine/threoine kinase, complete cds
431	1		-2.78	_	.0E+00 AB021684.1	NT	Marchantia polymorpha genes for 26S rRNA, 5S rRNA, 18S rRNA, 5.8S rRNA and 26S rRNA
8	L	26800	1.44	٢	.0E+00 AJ251660.1	LZ	Girardia tigrina mRNA for homeodomain transcription factor (so gene)
69			7.14	-	.0E+00 AL163218.2	Z	Homo sapiens chromosome 21 segment HS21C018
88	L			-	.0E+00 AF125984.1	LN	Aedes aegypti mucin-like protein MUC1 mRNA, complete cds
1417	16037		1.35	٢	.0E+00 X80416.1	TN	V.carteri Algal-CAM mRNA
1795	14944	28037	1.33	_	.0E+00 AB006531.1	IN	Plautia stali intestine virus RNA for nonstructural polyprotein, capsid protein precursor, complete cds
2554	15679	28803	1.11	1.0E+00	.0E+00 P48355	SWISSPROT	DNA GYRASE SUBUNIT B
2554			1.11	-	.0E+00 P48355	SWISSPROT	DNA GYRASE SUBUNIT B
2621	15744		96'0	1	0E+00 AA628453.1	EST_HUMAN	ar28g08.s1 Soares_total_fetus_Nb2HF8_9w Homo saplens cDNA clone IMAGE:1032830 3' similar to WP:C42D8.3 CE04204 ;contains element MER22 MER22 repetitive element ;
2940	16117	29129	4.51	1	.0E+00 P24008	SWISSPROT	3-OXO-5-ALPHA-STEROID 4-DEHYDROGENASE 1 (STEROID 5-ALPHA-REDUCTASE 1) (SR TYPE 1)
2940	16117	28130	4.51		.0E+00 P24008	SWISSPROT	3-OXO-5-ALPHA-STEROID 4-DEHYDROGENASE 1 (STEROID 5-ALPHA-REDUCTASE 1) (SR TYPE 1)
3032	i .	_	96'0		.0E+00 O14226	SWISSPROT	HYPOTHETICAL 67.9 KD PROTEIN C8F12.08C IN CHROMOSOME!
3269	<u> </u>	29463	1.16		1.0E+00 AA628453.1	EST_HUMAN	af26g08.s1 Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone INAGE:1032830 3' sImilar to WP:C42D8.3 CE04204 ;containo element MER22 MER22 repetitive element ;
3459	16626		0.73	Ĺ	1.0E+00 AF222761.1	TN	Rattus norvegious neuromedin U precursor (NmU) gene, exons 5 and 6
3688	13337		0.75		1.0E+00 U23808.1	NT	Xenopus laevis rhodopsin gene, complete cds
3772	2 16933	29939	1.61		1.0E+00 AJ223816.1	N	Agaricus bisporus mRNA for tyrosinase

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Top Hit Descriptor	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced	Homo sapiens hypothetical protein FLJ10139 (FLJ10139), mRNA	Hordeum vulgare gene encoding cysteine proteinase	Bos taurus micromolar calcium activated neutral protease 1 (CAPN1) gene, exons 11-20, and partial cds	Bos taurus micromolar calcium ectivated neutral protease 1 (CAPN1) gene, exons 11-20, and partial cds	Arabidopsis thaliana DNA chromosome 4, ESSA I FCA contig fragment No. 6	FIBER PROTEIN	UI-H-BI3-atx-d-09-0-UI.s1 NCI_CGAP_Sub5 Hamo sapiens cDNA done IMAGE:3068969 3'	Mus musculus subtitisin-like serine protease LPC (PC7) gene, exons 1 to 9, partial cds	Homo sapiens cell cycle protein (PA2G4) gene, exons 2 though 5	SRB-11 PROTEIN	601581891F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3936382 51	601581891F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3936382 5	V.carteri gene encoding valvoxopsin	insulin-like growth factor-binding protein 4 [cattle, pulmonary artery endothelial cells, mRNA, 2028 nt]	B-CELL RECEPTOR CD22 PRECURSOR (LEU-14) (B-LYMPHOCYTE CELL ADHESION MOLECULE) (BL-CAM)	Hamo sapiens endothelin-converting enzyme 2 (ECE2) mRNA, complete cds	ac79b08.s1 Stratagene (ung (#937210) Homo sapiens cDNA clone (MAGE:868791 3'	602/153792F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4294727 5'	601443950F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3848005 5	601443950F1 NIH_MGC_65 Homo saplens cDNA clone IMAGE:3848005 5	Rattus norvegicus mRNA for N-acetylglucosaminylitansferase III, complete cds	PEROXISOMAL HYDRATASE-DEHYDROGENASE-EPIMERASE (HDE) (MULTIFUNCTIONAL BETA- OXIDATION PROTEIN) (MFP) [INCLUDES: 2-ENOYL-COA HYDRATASE ; D-3-HYDROXYACYL COA DEHYDROGENASE ]	PEROXISOMAL HYDRATASE-DEHYDROGENASE-EPIMERASE (HDE) (MULTIFUNCTIONAL BETA- OXIDATION PROTEIN) (MFP) [INCLUDES: 2-ENOYL-COA HYDRATASE; D-3-HYDROXYACYL COA	DEHYDROGENASE
Top Hit Database Source	T &		- LN	FX		TN.	SSPROT	EST_HUMAN L	NT	±N ±N			EST_HUMAN 6	NT \	- TN	SWISSPROT (	Г	EST_HUMAN 8	EST_HUMAN 6		EST_HUMAN 6	_	SWISSPROT		SWISSPROT
Top Hit Acession No.	0E+00 AF223391.1	8922245 NT	DE+00 Z97022.1	DE+00 AF248054.1	0E+00 AF248054.1	0E+00 Z97341.2	0E+00 P04501	0E+00 AW452782.1	U75902.1	1.0E+00 AF104669.1	DE+00 P46506	0E+00 BE797716.1	0E+00 BE797716.1	0E+00 Y11204.1	0E+00 S52770.1	0E+00 P20273	0E+00 AF192531.1	0E+00 AA775191.1	0E+00 BF679213.1	0E+00 BE868267.1	0E+00 BE868267.1	0E+00 D10852.1	002207		0E+00 Q02207
Most Similar (Top) Hit BLAST E Value	1.0E+00	1.0E+00	1.0E+00	1.0E+00	1.0E+00	1.0E+00	1.0E+00	1.0E+00	1.0E+00 U75902.1	1.0E+00	1.0E+00	1.0E+00	1.0E+00	1.0E+00	1.0E+00	1.0E+00	1.0E+00	1.0E+00	1.0E+00	1.0E+00	1.0E+00	1.0E+00	1.05+00.002207		1.0E+00
Expression Signal	1.12	0.72	2.3	4.38	4.38	1.74	4.85	1.67	2.04	0.83	1.07	0.82	0.82	1.27	1.15	89.68	1.51	6.02	0.72	1.65	1.65	1.48	65		2.59
ORF SEQ ID NO:	30322		31568	32472	32473	32588	32763			33219			33350	33664	33826			34462		34749	34750		954		35164
Exon SEQ ID NO:	17330	17533		19157	19157	19259	19415	ı	1	19830	19923	<u> </u>	19950	20231	20371	20716	L		21070	l	21230	18496	_		21626
Probe SEQ ID NO:	4180	4390	5396	5971	5971	6077	6241	6248	6818	6671	6767	8795	6795	6916	7288	7647	7889	7903	8019	8148	8148	8335	8545		8545

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Top Hit Database Source	Most Similar (Top Hit Acession Database BLASTE No. Source
SWISSPROT	1.0E+00 P51784 SWISSPROT
UBRQUITIN CARBOXYL-TERMINAL HYDROLASE 16 (UBIQUITIN THIOLESTERASE 16) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE 16) (DEUBIQUITINATING ENZYME 16) (UBIQUITIN PROCESSING PROTEASE UBP-M)	
UBRQUITIN CARBOXYL-TERMINAL HYDROLASE 16 (UBIQUITIN THIOLESTERASE 16) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE 16) (DEUBIQUITINATING ENZYME 16) (UBIQUITIN PROCESSING PROTEASE UBP-M)	
EST_HUMAN	П
Simian immunodeficiency virus Gag protein (gag) gene, complete cds; Pol protein (pol) gene, partial cds; and Vif protein (vtf), Vpr protein (vpr), Tet protein (tat), Rev protein (rev), Vpu protein (vpu), Env protein (env), and Nef protein (nef) genes, >	æ.
NT Human immunodeficiency virus type 1 (HIV-1), Isolate SF33,	
EST_HUMAN	BE907592.1 EST_HUMAN
	6753429 NT
3429 NT	3429 NT
EST_HUMAN	1.1 EST_HUMAN
	Z
	U44952.1 NT
	6174562 NT
/4062 N	/4062 N
EST HUMAN   0V15007.51 SOMMES, SETESCHI CIGORISIS, NOTST HOITD SEPIETS CLINA CIGIE IMMOE. TOUGOU S  1   EST HUMAN   AV758825 BM Homo sepiens cCINA clone BMFAW CO4 6	Т
EST_HUMAN	EST_HUMAN
NT Human retinoblastoma susceptibility gene exons 1-27, complete cds	
NT (PBR1=proline-rich protein (intron 3) [human, Genomic, 898 nt]	
FIN	FIN
1000	1000
SWISSPROT	SWISSPROT
Ν	85.1 NT
SWISSPROT   SERINE/THREONINE PROTEIN KINASE MINIBRAIN	

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Probe SÉQ ID NO:	Exan SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
2990	19175	32496	0.83	9.9E-01	9.9E-01 Q09632	SWISSPROT	PROBABLE OXIDOREDUCTASE ZK1290.5 IN CHROMOSOME II
9461	22518		1.68	9.9E-01	9.9E-01 U65667.1	INT	Lycopersicon esculentum putative Mi1 copy 1 nematode-resistance gene
9755	22693		2.14	9.9E-01	9.9E-01 Q28642	SWISSPROT	B2 BRADYKININ RECEPTOR (BK-2 RECEPTOR)
536		26753	1.17	9.8E-01 P22567		SWISSPROT	AMINO-ACID ACETYLTRANSFERASE (N-ACETYLGLUTAMATE SYNTHASE) (AGS) (NAGS)
2370			1.26	9.8E-01		NT	Callithrix Jacchus UBE1 gene derived retroposon on the Y chromosome
2862	15976		1.29	· 9.8E-01	3.8E-01 AF174644.1	TN	Xenopus laevis rac GTPase mRNA, complete cds
3903	17062		0.67	9.8E-01	9.8E-01 BE957439.2	EST HUMAN	601653583R2 NIH_MGC_55 Homo sepiens cDNA clone IMAGE:3838461 3'
3903	17062	30062	0.67	9.8E-01	3.8E-01 BE957439.2	EST_HUMAN	601653583R2 NIH_MGC_55 Homa sapiens cDNA clane IMAGE:3838461 3'
7340	20420	COREC	4 42	9 RF-01	9 8E-01 A 1302158 1	FX	Enterchecterlaceae sp. JM983 partial groES gene for GroES-like protein and partial groEL gene for GroEL-like protein isolate. JM983
	1			2 200			Enterchacteriacege sp. JM983 partial groES gene for GroES-like protein and partial groEL gene for GroEL-
7349	20429	33891	4.42	9.8E-01	9.8E-01 AJ302158.1	L	Ilke protein, isolete JM983
7823	l		1.14	9.8E-01	9.8E-01 BF034016.1	EST_HUMAN	601456337F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE.3860049 5
7823	l		1.14	9.8E-01	9.8E-01 BF034016.1	EST_HUMAN	601456337F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3860049 5'
8916	21995	35534	0.94	9.8E-01 P38652	P38652	SWISSPROT	PHOSPHOGLUCOMUTASE (GLUCOSE PHOSPHOMUTASE) (PGM)
10653	23687		1.02	9.8E-01	9.8E-01 AA825565.1	EST_HUMAN	od55d04.s1 NCI_CGAP_GCB1 Homo saplens cDNA clone IMAGE:1371847 3'
11242	24311	37948		9.8E-01	9.8E-01 BE258705.1	EST_HUMAN	601110258F1 NIH MGC_16 Homo saplens cDNA clone IMAGE:3350750 5
11242	24311		1.84	9.8E-01	.8E-01 BE258705.1	EST_HUMAN	601110258F1 NIH_MGC_16 Homo saplens cDNA clone IMAGE:3350750 5'
							Homo sepiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a), castine transporter (CRTR),
12554	25377		2.43	9.8E-01	9.8E-01 U52111.2	·	CDM protein (CDM), adrenoleukodystrophy protein >
							Drosophila melanogaster sodium channel protein (para) gene, exons 9,10,11,12 and optional segments b, c, d
7309	┙	33851	2.73	9.7E-01		F	and e, partial cds
8701			1.9	9.7E-01	9.7E-01 AF149112.1	NT	Triticum aestivum stripe rust resistance profein Yr10 (Yr10) gene, complete cds
8707			1.54	9.7E-01	9.7E-01 M90544.1	NT	Salmonella typhimurium adenine-methyltransferase (mod) and restriction endonuclease (res)
9039		35661	0.73	9.7E-01	9.7E-01 BE799822.1	EST_HUMAN	601592165F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3945904 5'
11444	24505		3.56	9.7E-01	9.7E-01 BF511209.1	EST HUMAN	UFH-BI4-aci-e-07-0-UI.s1 NCL_CGAP_Sub8 Homo saplens cDNA clone IMAGE:3085140 3'
13208			3.17	9.7E-01	9.7E-01 AL114281.1	IN	Botrytis cinerea strain T4 cDNA library under conditions of nitrogen deprivation
4558	17696		0.74	9.6E-01	9.6E-01 AF197925.1	۲	Bromus inermis putative cytosolic phosphoglucomutase (pgm1) mRNA, complete cds
4558		30676	0.74	9.6E-01	9.6E-01 AF197925.1	TN	Bromus inermis putative cytosolic phosphoglucomutase (pgm1) mRNA, complete odd
4580	117717		1.28	9.6E-01	9.6E-01 AW 799674.1	EST_HUMAN ·	PM2-UN0053-240300-005-f12 UM0053 Homo sapiens cDNA
5872	Ė		3.51	9.6E-01	9.6E-01 Z70556.1	LN	Parvovirus B19 DNA, pattent C, genome position 2448-2994.
5872			3.51	9.6E-01	9.6E-01 Z70556.1	LN	Parvovirus B19 DNA, patient C, genome position 2448-2994
9889	20038	33447	9.0	9.6E-01	9.6E-01 Z97341.2	TN	Arabidopsis thaliana DNA chromosome 4, ESSA I FCA contig fragment No. 6

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	Τ,	_	_		_	_	_		_	_	<del>-</del>		<del>,</del>		_,	_	_		_	_		_					_	_		_	_	<u> </u>
Top Hit Descriptor	Helix lucorum presenilin (PS) mRNA, complete cds	P. falciparum complete gene map of plastid-like DNA (IR-A)	Rettus norvegicus (strain R21) Rps2r gene, complete cds	Homo sapiens ribosomal protein s4 Y isoform gene, complete cds	AV752605 NPD Homo sapiens cDNA clone NPDBAG06 5	AV752605 NPD Homo sapiens cDNA clone NPDBA G06 5'	Homo sepiens centrosomal protein 2 (CEP2), mRNA	Sphyma tiburo NADH dehydrogenase subunit 2 (NADH2) gene, mitochondrial gene encoding mitochondrial	protein, partial cus Louis conjune CCI 125 contain // OCE1003 mDNA	TOTAL SEPTEMBER VOIT 15 DIVIDING TOTAL SEPTEMBER 17 DIVIDING SEPTEMBER VOIT 15 DIVIDING SEPTEMBER VOIT	1010/2029/1 NIT WICK-ZI TORIO SEPRIS CURA GIORE INVACEL: 3906/1/2 3	6016/5639F1 NIH_MGC_21 Hamo sapiens culvA clone IMAGE: 39384/3 5	qd57d07.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1733581 3	RC1-CT0295-241199-011-b02 CT0295 Homo sepiens oDNA	601885163F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4103630 5'	UI-H-BI2-ahp-f-03-0-UI.s1 NCI_CGAP_Sub4 Homo sapiens cDNA clone IMAGE:2727677 3'	Bartonella clarridgeiae RNA polymerase beta subunit (rpoB) gene, partial cds	Pimpinella brachycarpa zinc finger protein (ZFP1) mRNA, complete cds	Human Fo-gamma-receptorIIA (FCGR2A) gene, exon 4	601466703F1 NIH_MGC_67 Hamo sapiens cDNA clone IMAGE:3869929 5	Homo sapiens epidemal growth factor receptor (avian erythroblastic leukemia viral (v-erb-b) oncogene Promoten (FGER) mRNA	Homo sapiens phytanoyl-CoA hydroxylase (PHYH) gene, exon 5	RC5-BT0503-271199-011-B01 BT0503 Homo sapiens cDNA	Bovine papillomavirus type 2, complete genome	Bovine papillomavirus type 2, complete genome	Homo sapiens nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 (NFKB1) gene, complete	רינים סיים מיינים	Spodoptera frugiperda methykenetatranydrofolate dehydrogenase mRNA, complete cds	Plesmodium falciparum mature parasite-infected enythrocyte surface antigen (MESA) gene, complete ods	oe09b03.s1 NCI_CGAP_Ov2 Homo sapiens cDNA clone IMAGE:1385357	Xenopus laevis CCCH zinc finger protein C3H-2 (C3H-2) mRNA, complete cds	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 34
Top Hit Database Source	NT	ΙN	NT	ΝŢ	EST_HUMAN	EST_HUMAN	F	ł	2 5	- A	ESI HOMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	NT.	TN	F	EST_HUMAN	ΤΙ	L	EST_HUMAN	FZ	NT.	F	Į.	TN.	L	EST_HUMAN	F	TN
Top Hit Acession No.	9.6E-01 AF197881.1	(95275.1	81138.1	9.6E-01 AF041427.1	9.8E-01 AV752605.1	9.6E-01 AV752605.1	11421722 NT		J914Z3.1	I N Lecon /	9.5E-01 BE902340.1	9.5E-01 BE902340.1	9.5E-01 AI190162.1	9.5E-01 AW861102.1		9.5E-01 AW 293799.1		9.4E-01 AF080595.1	9.4E-01 M90724.1	9.4E-01 BE781251.1	11410857	9.3E-01 AF242382.1	9.3E-01 BE071172.1	9.3E-01 M20219.1	M20219.1	V F243884 4	9.3E-01 Ar 213004. I	-36189.1	9.3E-01 AF270648.1	9.3E-01 AA847040.1	9.3E-01 AF061981.1	9.3E-01 AL161534.2
Most Similar (Top) Hit BLAST E Value	9.6E-01	9.6E-01	9.6E-01 L81138.1	9.6E-01	9.6E-01	9.6E-01	9.6E-01		9.6E-01 U91423.1	9.35-01	9.5E-01	9.5E-01	9.5E-01	9.5E-01	9.5E-01	9.5E-01	9.4E-01	9.4E-01	9.4E-01	9.4E-01	10	9.3E-01	9.3E-01	9.3E-01	9.3E-01	0.35	8.3E-01	9.3E-01 L36189.1	9.3E-01	9.3E-01	9.3E-01	9.3E-01
Expression Signal	0.63	1.52	0.92	1.42	3.91	3.91	1.31		3.68	1.0.1	2.1	2.1	0.71	1.04	1.56	1.57	5.72	2.17	0.79	1.86	* *	1.24	3.62	0.86	0.86	4	0	3.48	1.08	1.99	1.1	0.89
ORF SEQ ID NO:	34059		32675	38060	38496	38497			31656	78/34	30038	30039	35819	35933	38254	37548			35692				28934	30289	30290			32289		34856		35760
Exan SEQ ID NO:	20586	21667	22131	24408	24798	24798	25174			0/061	1/041	17041	22280			23923	16445	16463	22145		25075		15818	17298			-[	18986	20561	21339	22092	
Probe SEQ ID NO:	7512	8586	9052	11346	11808	11808	12225		12915	C\$67	3882	3882	9202	9306	11520	11737	3271	3289	9906	12496	1,004	1769	2699	4146	4146	5700	an/o	5795	7486	8257	9013	9137

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Probe SEQ ID NO:	Exan SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acessian No.	Top Hit Database Source	Top Hit Descriptor
13039	25683	31961	2.09	9.3E-01	11440298 NT	LN	Homo sapiens inositol 1,4,5-triphosphate receptor, type 2 (ITPR2), mRNA
13049	25688		1.22	9.3E-01	9.3E-01 AF271207.1	TN	Aedes triseriatus putative large subunit ribosomal protein rpL34 mRNA, complete cds
3311	16484	29505	3.92	9.2E-01		EST_HUMAN	601441338T1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:39161843'
4999			0.64	9.2E-01	9.2E-01 BF129973.1	EST HUMAN	601817814F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4041363 5'
5835			1.58	9.2E-01	7105410 NT	LN <sub>T</sub>	Mus musculus solute carrier family 30 (zinc transporter), member 4 (Slc30a4), mRNA
6109	19289	32624			1.1	EST_HUMAN	601461153F1 NIH_MGC_66 Homo saplens cDNA clone IMAGE:3864661 5
6770	19925	33320	0.65	9.2E-01	9.2E-01 M64703.1	LN	N.crassa valyt-tRNA synthetase (cyt-20/un-3) gene
9860			86.0		9.2E-01 AL161565.2	TN	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 65
9949	1			9.2E-01	6671677 NT	Ł	Mus musculus carbonic anhydrase 4 (Car4), mRNA
10472	23507	37120	3.6	9.2E-01	11430963 NT	TN	Homo sapiens lysosomal apyrase-like protein 1 (LALP1), mRNA
10627	23661	37269	1.64		9.2E-01 BF593251.1	EST HUMAN	7o58e06.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3578219 3' similar to SW:NU5M_TRYBB P04540 NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 5;
10883	L				9.2E-01 BE563811.1	EST_HUMAN	601334943F1 NIH_MGC_39 Homo saplens cDNA clone IMAGE:3688714 5
12022	25006				9.2E-01 BF132402.1	EST_HUMAN	601820312F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4052018 5'
200		0.700.0	7 62		0.45 04 TOSSZE 4	NAME IN FOR	ye52f01.s1 Soares fetal liver spleen 1NFLS Homo sepiens cDNA clone IMAGE:121369 3' similar to contains all remetiting element:
200	7007				THOOLE BOOK	NUMBER PROPERTY.	Homo sariens brootheffeel profein FI (20048 / FI (20048) mRNA
32	1		4.				
3275	16449	29468	1.28		9.1E-01 T26418.1	EST_HUMAN	AB200G8R Infant brain, LLNL array of Dr. M. Scares 1NIB Homo saplens cDNA clone LLAB200G8 5'
3275	i	29469	1.28		9.1E-01 T26418.1	EST HUMAN	AB200G8R Infant brain, LLNL array of Dr. M. Soares 1NIB Homo sapiens cDNA clone LLAB200G8 5'
6296	1		1.54	_	9.1E-01 L38033.1	FZ	Human pre-B cell stimulating factor homologue (SDF1b) mRNA, complete cds
6635	19794					SWISSPROT	INTER-ALPHA-TRYPSIN INHIBITOR HEAVY CHAIN H3 PRECURSOR (ITI HEAVY CHAIN H3)
7750		34300	17.46			EST_HUMAN	ob71g08.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1336862 3
7916	20967	34473	2.81	9.1E-01	9.1E-01 U72995.1	LN	Rattus norvegicus Rab3 GDP/GTP exchange protein mRNA, complete cds
10379		L	0.6		9.1E-01 P38432	SWISSPROT	P80-COILIN
12595	L		19.67		9.1E-01 AF050113.1	NT	Hamo sapiens uncoupling protein-3 (UCP3) gene, complete cds
3277	L_	29472	0.8	. 9.0E-01	7661625 NT	NT.	Homo sapiens DKFZP564M2423 protein (DKFZP564M2423), mRNA
, 3439	16607		0.73		9.0E-01 AL161515.2	NT ·	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 27
4219	17368	33367	99.0		N 8922310 NT	TN	Homo sepiens hypothetical protein FLJ10251 (FLJ10251), mRNA
4498	3 17638	30620	1.43		9.0E-01 AF099810.1	ΤN	Homo sapiens neurexin III-alpha gene, partial cds
5127	18252	31218	13.05		9.0E-01 AF017729.1	NT	Oryctolagus cuniculus Rad51 (RAD51) mRNA, complete ods
7551		34100			9.0E-01 L42547.1	느	Danio rerio LIM class homeodomain protein (ilm5) mRNA, complete cds
7579	9 20651		1.42		9.0E-01 D38621.1	LN.	Xenopus laevis gene for aldolase, complete cds

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Top Hit Descriptor	Danio rerio semaphorin Z1a mRNA, complete cds	Mycoplasma genitalium section 24 of 51 of the complete genome	Mus musculus neuromedin U precursor (Nmu) gene, partial ods; tPhLP (Tphlp) gene, partial ods; CLOCK (Clock) gene, complete ods; PFT27 (Pft27) gene, complete ods; and H5AR (H5ar) gene, complete ods	Fugu rubripes neural cell adhesion molecule L1 homolog (L1-CAM) gene, complete cds; putative protein 1 (PUT1) gene, partial cds; mitosis-specific chromosome segregation protein SMC1 homolog (SMC1) gene, complete cds; and calcium channel alpha-1 subunit>	Rabbit MHC fragment RLA-DF DNA	N 601882708F1 NIH_MGC_57 Hamo sepiens cDNA clone IMAGE:4095216 5	N 601882708F1 NIH MGC 57 Homo saplens cDNA clone IMAGE:4095216 5'	Otthone nana cytochrome-c oxidase subunit I (coxl) gene, partial cds; mitochondrial gene for mitochondrial product	Xyletla fastidiosa, section 90 of 229 of the complete genome	Chlamydophile pneumoniae AR39, section 21 of 94 of the complete genome		Pseudorables virus Ea glycoprotein M gene, complete cds	Homo sapiens peroxisomal 70 kD membrane protein mRNA, complete cds	Homo sapiens cell death-inducing DFFA-like effector B (CIDEB), mRNA	M.aeruginosa (HUB 5-2-4) DNA from plasmid PMA1	oc38h11.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1352037 3' similar to contains Alu repetitive element;contains element MER22 repetitive element;		Homo sapiens SOS1 (SOS1) gene, partial cds	Homo caplens AT-binding transcription factor 1 (ATBF1), mRNA	IN nn05f11.s1 NCI_CGAP_Pr4.1 Homo saplens cDNA clone IMAGE:1076877	Pseudomonas aeruginosa topoisomerase (top), putative transcriptional regulatory protein OhbR (ohbR), ortho- halahanande 1 3-dimensional page ISD partein OhbA (AphA) OhbC (AphC), ortho-halahanande 1 3-	ilabounteaa i.z-unolygenase peranci. Protein Crisch, Ono (crisch, crischiagea) i.z. dioxygenase alpha-ISP protein OhbB (ohbB), and put>	Г	"N qh36e06.x1 Soares_NFL_T_GBC_S1 Homo saplens cDNA clone IMAGE:1846786 3"		Pseudomonas aeruginosa PA01, section 524 of 529 of the complete genome	IN 602185541T1 NIH_MGC_45 Homo saplens oDNA clone IMAGE:4309906 3'
. Top Hit Database Source	F	ΤN	F	Ę	ΙN	EST HUMAN	EST_HUMAN	۲	F	μ	SWISSPROT	ΝΤ	N	FN	IN	EST HUMÂN	N.	NT LX	N	EST_HUMAN		Ę	EST HUMAN	EST_HUMAN	EST_HUMAN	۲	EST HUMAN
Top Hit Acession No.	9.0E-01 AF086761.1	9.0E-01 U39702.1	9.0E-01 AF146793.2	8.9E-01 AF026198.1	8.9E-01 X60986.1	8.9E-01 BF217939.1	8.9E-01 BF217939.1	8.9E-01 AF259667.1	8.9E-01 AE003944.1	8.9E-01 AE002186.2	026350	8.8E-01 AF310617.1	8.8E-01 M81182.1	T056978 NT	8.8E-01 Z28337.1	8.8E-01 AA808055.1	8.8E-01 D90911.1	8.7E-01 AF106953.2	5901893 NT	8.7E-01 AA595863.1		8.7E-01 AF121970.1	8.7E-01 AW897335.1	8.7E-01 AI239456.1	8.7E-01 AI239456.1	8.7E-01 AE004963.1	8.7E-01 BF570169.1
Most Similar (Top) Hit BLAST E Value	9.0E-01	9.0E-01	9.0E-01	8.9E-01	8.9E-01	8.9E-01	8.9E-01	8.9E-01	8.9E-01	8.9E-01	8.8E-01 O26350	8.8E-01	8.8E-01	8.8E-01	8.8E-01	8.8E-01	8.8E-01	8.7E-01	8.7E-01	8.7E-01		8.7E-01	8.7E-01	8.7E-01	8.7E-01	8.7E-01	8.元句
Expression Signal	0.68	0.48	1.41	2.6	1.28	0.82	0.82	0.92	2.72	4.02	2.11	99'0	69.0	1.07	2.23	7.56	2.13	2	. 0.98	5.32		4.12	0.66	0.66	99'0	2.07	1.08
ORF SEQ ID NO:		36673	38797	32309		33134	33135	35237	38766		30786			$\Big _{-}$	38049	38779		26704		29127				35752		36569	İ
SEO D NO:			25093	19004	19547	1	ı	21701	25060	25300	17799	18688	20766	ı	24400	25072	1	13672	15602	l		18246	21311			22978	1_
Probe SEQ ID NO:	9549	10035	12113	5814	6378	6590	9290	8621	12080	12423	4664	2488	7701	10436	11337	12092	12240	477	2475	2838		5120	8229	9130	9130	6866	10511

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Top Hit Descriptor	60218554171 NIH_MGC_45 Homo sapiens cDNA clone IMAGE:4309906 3'	QV6-NN1021-100800-337-c03 NN1021 Homo sapiens cDNA	601823684R1 NIH_MGC_79 Homo sapiens cDNA clone IMAGE:4043564 3'	601823684R1 NIH_MGC_79 Hamo sapiens cDNA clane IMAGE:4043564 3'	AV661898 GLC Homo saplens cDNA clone GLCGYG07 3'	Rat IGFII gene for insulin-like growth factor II	zd44e03.r1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:343518 5'	Homo sapiens cytochrome P450, subfamily XXVIIA (steroid 27-hydroxylase, cerebrotendinous xanthometrasis), polymeotide ( (CYP27A1b) mRNA	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 65	Drosophila melanogaster merlin (Dmerlin) mRNA, complete cds	Chicken lipoprotein lipase gene	Chicken lipoprotein lipase gene	polyprotein [Coxsackie B4 virus CB4, host≕mice, E2, originally derived from Edwards CB4 human strain,	Genomic RNA Complete, 7397 nt]	Grus canadensis recombination activating protein 1 (RAG-1) gene, partial cds	Grus cenadensis recombination activating protein 1 (RAG-1) gene, partial cds	Helicobacter pylori 26895 section 69 of 134 of the complete genome	Bacillus halodurans genomic DNA, section 12/14	Drosophila melanogaster collapsin response mediator protein (CRMP) mRNA, complete cds	Archaeoglobus fulgidus section 128 of 172 of the complete genome	Botrytis cinerea strain T4 cDNA library under conditions of nitrogen deprivation	Arabidopsis thaliana (ecotype Columbia) spl2 gene, exons 1-5	Bacteriophage D3, complete genome	601067107F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3453505 5'	Arabidopsis thallana DNA chromosome 4, contig fragment No. 68	SEGMENTATION PROTEIN PAIRED	SEGMENTATION PROTEIN PAIRED	Homo sapiens partial 5-HT4 receptor gene, exons 2 to 5	Cyanidium caldarium gene for SIgC, complete cds	Oyanidium caldarium gene for SigC, complete cds	Homo sapiens human immunodeficiency virus type I enhancer-binding protein 1 (HIVEP1), mRNA	Rattus norvegicus protein tyrosine phosphatase, non-receptor type 5 (Ptpn5), mRNA	Fowl adenovirus 8, complete genome
Top Hit Database Source	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN		EST_HUMAN	F			NT	Į.		NT	NT	LN	NT	NT	IN	IN	۲N	. IN	NT	EST HUMAN	NT	SWISSPROT	SWISSPROT	LN		LN	NT	N <sub>T</sub>	뒫
Top Hit Acession No.	8.7E-01 BF570169.1	3F363970.1	8.7E-01 BF107694.1	3F107694.1		8.6E-01 X17012.1	W69089.1	TN 0125034	8.6E-01 AL161565.2	J49724.1	X60547.1	6E-01 X60547.1		6E-01 S76772.1	4F143732.1	4F143732.1	8.6E-01 AE000591.1	4P001518.1	AF077837.1	4E000979.1	4L112162.1	8.5E-01 AJ011624.1	4F165214.1	BE542612.1	AL161572.2	P06601	8.5E-01 P06601	AJ243213.1	8.5E-01 AB006799.1	8.5E-01 AB006799.1	11418543 NT	8.5E-01 9507008 NT	AF083975.2
Most Similar (Top) Hit BLAST E Value	8.7E-01	8.7E-01	8.7E-01	8.7E-01	8.7E-01	8.6E-01	8.6E-01	20 E	8.6E-01	8.6E-01	8.6E-01 X80547.1	8.6E-01		8.6E-01	8.6E-01	8.6E-01	8.6E-01	8.6E-01	8.6E-01	8.6E-01	8.6E-01	8.5E-01	8.5E-01	8.5E-01	8.5E-01	8.5E-01	8.5E-01	8.5E-01	8.5E-01	8.5E-01	8.5E-01	8.5E-01	8.4E-01
Expression Signal	1.08	5.87	3.32	3.32	2.8	2.39	3.14	707	0.85	1.31	10.02	10.02		0.7	1.98	1.98	0.64	1.82	0.56	0.54	2.11	1.46	1.1	2.36	0.57	0.92	0.92	99.0	1.49	1.49	5.29	6:39	0.68
ORF SEQ ID NO:	37157	37782		38721			27123	aceac	1.				L	33042	33409	33410			34834				33427	34243	34784	L	L	35315	37198	37199			30980
Exon SEQ ID NO:	23546	24145	25017	25017	25940	13681	14057	46476	16871	17060		19202	L.	25825	20001	20001	20761	21194	21314	22927	25883	15835	20018	20759		L		21782	23593	23593	26056		18006
Probe SEQ ID NO:	10511	11070	12034	12034	12652	487	881	2044	3710	3901	6019	6019		8059	6848	6848	7696	8112	8232	9887	12856	2509	9989	7694	8180	8613	8613	8702	.10558	10558	12577	12585	4873

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					,		
	Exon SEQ ID NO:	ORF SEQ ID NO:	Express	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
5611	25808		2.75		8.4E-01 L78726.1	TN	Human fibroblast growth factor receptor 3 (FGFR3) gene, Intron 7
5611	25808	31872			8.4E-01 L78726.1	IN	Human fibroblast growth factor receptor 3 (FGFR3) gene, intron 7
7991	21041	34553	0.57	8.4E-01	8.4E-01 AF051142.1	NT	Mamestra brassicae pheromone binding protein 2 precursor (PBP2) mRNA, complete cds
10163	23200		3.42		8.4E-01 A J 248287.1	IN	Pyrococcus abyssi complete gename; segment 5/6
92	13941	26986			8.3E-01 M93437.1	TN	Thermus thermophilus cytochrome c-552 (cycA) and CycB (cycB) genes, complete cds
3164	l	29347				TN.	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 18
3912			0.69		8.3E-01 AB010879.1		Nicotiana tabacum mRNA for chloroplast ribosomal protein L10, complete cds
4120	17274	30273	3.17	1	8.3E-01 Y19177.1		Streptomyces antibiciticus polyketide biosynthetic gene cluster
5383	18585				3.3E-01 AL161540.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 40
9870	22910		4		8.3E-01 AI791952.1	EST_HUMAN	nn01f12.y5 NCI_CGAP_Co9 Homo saptens cDNA clone IMAGE:1076495 5' similar to contains THR.t1 THR repetitive element;
10316	23351	36958	1.32		8.3E-01 AF098070.1	: L	Droscophila melanogaster Lis1 homolog mRNA, complete cds
10423	23458		3.9		8.3E-01 AF108133.1	Į,	Mus musculus neuro-d4 gene, exons 3 through 12 and partial cds
							Methanobacterium thermoaufotrophicum from bascs 1270510 to 1283409 (section 109 of 148) of the
10911	23994	37627	2.18		8.3E-01 AE000903.1		complete genome
10930	24012		1.65	8.3E-01	7212472 NT	NT	Phytophthora infestans mitochondrion, complete genome
11584	24637		96.6		8.3E-01 AF020503.1	NT	Homo sepiens FRA3B common fragile region, diadenosine triphosphate hydrolase (FHIT) gene, exon 5
2111	15249	28369	2.72		8.2E-01 AB000489.1	IN	Rattus norvegicus mRNA for RPHO-1, complete cds
2156	15292		1.32			П	Mus musculus trophinin (Tnn) gene, complete cds
2744			96'0		1	EST_HUMAN	IL3-CT0219-161199-031-C08 CT0219 Homo saplens cDNA
4009					1.1		Horno sapiens mRNA for KIAA0674 protein, partial cds
4247			2.0		8.2E-01 Z72584.1		S. cerevísiae chromosome VII reading frame ORF YGL062w
4247	17393						S.cerevisiae chromosome VII reading frame ORF YGL062w
5217	18338		1.19		8.2E-01 AB000489.1		Rattus norvegicus mRNA for RPHO-1, complete cds
6781	19936		65.0	)	8.2E-01 X95283.1	IN IN	G.gallus mRNA for C-Serrate-1 protein
6781	19836				8.2E-01 X95283.1	님	G.gallus mRNA for C-Serrate-1 protein
6913	1				8.2E-01 AJ010142.1		Amanita muscarla mRNA for SCIII25 protein
7037	20173				8.2E-01 AW379433.1	EST_HUMAN	CM4-HT0243-081199-037-e01 HT0243 Homo sapiens cDNA
7419	25844	33966			B.2E-01 Z12126.1	TN	S.ccrevistac MET, LEU4, and POL1 genes encoding MET4 protsin, alpha-isoproplymalate (alpha-IPM) synthetase (partial), and DNA polymerase alpha (partial)
6298		ĺ	0.55		5.1	EST_HUMAN	601144885F2 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3160412 51
10231	23266					NT .	Homo saplens mRNA for KIAA0830 protein, partial cds
10264	23299	36897	1.51	8.2E-01	8.2E-01 AF052659.1	NT	Homo sapiens thioredoxin-related protein mRNA, complete cds

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Top Hit Descriptor	Oncorhynchus tshawytscha Isolate T-20 somatolactin precursor gene, exon 1	Oncorhynchus tshawytscha isolate T-20 somatolactin precursor gene, exon 1	MCKUSICK-KAUFMAN/BARDET-BIEDL SYNDROMES PUTATIVE CHAPERONIN	MCKUSICK-KAUFMANIBARDET-BIEDL SYNDROMES PUTATIVE CHAPERONIN	Molluscum contagiosum virus type 1 ORF1 and ORF2 DNA	OVARIAN TUMOR LOCUS PROTEIN	w14d02.r1 Soares_placenta_8to9weeks_ZNbHP8to9W Homo saptens cDNA clone IMAGE:252195 5' similar to gb:M36072 60S RIBOSOMAL PROTEIN L7A (HUMAN);	Mus musculus mRNA for NIPSNAP2 protein	Mus musculus TANK binding kinase TBK1 (Tbk1) mRNA, complete cds	Homo sepiens MHC class 1 region	Homo sapiens MHC class 1 region	Horno sapiens protein tyrosine phosphatase, non-receptor type 2 (PTPN2) mRNA	MELANOCYTE STIMULATING HORMONE RECEPTOR (MSH-R) (MELANOTROPIN RECEPTOR) (MELANOCORTIN-1 RECEPTOR) (MC1-R)	Mus musculus putative collagen alpha-2 (XI) chain (COL11A2) gene, partial cds	NEURONAL MEMBRANE GLYCOPROTEIN M6-B	NEURONAL MEMBRANE GLYCOPROTEIN M6-B	CYTOCHROME B	Drosophila melanogaster putative inorganic phosphate cotransporter (Picot) gene, partial eds; putative sodium channel (Nach) and putative am/asse-related protein (Amyrel) genes, complete ods; and putative serifie-	enriched protein (gprs) gene, partial cd>	Drosophila melanogaster putative inorganic phosphate cotransporter (Picot) gene, partial cds; putative sodium	channel (Nach) and putative amylase-related protein (Amyrel) genes, complete cds; and putative serine-	enriched protein (gprs) gene, partial cd>	Bacillus halodurans genomic DNA, section 11/14	Bacillus helodurans genomic DNA, section 11/14	xn01h03.x1 NC _CGAP_Kd11 Homo sapiens cDNA done IMAGE:2692469 3' similar to SW:LYAR_MOUSE Q08298 CELL GROWTH REGULATING NUCLEOLAR PROTEIN ; contains MER22.br PTR5 repetitive	element;	PROBABLE E4 PROTEIN	KK9972F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA clone KK9872 5' similar to EST(CLONE C-0PE11)	Trepanema pallidum section 42 of 87 of the complete genome
Top Hit Database Source	F	LZ FZ		SWISSPROT	LZ LZ	SWISSPROT	EST HUMAN	Į.	LN TN	NT TN	I IN		SWISSPROT		SWISSPROT	SWISSPROT		<u>.</u>	E			NT		Į.	~	EST_HUMAN	SWISSPROT	_	뒫
Top Hit Acession No.	.2E-01 AF223888.1				2E-01 L10127.1		3.2E-01 H87398.1	3.2E-01 AJ001281.1		8.1E-01 AF055066.1	8.1E-01 AF055066.1	4506290 NT	001727	3.1E-01 U16790.1	013491	Q13491			8.1E-01 AF022713.2			8.1E-01 AF022713.2	8.1E-01 AP001517.1	8.1E-01 AP001517.1		8.1E-01 AW242647.1	P06425		8.1E-01 AE001226.1
Most Similar (Top) Hit BLAST E Value	8.2E-01	8.2E-01	8.2E-01 Q9JI70	8.2E-01 Q9JI70	8.2E-01	8.2E-01 P10383	8.2E-01	8.2E-01	8.1E-01	8.1E-01	8.1E-01	8.1E-01	8.1E-01 Q01727	8.1E-01	8.1E-01 Q13491	8.1E-01	8.1E-01 047477		8.1E-01			8.1E-01	8.1E-01	8.1E-01		8.1E-01	8.1E-01 P06425	8.1E-01	8.1E-01
Expression Signal	0.54	0.54	3.78	3.78	4.72	6.12	3.97	3.01	1.38	2.77	277	0.63	0.63	0.89	2.17	2.17	2.0		1.1			1.1	0.91	0.91		1.14	0.58	0.62	0.54
ORF SEQ ID NO:				37240		38715	38722			29723			32321			ľ			34693			34694		35429		36691		37267	
Exan SEQ ID NO:	1	23463		ı	ı	25013	25018	l	l	16712	16712	17865	19015	L	19915				21177			21177		21887		22048		ŀ	23802
Probe SEQ ID NO:	10428	10428	10596	10596	11942	12030	12035	12607	2817	3547	3547	4730	5825	6445	62.29	6229	7681		8095			8095	8088	8808		6968	10330	10823	10769

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	Top Hit Descriptor	RCG-TN0080-220800-025-d10 TN0080 Homo sapiens cDNA	RC0-TN0080-220800-025-d10.TN0080 Homo sapiens cDNA	Thermotoga maritima section 23 of 136 of the complete genome	Staphylococcus aureus partial pta gene for phosphate actyltransferase allele 15	Bos faurus futb and rtif genes	602072473F1 NCI_CGAP_Brn67 Homo saplens cDNA clone IMAGE:4215091 5'	Saimiri boliviensIs olfactory receptor (SBO27) gene, partial cds	Mus musculus gene for cviductal glycoprotein, complete cds	G.gallus mRNA for nicotinic acetylcholine receptor (nAChR) beta 3 subunit	Mus musculus myosin IXb (Myo9b), mRNA	RCO-NN1012-270300-021-h06 NN1012 Homo sapiens cDNA	Rice stripe virus RNA 3	QV3-0T0065-280600-250-c09 OT0065 Homo sapiens cDNA	Gallus galluc PPAR gamma mRNA for peroxisome proliferator-activated receptor, complete cds	CREB-BINDING PROTEIN	Lymantria dispar nuclear polyhedrosis virus gene for DNA polymerase, complete cds	Ureaplasma urealyticum section 31 of 59 of the complete genome	Homo saplens mRNA for KIAA1452 protein, partial cds	Haemophilus influenzae Rd section 54 of 163 of the complete genome	Oryctolagus cuniculus mRNA for mitsugumin29, complete cds	Danio rerio Trp4-associated protein Tap1A (tap1A) mRNA, complete cds	Gallus gallus SOX8 transcription factor (SOX8) mRNA, complete cds	601192033F1 NIH_MGC_7 Homo sapiens cDNA done IMAGE:3535785 5'	Mus musculus embigin (Emb), mRNA	Mus musculus embigin (Emb), mRNA	Mus musculus enabled homdog (Drosophila) (Enah), mRNA	S.pneumoniae dexB, cap3A, cap3B and cap3C genes and orfs	S.pneumoniae dexB, cap3A, cap3B and cap3C genes and orfs	Chrysomya bezziana peritrophin-48 precursor, gene, complete cds	Humen mRNA for prostacyclin cynthasc, complete ods	P.sativum GR gene	Giardia lamblia variant-specific surface protein G3M-B (vspG3M-B) mRNA, partial cds	SMALL HYDROPHOBIC PROTEIN	AV700860 GKC Homo sapiens cDNA clone GKCDRE123'
	Top Hilt Database Source	EST_HUMAN	EST_HUMAN	Ā	ᅜ	Ł	EST_HUMAN	M	ħ	NT	ΤN	EST_HUMAN	NT	EST_HUMAN	TA	SWISSPROT	TN	NT	NT	ΝΤ	N	ΝΤ	LN	EST_HUMAN	NT	NŢ	TN	LN L	ΙΝ	TN	NT	NT	ΤN	SWISSPROT	EST_HUMAN
S)	Top Hit Acession No.	8.1E-01 BE938558.1	8.1E-01 BE938558.1	8.1E-01 AE001711.1	8.0E-01 AJ271510.1	8.0E-01 AJ132772.1	8.0E-01 BF530962.1	8.0E-01 AF127897.1	8.0E-01 AB006183.1	X83739.2	7667352 NT	8.0E-01 AW901489.1	Y11095.1	8.0E-01 BE833326.1	8.0E-01 AB045597.1	292793	D11476.1	7.9E-01 AE002130.1	7.9E-01 AB040885.1	J32739.1	7.9E-01 AB004816.1	7.9E-01 AF130459.1	7.9E-01 AF228664.1	BE263612.1	6753745 NT	6753745 NT	6753753 NT	247210.1	247210.1	7.9E-01 AF139718.1	J38145.1	X90996.1	J01912.1	P19719	7.9E-01 AV700860.1
	Most Similar (Top) Hit BLAST E Value	8.1E-01	8.1E-01	8.1E-01/	8.0E-01	8.0E-01	8.0E-01	8.0E-01	8.0E-01	8.0E-01 X83739.2	8.0E-01	8.0E-01	8.0E-01 Y11095.1	8.0E-01	8.0E-01	8.0E-01 Q92793	7.9E-01 D11476.1	7.9E-01	7.9E-01	7.9E-01 U32739.1	7.9E-01	7.9E-01	7.9E-01	7.9E-01	7.9E-01	7.9E-01	7.9E-01	7.9E-01 Z47210.1	7.9E-01 Z47210.1	7.9E-01	7.9E-01 D38145.1	7.9E-01 X90996.1	7.9E-01 U01912.1	7.9E-01 P19719	7.9E-01
	Expression Signal	2.62	2.62	2.22	2.62	10.2	1.95	1.32	1.29	6.77	1	2.66	1.21	0.48	0.48	1.43	0.75	0.92	28.32	1.06	9.03	4.11	3.57	0.87	0.84	0.84	99.0	0.93	0.93	99.0	0.68	2.68	3.24	5.43	1.17
	ORF SEQ ID NO:	38459	38460	32102		26549		29334	23572	30775	31196		35338		37483	37902	26697				28603	. 28604				30853		31325	31326		23003	34903	36390		36934
	Exon SEQ ID NO:	24764	24764	25221	13404	13516	15233		16557	17791	18224	21261	21802	23669	23860	24267	13661	13915	14787	14839	15468	15469	16769	17557	17869	17869	18331	<u> </u>	18357	18402	19642	21382	22811		1
	Probe SEQ ID NO:	11772	11772	12303	181	289	2093	3146	3387	4655	9609	8179	8722	10635	10827	11198	466	733	1835	1887	2337	2338	3806	4416	4734	4734	5210	5235	6235	6283	6475	8300	9747	10255	10298

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signel	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
10729	23762	37369	0.78	7.9E-01	7.9E-01 AB000631.1	LΝ	Streptococcus mutans DNA for sigma 42 protein, dTDP-4-keto-L-rhamnose reductase, complete cds
10845		37498	0.61	7.9E-01	7.9E-01 P15305	SWISSPROT	DYNEIN HEAVY CHAIN (DYHC)
11256	24325		1.75	7.9E-01	7662471 NT	NT	Homo capiens KIAA1072 protein (KIAA1072), mRNA
11487	24546	38218	1.94	7.9E-01 P19022	P19022	SWISSPROT	NEURAL-CADHERIN PRECURSOR (N-CADHERIN)
668	14074		1.49	7.8E-01	7.8E-01 Z43785.1	EST_HUMAN	HSC1KH041 normalized Infant brain cDNA Homo sapiens cDNA clone c-1kh04
2349			6:99	7.8E-01	7.8E-01 AW959567.1	EST_HUMAN	EST371637 MAGE resequences, MAGF Homo sepiens cDNA
4823	17956		0.73	7.8E-01	7.8E-01 U87305.1	Ā	Rattus norvegicus transmembrane receptor Unc5H1 mRNA, complete cds
5149	18271		0.89	7.8E-01	7.8E-01 AW753353.1	EST_HUMAN	RC3-CT0254-130100-023-c02 CT0254 Homo sapiens cDNA
6194	19370	32721	2.26	7.8E-01	7.8E-01 AF116856.1	IN	Sphenodon punctatus alpha enolase mRNA, partial cds
	l					٠,	INTERLEUKIN-6 PRECURSOR (IL-6) (B-CELL STIMULATORY FACTOR 2) (BSF-2) (INTERFERON
6348			2.28	7.8E-01 P05231		SWISSPROT	BETA-2) (HYBRIDOMA GROW TH FACTOR)
6591	19761	33136	0.84	7.8E-01	7.8E-01 AL445066.1	NT	Thermoplasma acidophilum complete genome; segment 4/5
8698	21768	35299	1.13	7.8E-01	7.8E-01 BF108927.1	EST_HUMAN	7154d05.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:3525176 3
9434	22508		1.53	7.8E-01	7.8E-01 Y10159.1	NT	D.discoideum racGAP gene
9533	22598	36170	0.56	7.8E-01	4826873 NT	Ā	Homo sapiens nucleoporin 214kD (CAIN) (NUP214), mRNA
10329	23364		1.28	7.8E-01	7.8E-01 Q25452	SWISSPROT	MUSCLE CALCIUM CHANNEL ALPHA-1 SUBUNIT (MDL-ALPHA1)
12571	26033		1.92	7.8E-01	7.8E-01 L29260.1	NT	Arabidopsis thaliana 1-amino-1-cyclopropanecarboxylate synthase (ACS5) gene, complete cds
146	13371	26403	5.78	7.7E-01	7.7E-01 AF184345.1	LΝ	Lycopersicon hirsutum ADP-glucose pyrophosphorylase large subunit (AGP-L1) mRNA, complete cds
	1						Mus musculus major histocompatibility locus class II region: major histocompatibility protein class II alpha
							chain (IAalpha) and major histocompatibility protein class il beta chain (IEbeta) genes, complete cds;
744	13925		1.72	7.7E-01	7.7E-01 AF050157.1	뉟	butyrophilin-like (NG9), butyrophilin-li>
2776	Ι.	29003	1.34	7.7E-01	7.7E-01 033915	SWISSPROT	CITRATE SYNTHASE
							Homo sapiens UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyliransferase 7
3438	16606		0.89	7.7E-01	8393408 NT	M	(GaINAC-T7) (GALNAC-T7), mRNA
3689	16851	29859	3.86	7.7E-01	7.7E-01 AF118085.1	MT	Homo sapiens PR01975 mRNA, complete cds
4516	17655	30643	3.38	7.7E-01	7.7E-01 AF199488.1	NT	Cofurnix cofurnix japonica sub-species japonica beta-actin mRNA, partial cds
4516	17655	30644	3.38	7.7E-01	7.7E-01 AF199488.1	IN	Coturnix coturnix japonica sub-species japonica beta-actin mRNA, partial cds
5678	18872		1.39	7.7E-01	7.7E-01 P16553	SWISSPROT	RAFFINOSE INVERTASE (INVERTASE)
5678	18872		1.39	7.7E-01	7.7E-01 P16553	SWISSPROT	RAFFINOSE INVERTASE (INVERTASE)
9209	19258	32587	1.41	7.7E-01	7.7E-01 R08600.1	EST_HUMAN	yr24b02.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:127755 3'
10049	23087		0.68		7.7E-01 AB021134.1	NT	Daphria magna hemoglobin gene cluster (dhb3, dhb1 and dhb2 genes), complete cds
12452	25317		7.14	7.7E-01	11497621 NT	NT	Archaeoglobus fulgidus, complete genome

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				_	_			_	_					_	_		_		_						· —	-	
Top Hit Descriptor	Arabidopsis thaliana 3-methylcrotonyl-CoA carboxylase non-blotinylated subunit (MCCB) mRNA, complete cds	Arabidopsis thaliana 3-methylorotony-CoA carboxylase non-blotinylated subunit (MCCB) mRNA, complete cds	MATING-TYPE PROTEIN A-ALPHA Z4	aq14b12.x1 Stanley Frontal NS pool 2 Homo sapiens cDNA clone IMAGE:2030879	aq14b12x1 Stanley Frontal NS pool 2 Homo sapiens cDNA clone IMAGE:2030879	Rattus norvegicus calcium-independent alpha-latrotoxin receptor mRNA, complete cds	Mus musculus neuromedin U precursor (Nmu) gene, partial ods; tPhLP (Tphlp) gene, partial ods; CLOCK (Clock) gene, complete cds; PFT27 (Pft27) gene, complete cds; and H5AR (H5ar) gene, complete ods	Mus musculus advillin (Advil-pending), mRNA	Mus musculus advillin (Advil-pending), mRNA	GLUTAMATE (NIMDA) RECEPTOR SUBUNIT EPSILON 3 PRECURSOR (N-METHYL D-ASPARTATE: RECEPTOR SUBTYPE 2C) (NR2C) (NIMDAR2C)	GLUTAMATE [NMDA] RECEPTOR SUBUNIT EPSILON 3 PRECURSOR (N-METHYL D-ASPARTATE	RECEPTOR SUBTYPE 2C) (NR2C) (NMDAR2C)	Mus musculus cytochrome P450, 2b9, phenobarbitol inducible, type a (Cyp2b9), mRNA	MUSCARINIC ACETYLCHOLINE RECEPTOR M2	MUSCARINIC ACETYLCHOLINE RECEPTOR M2	H.aspersa mRNA for neurofilament NF70	H.aspersa mRNA for neurofilament NF70	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 88	Homo sapiens mRNA for KIAA0895 protein, partial cds	Homo seplens chromosome 21 segment HS21C101	Homo sapiens FRA3B common fragile region, diadenosine triphosphate hydrolase (FHIT) gene, exon 5	Drosophila melanogaster tyrosine kinase receptor protein (eph) mRNA, complete cds	Homo saplens dentin sialophosphoprotein precursor (DSPP) gene, complete cds	tr14b09.x1 NCI_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2167577 3' similar to contains Alu	repetitive element; contains element MIR repetitive element ;	Homo sapiens mRNA for KIAA0534 protein, partial cds	Maha pusilia actin (Act1) mRNA, complete cds
Top Hit Database Source	IN	LN	SWISSPROT	EST_HUMAN	HUMAN		. LN			SWISSPROT	Π	SWISSPROT		SWISSPROT	ISSPROT					NT	F	ĮN.	ΕN		T HOMAN		Į.
Top Hit Acession No.	6E-01 AF059510.1	6E-01 AF059510.1		.6E-01 Al253399.1			6E-01 AF146793.2	6857752 NT	6857752 NT	6E-01 001098			6753577			.6E-01 X86347.1		.6E-01 AL161592.2	.6E-01 AB020702.1	.5E-01 AL163301.2	5E-01 AF020503.1	.5E-01 AF052730.1	5E-01 AF163151.2		T		4E-01 AF112538.1
Most Similar (Top) Hit BLAST E Value	7.6E-01	7.6E-01	7.6E-01	7.6E-01	7.6E-01	7.6E-01	7.6E-01	7.6E-01	7.6E-01	7.6E-01		7.6E-01 Q01098	7.6E-01	7.6E-01	7.6E-01	7.6E-01	7.6E-01	7.6E-01	7.6E-01	7.5E-01	7.5E-01	7.5E-01	7.5E-01		7.4E-01	7.4E-01	7.4E-01
Expression Signal	5.26	5.26	99.0	0.74	0.74	0.84	154	2.38	238	0.53		0.53	1.33	5.24	5.24	2.29	2.29	2.78	8.21	1.31	1.08	8.0	5.2		1.61	0.97	0.97
ORF SEQ ID NO:	32748	32749	33193	31501		33472	34855	34924	34925	35137		35138	35789	36100	36101	11488	38412				26807	34240		İ			29983
Exan SEQ ID NO:	19399	19399	19806	18509	L.	20061	24337	21400	21400	21601	L		22245			24719	24719	24995	25157	13719	13787		25354		- 1		16980
Probe SEQ ID NO:	6224	6224	6647	0669	0669	7196	8255	8318	8318	8520		8520	9167	9479	9479	11639	11639	12010	12203	526	597	7690	12521		1154	2419	3820

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				•			
Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Vatue	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
4010	17167	30175	0.71	7.4E-01	4E-01 AF133310.1	TN	Vibrio cholerae phage CTXphi Calcutta-rstR-a (rstR-a) and Calcutta-rstR-b (rstR-b) genes, complete cds
4429	17569	30551	8.12	7.4E-01	.4E-01 AL163246.2	Ę	Homo sapiens chromosome 21 segment HS21C046
8027	21110	34628	1.25	7.4E-01	.4E-01 AL161551.2	NT	Arabidopsis thallana DNA chromosome 4, contig fragment No. 51
8027	21110	34629	1.25	7.4E-01		IN	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 51
8834	21913		1.01	7.4E-01	.4E-01 BF346266.1	EST_HUMAN	602018456F1 NCI_CGAP_Brn67 Homo saplens cDNA clone IMAGE:4154340 5'
- 8	00070	_	,	_	7 00000	ļ.	Ratus norvegicus leukocyte common antigen receptor (LAR) gene, trans-spliced atternative untranslated
0100	69617				4E-01 U8/900.1	- HOL	ESAETODEET NILL MOD & Lower conjuing Albae IMAGE 19824474 R
9298	22374	35925	98.9	7.4E-01	.4E-01 BE747503.1	EST_HUMAN	5015/3020F1 NIM MGC_9 Home sapiens GUIVA gione IMAGE 3641/4 5
9357	22432	35990	1.24	7.4E-01	.4E-01 AA187986.1	EST_HUMAN	zp67h01.s1 Stratagene endothelial cell 837223 Homo sapiens cDNA clone IMAGE:625297 3' similar to SW:TCPQ_MOUSE P42832 T-COMPLEX PROTEIN 1, THETA SUBUNIT;
10613	23647	37256	0.7	7.4E-01	11424933	. LN	Homo sapiens NY-REN-45 antigen (LOC51133), mRNA
12170	25133		3.69	7.4E-01	6753217 NT	NT	Mus musculus complement component 1 inhibitor (C1nh), mRNA
12287	25213		1.7	7.4E-01	.4E-01 AI472641.1	EST_HUMAN	ta13h01.x1 NCI_CGAP_Lym5 Homo sapiens cDNA clone IMAGE:2043985 3'
4083	17238		67.0	4	.3E-01 AP000062.1	LN	Aeropyrum pernix genomic DNA, section 5/7
4738	17873	30858	8.0	<u>.                                    </u>	.3E-01 AE001166.1	NT	Borrella burgdorferi (section 52 of 70) of the complete genome
4822	17955		2.38	_	.3E-01 AF225421.1	NT	Homo sapiens HT017 mRNA, complete cds
6741	19897	33287	5.5	7	.3E-01 L35772.1	NT	Mus musculus antigen (CD72) gene
6741	19897	33288		1	.3E-01 L35772.1	TN	Mus musculus antigen (CD72) gene
7243	25841	33771		_	.3E-01 AJ011418.1	NT	Lycopersicon esculentum mRNA for ubiquitin ectivating enzyme
7617	ı	34163			.3E-01 Z14133.1	TN	D.melanogaster Chc mRNA for clathrin heavy chain
7718	ı		7,25	۷	.3E-01 M26511.1	NT	V. alginolyticus sucrase (scrB) gene, complete cds
7718	20782			7	.3E-01 M26511.1	TN	V.alginolyticus sucrase (scrB) gene, complete cds
11714	24754	38448	3.29	_	.3E-01 AA678019.1	EST_HUMAN	zi25508.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:431799 3'
11714	24754	38449		7	.3E-01 AA678019.1	EST_HUMAN	zi25508.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:431799 3'
854	14031				.2E-01 L29281.1	IN	Rattus norvegicus initiation factor-2 kinase (elF-2a) mRNA, complete cds
2012	15152	28257	3.43	_		NT	N:tabacum NeiF-4A13 mRNA
2532	15657	28781	1.96		.2E-01 AB009605.1	NT	Gallus gallus gene for melanocortin 2-receptor, complete cds
3135	16311	29323		4	.2E-01 AF198100.1	NT	Fowhax virus, complete gename
3541	16705	71762	2.36		.2E-01 AF065606.1	LN.	Giardia intestinalis variant-specific surface protcin (vsp417-8) genc, vsp417-6/A-l allele, complete cds
3702	16863		1.35	2	2E-01 AB002307.1	TN	Human mRNA for KIAA0309 gene, partial cds
3975	l		1.57	7		EST_HUMAN	602035589F1 NCI_CGAP_Bm64 Homo saplens cDNA done IMAGE:4183222 5
4173	17323		0.73	4	2E-01 AF108093.1	LN	Homo sapiens IA-2 gene, inton 18

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·			<u>.                                    </u>	_	_,	_,		_	_		_	_,			_	_	_		_		_		_	_					
Top Hit Descriptor	Limesenteroides gene for sucrose phosphorylase (EC 2.4.1.7)	Homo sapiens transcription factor IGHM enhancer 3, JM11 protein, JM4 protein, JM6 protein, T54 protein, JM10 protein, A4 differentiation-dependent protein, triple LIM domain protein 6, and synaptophysin genes, complete cds; and L-type calcium channel a>	Horno sapiens transcription factor IGHM enhancer 3, JM11 protein, JM4 protein, JM5 protein, T54 protein, JM10 protein, A4 differentiation-dependent protein, triple LIM domain protein 6, and synaplophysin genes,	complete cds; and L-type calcium channel a>	Arabidopsis thallana DNA chromosome 4, contig fragment No. 63	Scianum tuberosum cold-stress inducible protein (C17) gene, complete cds	Oryctolagus cunicutus RING-finger binding protein mRNA, partial cds	AV743773 CB Homo sapiens cDNA clone CBMAFD06 5'	602118381F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4275381 5'	Rattus norvegicus cytocentrin mRNA, complete cds	Dictyocaulus viviparus nematode polyprotein antigen precursor (DvA) mRNA, complete cds	Aeropyrum pemix genomic DNA, section 6/7	B.thuringiensis PK1 & cap genes, putative	Rana catesbetana mRNA for bulfrog skeletal muscle calcium release channel (ryanodine receptor) alpha	Scrorm(KyK1), complete cas	Homo sapiens partial TCF-4 gene for T-cell transcription factor-4, exons 15-16	Mus musculus otogelin (Olog), mRNA	Mus musculus atogelin (Otog), mRNA	602155438F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4296344 5'	602155438F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4296344 5	Drosophila melanogaster 6-pyruvoyitetrahydropterin synthase (pr) gene, complete cdc	RC1-BT0567-301299-011-d09 BT0567 Homo sapiens cDNA	RC1-BT0567-301299-011-409 BT0567 Homo saplens cDNA	601496330F1 NIH_MGC_70 Homo saptens cDNA clone IMAGE:3898495 5'	Human T-cell receptor germline gamma-chain J2 gene	zu06h11.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:731109 3'	Horno sapiens mRNA for KIAA0614 protein, partial cds	Homo sapiens mRNA for KIAA0614 protein, partial cds	yz73e07.s1 Soares_multiple_sclerosis_2NbHMSP Homo sepiens cDNA clone IMAGE:288708 3' sImilar to contains Alu repetitive element;
Top Hit Database Source	N-	Ł		Į.	L	N T	NT	EST_HUMAN	EST_HUMAN	<u>N</u>	NT	NT	Ę		z	FZ	LN	NT	EST_HUMAN	EST_HUMAN	IN	EST_HUMAN	EST_HUMAN	EST_HUMAN	۲	EST_HUMAN	FN	L	EST_HUMAN
Top Hit Acession No.	2E-01 D90314.1	2E-01 AF196779.1		2E-01 AF196779.1	2E-01 AL161563.2	2E-01 U69633.1	2E-01 AF236061.1	2E-01 AV743773.1	.2E-01 BF670061.1		2E-01 U02568.1	.2E-01 AP000063.1	Æ-01 Y10168.1		.1E-01 D21070.1	.1E-01 AJ270777.1	7305360 NT	7305360 NT	.1E-01 BF681034.1	.1E-01 BF681034.1	1E-01 U36232.1	1E-01 BE074185.1	1E-01 BE074185.1	1E-01 BE904405.1	1E-01 M12961.1	1E-01 AA421492.1	.0E-01 AB014514.1	0E-01 AB014514.1	7.0E-01 N62412.1
Most Similar (Top) Hit BLAST E Value	7.2E-01	7.2E-01		7.2E-01	7.2E-01	7.2E-01	7.2E-01	7.2E-01	7.2E-01	7.2E-01	7.2E-01	7.2E-01	7.2至-01		7.1E-01	7.1E-01	7.1E-01	7.1E-01	7.1E-01	7.1E-01	7.1E-01	7.1E-01	7.1E-01	7.1E-01	7.1E-01	7.1E-01	7.0E-01	7.0E-01	'
Expression Signal	2.68	1.07		1.07	0.65	0.59	1.31	0.54	2.25	3.26	1.51	4.37	1.46		11.37	16.1	3.07	3.07	1.73	1.73	6.48	1.12	1.12	1.6	1.1	2.64	0.95	0.95	1.29
ORF SEQ ID NO:	31007	31317		31318	31395	33903	35265		37192	37690	31530				26928	29320	30453	30454	32579	32580	33606	35552	35553	36700	37265		27479		
Exan SEQ ID NO:	18022	İ	1	18347	1	1	Ì	22241	23583	24058	18491	25488	26075		13892	18308	17467	17467	19251	l	ı	ı	ı	ı	l	1	L.	14415	
Probe SEQ ID NO:	4892	5225		5225	5308	7362	8648	9163	10548	10977	12530	12737	12784		730	3130	4324	4324	6009	6909	7088	8934	8934	10058	10621	12505	1257	1257	2521

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Top Hit Descriptor	yz73e07.s1 Soares_multiple_sclerosis_2NbHMSP Homo sapiens cDNA clone IMAGE:288708 3' similar to contains Alu repetitive element;	Homo sapiens chromosome 21 segment HS21C101	Arabidopsis thaliana mRNA for chlorophyll b synthase, complete cds	Escherichia coli K-12 MG1655 section 143 of 400 of the complete genome	Clostridium acetobutylicum mannitol-specific phosphotransferase system (PTS) system, mtlA, mtlR, mtlF,	and mtlD genes, complete cds	Clostridium acetobutyficum mannitol-specific phosphotransferase system (PTS) system, mtlA, mtlR, mtlF, end mtD genes, complete cds	AV763842 MDS Homo saplens cDNA clone MDSCHE04 5'	AV763842 MDS Homo saplens cDNA clone MDSCHE04 5'	Bacteriophage N15 virlon, complete genome	Candida albicans equalene epoxidase (CAERG1) gene, complete cds and translational regulator gene, partial cds	Candida albicans squalene epoxidase (CAERG1) gene, complete cds and translational regulator gene, partial	SDO	nn28a09.s1 NCI_CGAP_Gas1 Homo saptens cDNA clene IMAGE:1085176 3	Chlamydia muridarum, section 3 of 85 of the complete genome	Mus musculus mRNA for immunoglobulin gamma heavy chain variable region, isolate PC 2811	601465594F1 NIH_MGC_67 Homo saplens cDNA clone IMAGE:3868943 5'	Branchlostoma belcheri BbNA3 πRNA for notochord actin, complete cds	Drosophila melanogaster mRNA for A-klnase anchor protein DAKAP550, partial	601177333F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3532328 5'	Strongylocentrotus purpuratus myosin V, complete cds	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 69	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 69	Entamoeba dispar cation transporting ATPase (atpase) gene, partial cds	Musa acuminata pectate lyase 1 (PL1) mRNA, complete cds	Musa acuminata pectate lyase 1 (PL1) mRNA, complete cds	601880580F1 NIH_MGC_55 Homo capienc cDNA clone IMAGE:4109419 5'	Homo sapiens DAN gene, complete cds	Homo sapiens DAN gene, complete cds	FORKHEAD BOX PROTEIN C2 (FORKHEAD-RELATED PROTEIN FKHL14) (MESENCHYME FORK HEAD PROTEIN 1) (MFH-1 PROTEIN) (TRANSCRIPTION FACTOR FKH-14)
Top Hit Database Source	T_HUMAN	NT	K	L		LN L	LN	EST HUMAN	Г	LΝ	LN.			T_HUMAN	NT .		T_HUMAN	. LN	TN	EST_HUMAN	NT	NT	N	N	F	٦	EST_HUMAN	L L	IN	SWISSPROT
Top Hit Acession No.	.0E-01 N62412.1	.0E-01 AL163301.2	.0E-01 AB021316.1	.0E-01 AE000253.1		.0E-01 U53868.1	0E-04   153868 4	.0E-01 AV763842.1	.0E-01 AV763842.1	30464	9E-01 U69674.1		.9E-01 U69674.1	.9E-01 AA593530.1	.9E-01 AE002271.2	.9E-01 Y17373.1	.9E-01 BE782751.1	.9E-01 AB035662.1	.9E-01 Y18278.1	.9E-01 BE296188.1	.9E-01 AF248863.1	1.9E-01 AL161573.2	6.9E-01 AL161573.2	6.9E-01 AF118046.1	6.9E-01 AF206319.1	6,9E-01 AF206319.1	6.9E-01 BF242367.1	.9E-01 D89013.1	.9E-01 D89013.1	Q99958
Most Similar (Top) Hit BLAST E	7.0E-01	7.0E-01	7.0E-01	7.0E-01		7.0E-01	7.05-04	7.0E-01	7.0E-01	7.0E-01	6.9E-01		6.9E-01	6.9E-01	6.9E-01	6.9E-01	6.9E-01	6.9E-01	6.9E-01	6.9E-01	6.9E-01	6.9E-01	6.9E-01	6.9E-01	6.9E-01	6.9E-01	6.9E-01	6.9E-01	6.9E-01	6.9E-01 Q99958
Expression Signal	1.29	2.32	0.89	6.52		0.58	85.0	1.47	1.47	1.47	6.3		6.3	2.91	1.71	15.79	. 97.22	0.82	0.85	1.12	0.58	2.94	2.94	99.0	0.56	0.56		2.11		
ORF SEQ ID NO:	28771					36150	38151		38103		27224				29484			32405	32627	33029	34542		34770							
Exon SEQ ID NO:	15647	18291	ı	l	1	22582	22882	1	24443	ı	L	<u> </u>			16465	16696		19091	19292	19666			21250		1	١			24592	
Probe SEQ ID NO:	2521	5169	6073	8573		9517	0517	11382	11382	13133	992		992	1338	3291	3531	5311	5902	6112	9200	7979	8168	8168	9372	9886	9886	10619	11536	11536	12146

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Table 4
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	Top Hit Descriptor	Glardia intestinalis carbamate kinase gene, complete cds	Synechocystis sp. PCC6803 complete genome, 27/27, 3418852-3573470	aj75a05.s1 Soares_parathyrold_tumor_NbHPA Homo sapiens cDNA clone IMAGE:14022563' similar to gb:X56411_ma1 ALCOHOL DEHYDROGENASE CLASS II PI CHAIN (HUMAN);	Rat(hooded) protactin gene : exon iii and flanks	Homo sapiens hevin (HEVIN) mRNA	Homo sapiens mRNA for KIAA1345 protein, partial cds	nv13e07.s1 NCL_CGAP_Pr22 Homo sapiens cDNA clone INAGE:1220100 3' similar to gb:X13546_ma1 Human HMG-17 gene for non-histone chromosomal protein (HUMAN);	Stagonospora avanae bgl1 gene for beta-glucosidase, exons 1-4	Stagonospora avenae bgl1 gene for beta-glucosidase, exons 1-4	Mus musculus zinc finger protein (Peg3) mRNA, complete cds	Mus musculus zinc finger protein (Peg3) mRNA, complete cds	Anopheles gambiae strain M2 translation initiation factor 4C (1A) (eIF-4C) mRNA, complete cds	Mus musculus major histocompatibility complex region NG27, NG28, RPS28, NADH oxidoreductase, NG29, KIFC1, Fas-binding protein, BING1, tapasin, RalGDS-iike, KE2, BING4, bela 1,3-galactosy transferase, and	RPS18 genes, complete cds; Sacm21 gene, partial>	Mus musculus major histocompatibility complex region NG27, NG28, RPS28, NADH oxidoreductase, NG29,	KIFC1, Fas-binding protein, BING1, tapasin, RalGDS-like, KE2, BING4, beta 1,3-galactosyl transferase, and	KPS18 genes, complete cds; Secmz1 gene, partai>	Homo sapiens nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 (NFKB1) gene, complete cds	Homo sapiens nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 (NFKB1) gene, complete	sþó	Quail fast skeletal muscle troporin I gene, complete cds	zx12g12.s1 Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:786310 3' similar to	Contains element I Any I repetuve eterrem,	Drosophila melanogaster Mst85C gene, complete cds; NMDMC isoform (Nimdmc) gene, complete cds,	alternatively spliced; and franscription factor (Kelish) gene, complete cos, alternatively spliced	Mus musculus Wiskott-Aldrich syndrome protein (Wasp), mRNA	S.tuberosum mRNA for glucose-6-phosphate dehydrogenase	M.barken ATPase alpha and beta subunit (atpA and atpB) genes, complete cds	M. barkeri ATPase alpha and beta subunit (atpA and atpB) genes, complete cds
	Top Hit Database Source	NT	NT S	EST HUMAN 9	Г			HUMAN	Т	N	N N	NT N	NT	<u> </u>	TA LA	2	-	L	. N	-	NT	) IN		EST HUMAN						N N
26	Top Hit Acession No.	6.8E-01 AF017784.1	6.8E-01 D90917.1	6.8E-01 AA854475.1	J00762.1	4758521	6.8E-01 AB037766.1 NT	6.8E-01 AA687936.1	6.8E-01 AJ276675.1	6.8E-01 AJ276675.1	6.8E-01 AF038939.1	6.8E-01 AF038939.1	6.8E-01 AF164151.1		6.8E-01 AF110520.1			6.8E-01 AF110520.1	6.7E-01 AF213884.1		6.7E-01 AF213884.1	6.7E-01 M12132.1		6.7E-01 AA451864.1		6.7E-01 AF186073.1	6678580 NT	6.7E-01 X74421.1	6.7E-01 J04836.1	6.7E-01 J04836.1
	Most Similar (Top) Hit BLAST E Value	6.8E-01	6.8E-01	6.8E-01	6.8E-01	6.8E-01	6.8E-01	6.8E-01	6.8E-01	6.8E-01	6.8E-01	6.8E-01	6.8E-01		6.8E-01	·		6.8E-01	6.7E-01		6.7E-01	6.7E-01		6.7E-01		6.7E-01	6.7E-01	6.7E-01	6.7E-01	6.7E-01
	Expression Signal	1.94	1.41	1,43	1.32	0.62	1.06	572	2.4	2.4	1.91	1.91	1.57		1.97			1.97	30.38		25.24	1.14		1.98		5.15	5.81	0.62	1.44	1.44
-	ORF SEQ ID NO:	27212		27883					38056		38098	38097			38594			38595	26559		26588			28477						31895
	Exan SEQ ID NO:	14152	l	l	L	18109				ı	1	l	١		24893	1		24893	13525		13580	15104	ì	15348		16058	16236	17712	18820	18820
	Probe SEQ ID NO:	979	2739	2890	4694	4980	9838	10567	11344	11344	11376	11376	11579		11906			11906	300		349	1961		2214		2235	3060	4575	5626	2626

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-		-	_	_	_	_	_	_	_	_	_	_	_	_			_		_	_			7	_	_		-	_	_	_	
	Top Hit Descriptor	Helicobacter pylori, strain J99 section 47 of 132 of the complete genome	Gallid herpesvirus 2, complete genome	Gallid herpesvirus 2, complete genome	601650177R1 NIH_MGC_71 Hama sapiens cDNA done IMAGE:3905778 3'	601650177R1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3905778 3'	Pseudomonas aeruginosa PA01, section 167 of 529 of the complete genome	Helicobacter pylori, strain J99 section 47 of 132 of the complete genome	Human placental protein 14 (PP14) gene, complete cds	CM3-HT0769-010600-197-c03 HT0769 Homo sapiens cDNA	N-ACETYLGLUCOSAMINYL-PHOSPHATIDYLINOSITOL BIOSYNTHETIC PROTEIN GP11	EST 48065 Fetal spleen Homo sepiens cDNA 3' end	Homo sapiens SLIT1 protein (SLIL2) mRNA, partial cds	Homo sapiens lens epithelium-derived growth factor gene, alternatively spliced, complete cds	Homo sapiens sema domain, seven thrombospondin repeats (type 1 and type 1-like), transmembrane domain (TAA) and chart edential domain (company for CEMARA) mBNA	(Tim) and short cyclobasing domain; Semaphoni) of (Sewhor) interval	Cabicans random DNA marker, 282bp	Human hereditary haemochromatosis region, histone 2A-like proteln gene, hereditary haemochromatosis (HLA-H) gene, RoRet gene, and sodium phosphate transporter (NPT3) gene, complete cds	Mus musculus kinesin light chain 2 (Klc2), mRNA	Pseudomonas aeruginosa PA01, section 19 of 529 of the complete genome	Pseudomonas aeruginosa PA01, section 19 of 529 of the complete genome	AV660506 GLC Homo sapiens cDNA clone GLCGID04 3'	AV704700 ADB Homo sapiens cDNA clone ADBCAF11 5	Homo sapiens chromosome 21 segment HS21C078	AU118198 HEMBA1 Homo sapiens cDNA clone HEMBA1003079 5'	H.vulgaris Na,K-A TPase alpha subunit mRNA, complete cds	H.vulgarls Na,K-ATPase alpha subunit mRNA, complete cds	Mus musculus gene for Tob2, complete ods	Homo sapiens interleukin 10 receptor, alpha (IL10RA) mRNA	Homo sapiens SPP2 gene for secreted phosphoprotein 24 precursor, exons 1-8	Phaseolus vulgaris ATPase gamma subunit mRNA, nuclear gene encoding mitochondrial protein, partial cds
2011100	Top Hit Database Source	TN	N⊤	NT.	EST_HUMAN	EST_HUMAN	F	NT	TN	EST_HUMAN	SWISSPROT	EST_HUMAN	LN FN	ΙΝ	ŀ	Z	μ	TN	F	N	ΤN	EST_HUMAN	EST_HUMAN	F	EST_HUMAN	NT	ΝŢ	۲	NT	TN	NT
8.110	Top Hit Acession No.	6.7E-01 AE001486.1	±N 2635035 NT	9635035 NT	6.7E-01 BE966241.2	6.7E-01 BE966241.2		6.7E-01 AE001486.1	6.7E-01 M34046.1	6.7E-01 BF354649.1	014357	6.7E-01 AA342521.1	6.6E-01 AF075240.1	6.6E-01 AF199339.1	4500000	1 N 08890C4	6.6E-01 Y07669.1	6.6E-01 U91328.1	6680577 NT	6.6E-01 AE004458.1	6.6E-01 AE004458.1	6.6E-01 AV660506.1	6.6E-01 AV704700.1	6.6E-01 AL163278.2	6.6E-01 AU118198.1	6.5E-01 M75140.1	6.5E-01 M75140.1	6.5E-01 AB041225.1	4504632 NT	6.5E-01 AJ272265.1	6.5E-01 U28921.1
,	Most Similar (Top) Hit BLAST E Value	6.7E-01	6.7E-01	6.7E-01	6.7E-01	6.7E-01	6.7E-01	6.7E-01	6.7E-01	6.7E-01	6.7E-01 O14357	6.7E-01	6.6E-01	6.6E-01	10.0	9.5E-01	6.6E-01	6.6E-01	6.6E-01	6.6E-01	6.6E-01	6.6E-01	6.6E-01	6.6E-01	6.6E-01	6.5E-01	6.5E-01	6.5E-01	6.5E-01	6.5E-01	6.5E-01
	Expression Signal	62.0	1.3	1.3	65.0	0.59	3.97	0.94	1.04	2.06	2.75	2.48	26.0	1.13	9	1.16	4.58	2.48	3.82	0.62	0.62	3.7	0.58	2.34	0.51	2.02	2.02	5.5	1.73	7.71	2.88
	ORF SEQ ID NO:	32594	L	32984	33304			34042		, (						1	29913		32990		33809		35384				26849	,			31258
	Exen SEQ ID NO:	19265	i _	19620	19910	19910	L	l	23383	24265	1	J	15695	Ι.	J		16909	17373	19629	_	L	20916		22905	<u>1                                    </u>	13825	13825		17300	17540	18296
	Probe SEQ ID NO:	6083	6453	6453	6754	6754	7468	7495	10348	11196	11746	11959	2570	2765	of UC	32/8	3748	4225	6462	7272	7272	7862	8764	3865	10207	640	640	3519	4148	4397	5174

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nilar Top Hit Acession Database Top Hit Source Source	8.5E-0-1 P18480 SWISSPROT (TRANSCRIPTION FACTOR TYE4)	6.5E-01 D88348.1 NT Chicken mRNA for 115-kDa melanosomal matrix protein, complete cds	П	EST_HUMAN	EST_HUMAN	5E-01 AF119676.1 NT Mus muscultus small GTP-binding protein RAB26 (Rab25) gene, complete cds	5E-01 H87583.1 EST_HUMAN   yw17f06.r1 Sogres_placenta_8tb9weeks_ZNbHP8tc9W Homo sepiens cDNA clone IMAGE:252515.5	EST_HUMAN	6.5E-01 AU138078.1 EST_HUMAN AU138078 PLACE1 Homo sapiens cDNA clone PLACE1007810 5	Plasmodium berghei cytochrome c oxidase subunit III, cytochrome c oxidase subunit I, and cytochrome b	LANGE HOL	ES L	Ę		Γ	6.4E-01 Y12488.1 NT M.musculus whn gene	6.4E-01 Y12488.1 NT M.musculus whn gene	ħ	3320 NT	NT	EST_HUMAN	.1 EST HUMAN	SWISSPROT	· IN	NT	IN	NT	TN	EST_HUMAN	LN	3E-01   L27798.1 NT Streptococcus dysgalactiee (mag) gene, complete cds
						1							Τ	Τ	Γ				11418320 NT				Г								
Most Similar (Top) Hit BLAST E Value	6.5E-01 P1	6.5E-01 D8	6.5E-01 X0	· 6.5E-01 Al.	6.5E-01 T7	6.5E-01 AF	6.5E-01 H8	6.5E-01 AA	6.5E-01 AL	0	0.00-01A	0.0E-01 BC	8 4F-04   14	6.4E-01 U4	6.4E-01 AE	6.4E-01 Y1	6.4E-01 Y1	6.4E-01 AE	6.4E-01	6.4E-01 UE	6.4E-01 BF	6.4E-01 A	6.3E-01 PO	6.3E-01 U3	6.3E-01 UE	6.3E-01 U7	6.3E-01[U7	6.3E-01 Y1	6.3E-01 BE	6.3E-01 L2	6.3E-01 L2
Expression Signal	1.86	1.3	0.74	66.0	0.86	2.53	2.55	2.98	3.38	1	3.0	8.09	2 2	4.42	1.46	0.74	0.74	1.58	0.5	7.31	1.31	19.53	3.78	1.85	3.29	3.65	3.65	0.93	0.84	1.01	1.01
ORF SEQ ID NO:	31795	33428		34404		37186	37583				30300		26843		L		30732	36432		36933	36949		26682	26765	28493		28885		32713		33282
Exan SEQ ID NO:	25807	1		20901	23080	23577	23954	24008			_	25386	L	Ţ	Į	L	)	21891	23257	23329	23344	25461	13643	13741	15364	L	15769	16257	19365	19889	19889
Probe SEQ ID NO:	5559	6865	7760	7846	10042	10542	10869	10925	11030		11899	12300	Cac	3545	3964	4614	4614	8812	10221	10294	10309	12693	447	548	2230	2646	2646	3081	6189	6733	6733

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					,		
Probe SEQ ID NO:	Exon SEQ 1D NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Velue	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
87.18	21798			6.3E-01	6.3E-01 BE902044.1	EST_HUMAN	601676889F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3959351 5
2087	22166	35712	0.79	6.3E-01	6.3E-01 S62927.1	. IN	glycoprotein Ilia (Alu 1 and 3 fusion junction) [human, Genomic Mutant, 300 nt]
9421	22495	36062	99.0		3.3E-01 BF216984.1	EST HUMAN	601884050F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4102596 5'
9620	22675		3.14	6.3E-01	9627521 NT	ΤN	Variola virus, complete genome
9620	22675		3.14		9827521 NT	ΙΝ	Variola virus, complete genome
10142					6.3E-01 AE002329.2	NT	Chlanydia muridarum, section 59 of 85 of the complete genome
10641	23675		1.59	6.3E-01		Ŋ	S.cerevisiae chromosome VII reading frame ORF YGR218w
10747	23780		1	6.3E-01	6.3E-01 AE000313.1	LN	Escherichia coli K-12 MG1655 section 203 of 400 of the complete genome
10781	23814		0.48		6.3E-01 AW795395.1	EST_HUMAN	PM0-UM0018-130500-003-g12 UM0018 Hamo saplens cDNA
14044	04070		2, 1		6 3 1 0 4 8 7 7 7 1 5 1	NAMI IL TOR	INDBN06.s1 NCI_CGAP_Co10 Homo sapiens cDNA clone IMAGE:1161371 3' similar to TR:002916 002916. HI ARK
2007					0.0E-01 A20, 77 10.1	TOTAL TOTAL	CAL BITO43 A00000 A48 RIA43 Homo canions cDNA
11620		1			0.3E-01 AIBU4100.1	DAMES DE LA COMPANA	HYDOTHETICAL 13 7 KD PROTEIN IN INOLING INTERGENIC REGION
80/11	L	۱			747003	TOURS WE	IN CHILD TO THE TOTAL TO THE THE THE THE THE THE THE THE THE THE
11888	24876	385/3	2.12		5.3E-01 P360/3	SWISSPRO	Refa violants mitochondron, complete genome
2000	L	1			ŀ		Muse muser the Leastin complex 2, name for (Krt2-Rn) mBNA
12262		31546	2		2820	N I	Mus linusculus na auti contines 2, gene og (nr.cz.og), minnes
12358			1.6		7.1	Į.	Homo sapiens 3-phosphoadenosine 5-phosphosuirate synmetase (FAF-55) mkn/A, complete cos
12582	26029		4.27		1	뒫	C.limicola pscD gene
5991	19178	32497	2.15		6.2E-01 Q10135	SWISSPROT	HYPOTHETICAL 142.5 KD PROTEIN C23E2.02 IN CHROMOSOME I
7664	20731		3.59		6.2E-01 AF022253.1	NT	Mus musculus calcium-sensing receptor related protein 4 (Casr-rs4) mRNA, partial cds
77.45	010	04760	4.6		6 2E-04 A1 024427 3	. <del></del> .	Mus musculus chromosome X contigA; putative Magea9 gene, Caltractin, NAD(P) steroid dehydrogenase and Zho finas mutain 185.
8497	1			L	6.2E-01 H72255.1	EST HUMAN	ys01e08.s1 Soares fetal liver spieen 1NFLS Homo sepiens cDNA clone IMAGE:213542.3'
00.87					R 2E.01 AE034411 1	i F	Lycopersicon esculentum cytosolic Cu,Zn supercolde dismutase (Sod) gene, partial ods; and dehydroquinate dehydratase/shikimate:NADP oxidoreductase gene, complete ods
9648	1			L	BE562687.1	EST HUMAN	601336146F1 NIH_MGC_44 Homo sepiens cDNA clone IMAGE:3690010 5
9710	1				6.2E-01 M24461.1	LN	Human pulmonary surfactant-associated protein SP-B (SFTP3) mRNA, complete cds
10283	ı	36919	6.83		6.2E-01 AL161511.2	NT	Arabidopsis thallana DNA chromosome 4, contig fragment No. 23
10426	23461	37067	0.63	6.2E-01	11420793 NT	LΝ	Hamo sapiens polassium vallage-gated channel, Shab-related subfamily, member 1 (KCNB1), mRNA
10426	23461	37068	0.63	6.2E-01	11420793 NT	F	Homo sapiens potassium voltage-gaited channel, Shab-related subfamily, member 1 (KGNB1), mRNA
10756	23789	37405	5.75		6.2E-01 P27410	SWISSPROT	NON-STRUCTURAL POLYPROTEIN (CONTAINS: RNA-DIRECTED RNA POLYMERASE ; THIOL PROTEASE P3C ; HELICASE (2C LIKE PROTEIN); COAT PROTEIN]

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. Top Hit Descriptor	NON-STRUCTURAL POLYPROTEIN (CONTAINS: RNA-DIRECTED RNA POLYMERASE ; THIOL PROTEASE P3C ; HELICASE (2C LIKE PROTEIN); COAT PROTEIN)	Mus musculus secreted acidic cysteine rich glycoprotein (Sparc), mRNA	Caenorhabditis elegans N2 CeMyoD (hih-1) alternatively spliced genes, complete cds	Rat TRPM-2 gene, complete cds	Rat TRPM-2 gene, complete cds	xd50h03.x1 NCJ_CGAP_Ov23 Homo sapiens dDNA clone IMAGE:2597237 3' similar to gb:X12671_ma1 HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN A1 (HUMAN);	SUSHI REPEAT-CONTAINING PROTEIN SRPX PRECURSOR (DRS PROTEIN) (DOWN-REGULATED	BY V-SRC)	Arabidopsis thallana putative zinc transporter (ZIP1) mRNA, complete cds	Homo sapiens mitogen-activated protein kinase kinase kinase kinase 4 (MAP4K4), mRNA	Homo sapiens mitogen-activated protein kinase kinase kinase kinase 4 (MAP4K4), mRNA	Homo sapiens G-protein coupled receptor EDG-7 mRNA, complete cds	Homo sapiens G-protein coupled receptor EDG-7 mRNA, complete cds	Pseudomonas aeruginosa PA01, section 13 of 529 of the complete genome	Homo sapiens dopamine transporter (SLC6A3) gene, complete cds	Sus scrofa neural cell adhesion molecule (NCAM) gene, 3' UTR and microsatellite repeat region	hyaluronan-binding protein=hepatocyte growth factor activator homolog [human, plasma, mRNA, 2408 nt]	hyaluronan-binding protein-hepatocyte growth factor activator homolog (human, plasma, mRNA, 2408 nt)	M.mazsi orfA, orfB, and orfC of archaeal ABC-transporter system	Homo sapiens DNA for amyloid precursor protein, complete cds	Homo saplens adaptor-related protein complex 3, mu 2 subunit (CLA20), mRNA	Human respiratory syncytial virus strain CH93-53b attachment protein (G) gene, complete cds	Vital hemorrhagic septicemia virus N, P, M, G, Nv, L genes, French strain 07-71	Homo sapiens Notch3 (NOTCH3) gene, exons 26, 27, and 28	D(2) DOPAMINE RECEPTOR .	UI-H-BI1-aeb-a-10-0-UI.s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2718619 3'	Musca domestica insecticide-susceptible strain voltage-sensitive sodium channel mRNA, complete cds	MACROPHAGE-STIMULATING PROTEIN RECEPTOR PRECURSOR (MSP RECEPTOR) (P185-RON) (CDW136) (CD136 ANTIGEN)
Top Hit Database Source	SWISSPROT	۲	TN	FZ	TN	EST_HUMAN		SWISSPROT	LN	N	LN.	M	LN LN	NT	TN	NT	NT	Ł	LN	FZ.	NT	LΝ	LΝ	Ę	SWISSPROT	EST_HUMAN	·	SWISSPROT
Top Hit Acession No.		9678076		6.1E-01 M64733.1	6.1E-01 M64733.1	6.1E-01 AW105653.1			6.1E-01 AF033535.1	11431065 NT	11431065 NT	6.1E-01 AF236117.1	6.1E-01 AF236117.1	6.1E-01 AE004452.1		6.1E-01 AF025993.1	6.1E-01 S83182.1	6.1E-01 S83182.1	6.1E-01 X95287.1	6.0E-01 D87675.1	TN 6662089	6.0E-01 AF065253.1		6.0E-01 AF058895.1	P20288	6.0E-01 AW139713.1	6.0E-01 U38813.1 .	Q04912
Most Similar (Top) Hit BLAST E Value	6.2E-01 P27410	6.1E-01	6.1E-01	6.1E-01	6.1E-01	6.1E-01		6.1E-01 Q63769	6.1E-01	6.1E-01	6.1E-01	6.1E-01	6.1E-01	6.1E-01	6.1E-01	6.1E-01	6.1E-01	6.1E-01	6.1E-01	6.0E-01	6.0E-01	6.0E-01	6.0E-01	6.0E-01	8.0E-01 P20288	6.0E-01	6.0E-01	6.0E-01 Q04912
Expression Signal	5.75	6.27	1.33	3.4	3.4	0.67		0.69	3.47	1.51	1.51	4.02	20.44	1.05	0.92	0.47	1.77	1.77	1.16	1.79	4.74	1.83	0.87	1.26	1.96	2.5	2.74	0.68
ORF SEQ ID NO:	37406		Ŀ		33565		L.	33787			35613			36686	36883	37489	38718	38719		26730		27623			31567	L	33216	
Exan SEQ ID NO:	23789	15595	ı	20146	20145	20283	l	20337		22074		22670	l	L.	23287		25016	25016		上	13767		L.	L	18597	18753	19828	19955
Probe SEQ ID NO:	10756	2468	5653	2009	7009	7160		7254	8428	8995	8995	9615	9615	10047	10252	10833	12033	12033	13062	204	575	1393	3917	4306	5395	5655	6999	0089

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	Top Hit Descriptor	Strongylocentrotus purpuratus kinesin light chain isoform 2 mRNA, complete cds	Strongylocentrotus purpuratus kinesin light chaln Isoform 2 mRNA, complete cds	Homo sapiens partial LMO1 gene for LIM domain only 1 protein, exon 1	SEGMENTATION PROTEIN FUSHI TARAZU	SEGMENTATION PROTEIN FUSHI TARAZU	Homo sapiens genes for leukotriene B4 receptor BLT2, leukatriene B4 receptor BLT1, complete cds	PEROXISOMAL MEMBRANE PROTEIN PER9 (PEROXIN3)	RC2-FN0094-190700-017-d08 FN0094 Homo saplens cDNA	Gallus gallus mRNA for Hyperion protein, 419 kD isoform	Gallus gallus mRNA for Hyperlon protein, 419 kD isoform	#08f07.x1 NCI_CGAP_Pr28 Homo sapiens cDNA clone IMAGE:2095621 3'	Horno sapiens nuclear factor (erythroid-derived 2)-like 3 (NFE2L3), mRNA	zj93g05.s1 Scares_fetal_liver_spleen_1NFLS_S1 Homo saplens cDNA clone IMAGE:462776 31	Horno sapiens RNA binding motif protein 3 (RBM3), mRNA	Mus musculus cGMP-Inhibited phosphodiesterase (Pde3a), mRNA	RC1-HT0375-030500-015-c03 HT0375 Homo sapiens cDNA	Haemophilus influenzae Rd section 16 of 163 of the complete genome	Homo sapiens chromosome 21 segment HS21C067	Homo sapiens chromosome 21 segment HS21 C067	Pterodroma neglecta cytochrome b (cytb) gene, mitochondrial gene encoding mitochondrial protein, complete	Rattus norvegicus cenexin 2 mRNA, partial cds	Ovis aries SRY gene promoter region	Homo sapiens low density lipoprotein receptor-related protein II (LRP2) gene, excn 1 and partial cds	Homo sapiens gene for histamine H2 receptor, promoter region and complete cds	G.gallus gene for skeletal alpha-actinin, exon EF2	Synechocystis sp. PCC6803 complete genome, 13/27, 1576593-1719643	egionella pneumophila gono for iron cuperoxide dismutase, complete cds	Chlamydia trachomatis strain K/UW31/Cx major outer membrane protein (omp1) gene, complete cds	E6 PROTEIN	VASCULAR ENDOTHELIAL-CADHERIN PRECURSOR (VE-CADHERIN) (CADHERIN-5)
מוופוס ביים וווסכים פופווים	Top Hit Datebase Source	NT			SWISSPROT	SWISSPROT	TN TN	SWISSPROT P	EST_HUMAN R		NT TN	T_HUMAN	NT	EST_HUMAN   Z					ا LN	⊥NT				H LN	⊢N		S LN	I.		П	SWISSPROT
Sign Sign Sign Sign Sign Sign Sign Sign	Top Hit Acession No.			6.0E-01 AJ277661.1			6.0E-01 AB008193.1		6.0E-01 BE837779.1	6.0E-01 AJ131892.1	6.0E-01 AJ131892.1	6.0E-01 AI420623.1	11421663	6.0E-01 AA706087.1	5803136 NT	FN 6065303 NT	6.0E-01 BE157617.1	5.9E-01 U32701.1	5.9E-01 AL163267.2	5.9E-01 AL163267.2	11001	5 0F-01 07 454 1.1	5.9E-01 AF026568.1	5.9E-01 AF065440.2	5.9E-01 AB023486.1	X68801.1	5.9E-01 D90911.1	5.9E-01 D12922.1	5.9E-01 AF063204.2	5.9E-01 P06463	5.9E-01 P55284
	Most Similar (Top) Hit BLAST E Value	6.0E-01 L10234.1	6.0E-01 L10234.1	6.0E-01	6.0E-01 P02835	6.0E-01 P02835	6.0E-01	6.0E-01 Q01497	6.0E-01	6.0E-01	6.0E-01	6.0E-01	6.0E-01	6.0E-01	6.0E-01	6.0E-01	6.0E-01	5.9E-01	5.9E-01	5.9E-01	Lo	1.8E-01	5.9E-01	5.9E-01	5.9E-01				5.9E-01	5.9E-01	5.9E-01
	Expression Signal	0.77	77.0	6.49	4.15	4.15	1.57	1.04	0.61	1.38	1.38	2.74	2.08	1.46	1.44	5.46	8.12	1.09	5.23	5.23		3 05	0.66	1.95	3.08	0.63	0.48	0.48	1.0.1	0.64	1.28
	ORF SEQ ID NO:	33705	33706	34056	34922	34923	36664				38022		32052			31766	-			29531		2/006	31374	33140			34795		36385		37033
	Exan SEQ ID NO:	20268		20583	ı	21397	23066		23629	ı		ı	25440	1	ı	1	ı	1	16518	l	l	1/0/5	L			1	l	I	22807	L	23426
	Probe SEQ ID NO:	9269	6955	7509	8315	8315	10028	10480	10594	11312	11312	11846	12663	12781	12953	12998	13032	1025	3343	3343		3910	5289	6594	7416	7556	8188	8839	9743	10117	10391

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					,		
Probe SEQ ID	Exon SEQ ID	ORF SEQ	Expression	Most Similar (Top) Hit	Top Hit Acession	Top Hit Database	Top Hit Descriptor
ë Ž	Ö	 ≥ ⊇	12 D	Value	į	Source	
10908	23991	37624	2.24	5.9E-01	9E-01 Q9X0I3	SWISSPROT	THYMIDYLATE KINASE (DTMP KINASE)
10916	23999	37632	1.71	5.9E-01	9E-01 AF197944.1	INT	Xencpus laevis receptor protein tyrosine phosphatase delta (XPTP-D) mRNA, complete cds
11203	24272	37908	2.76	5.9E-01	5.9E-01 AW937175.1	EST_HUMAN	PM1-DT0041-190100-002-h03 DT0041 Homo sapiens cDNA
11469	24528	38201	1.98	5.9E-01	5.9E-01 AF064626.1	TN	Mus spretus strain SPRET/Ei CD48 antigen (Cd48) gene, partial cds
12302	25220	32101	1.78	5.9E-01	5.9E-01 L42320.1	NT	Oryciclegus cuniculus alpha 1 anti-trypsin (alpha 1 AT) gene, promoter region
12549			1.92	5.9E-01	AB017705.1	NT	Aspergillus aryzae pyrG gene for arotidine-5'-phosphate decarboxylase, complete cds
12799	25533		4.82	5.9E-01	5.9E-01 P34926	SWISSPROT	MICROTUBULE-ASSOCIATED PROTEIN 1A [CONTAINS: MAP1 LIGHT CHAIN LC2]
1958	15101	28201	1.26	5.8E-01	P40472	SWISSPROT	SIM1 PROTEIN
4092	17247	30252	1.11	5.8E-01	BF695738.1	EST_HUMAN	601852474F1 NIH_MGC_58.Homo sapiens cDNA done IMAGE:4078131 5'
4637	17773		3.59	5.8E-01	AB009077.1	NT	Vigna radiata mRNA for proton pyrophosphatase, complete cds
4917	18047		2.22	5.8E-01	AF110846.1	NT	Megaselia scalaris sex-lethal homolog (Megsxl) gene, partial cds, alternatively spliced products
5490	18689		1.02	5.8E-01	AE002152.1	LN	Ureaplasma urealyticum section 53 of 59 of the complete genome
5648	18842	32123	0.81	5.8E-01		SWISSPROT	POTENTIAL 5'-3' EXONUCLEASE
6313				5.8E-01		EST_HUMAN	HUM500E06B Human placenta polyA+ (TFujiwara) Homo sapiens cDNA clone GEN-500E06 5'
6442	19609	32972	89.0	5.8E-01	5.8E-01 D50601.1	LΖ	Shigella sonnei DNA for 26 ORFs, complete cds
6952	20265		2.37	5.8E-01	565091.1	Į.	cyclic AMP-regulated phosphoprotein [rats, mRNA, 1030 nt]
							yn91b03.st Soares adult brain N2b5HB55Y Homo saplens cDNA clone IMAGE:175757 3' similar to
8071	21153		2.87	5.8E-01	8E-01 H415/1.1	ı	gescolor internase indocen process (notable).
8278	21360	34878	99.0	5.8E-01	Al280051.1		qh85d10.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1853779 3
8278	21360	34879	99'0	5.8E-01	5.8E-01 AI280051.1	EST_HUMAN	qh85d10x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1853779 31
8385	21466	34991	2.71	5.8E-01	P14328	SWISSPROT	SPORE COAT PROTEIN SP98
8385	21466	34992	2.71	5.8E-01		SWISSPROT	SPORE COAT PROTEIN SP96
9092	22171	35716	10.4	5.8E-01		L L	Homo sapiens partial TCF-4 gene for T-cell transcription factor-4, excns 6-11
9172	22250	35793		5.8E-01	Q27368	SWISSPROT	TRANSCRIPTION FACTOR EZF
9173	22251	35794	0.57	5.8E-01	0.20471	SWISSPROT	PUTATIVE CASEIN KINASE I F46F2.2 IN CHROMOSOME X
9795			0.79	5.8E-01	BF031606.1	EST_HUMAN	601557774F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:3827298 5'
11237	L	37943	7.26		AJ243213.1	NT	Homo sapiens partial 5-HT4 receptor gene, exons 2 to 5
11291	24357		3.35		BF700092.1	EST_HUMAN	602127577F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4284403 5'
11407	24468		1.44	5.8E-01	5.8E-01 BF700092.1	EST_HUMAN	602127577F1 NIH_MGC_56 Hamo sapiens cDNA clone IMAGE:4284403 5'
3108	16284		0.73	5.7E-01	6755253		Mus musculus plasmacytoma variant translocation 1 (Pvt1), mRNA
3295	16469	29488	1.46	5	.7E-01 Q9WTJ2	SWISSPROT	PUTATIVE TRANSCRIPTION FACTOR OVO-LIKE 1 (MOVO1) (MOVO1A)
3593	16757		2.84	5	7E-01 AB033503.1	<u> </u>	Populus euramericana peacs-2 mRNA for 1-aminocyclopropane-1-carboxylate synthase, complete cds
6485	1	33014		8	.7E-01 BF035413.1	EST HUMAN	601454952F1 NIH_MGC_68 Homo saplens cDNA clone IMAGE:3858590 5'
	İ			]			

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Top Hit Descriptor	238c06.r1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:665674 5' Botrvits cherea strain T4 cDNA library under conditions of nitrosen dearivation	PYRROLINE-5-CARBOXYLATE REDUCTASE (P5CR) (P5C REDUCTASE)	Mus musculus Kong1, Ltrpc5, Wash2, Tapa-1, Tssc4 and Tssc6 genes, alternative transcripts	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 32	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 32	602067712F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4066610 5'	MR3-HT0736-180700-003-802 HT0736 Homo sapiens cDNA	601654814R1 NIH_MGC_57 Homo saplens cDNA clone IMAGE:3839763 3'	Homo sepiens mRNA for KIAA0740 protein, partial cds	Homo saplens mRNA for KIAA0740 protein, partial cds	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 13	Chicken TBP gene, exon8, complete cds	AV684703 GKC Homo saplens cDNA clone GKCFSF05 5'	AV684703 GKC Homo saplens cDNA clone GKCFSF05 5'	Homo sapiens MUC3A gene for intestinal mucin, partial cds	601514007F1 NIH_MGC_71 Hamo sapiens cDNA clone IMAGE:3915457 5'	ng75g10.s1 NCI_CGAP_Pr6 Homo saplens cDNA clone IMAGE:940674 similar to contains element PTR7 reportitive element;	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 13	HIGH AFFINITY POTASSIUM TRANSPORTER	602132029F1 NIH_MGC_81 Homo saplens cDNA clone IMAGE:4271334 5	Rattus norvegious Propionyl Coenzyme A carboxylase, beta polypeptide (Pccb), mRNA	GAG POLYPROTEIN [CONTAINS: INNER COAT PROTEIN P12; CORE PROTEIN P15; CORE SHELL PROTEIN P30; NUCLEOPROTEIN P10]	GAG POLYPROTEIN (CONTAINS: INNER COAT PROTEIN P12; CORE PROTEIN P15; CORE SHELL PROTEIN P30; NUCLEOPROTEIN P10]	Homo saplens superkiller viralicidic activity 2 (S. cerevisiae homolog) Hike (SKIV2L), mRNA	yo'8a10.s1 Soares adult brain N2b5HB55Y Homo saplens cDNA.clone IMAGE:1782663'	Rabbit oral papillomavirus, complete genome	FOS-RELATED ANTIGEN-1	Melanoplus sanguintpes entomopoxyfrus, complete genome	Bos taurus MHC class II beta-chain BoLA-DIB1 gene, partial cds
Top Hit Database Source	EST_HUMAN	SWISSPROT	TN	IN	TN	EST_HUMAN	EST_HUMAN	EST_HUMAN	IN	IN	ΙN	١N	EST_HUMAN	EST_HUMAN	F	EST_HUMAN	EST_HUMAN	뉟	SWISSPROT	9.1 EST_HUMAN	FZ	SWISSPROT	SWISSPROT	LZ	EST_HUMAN	F	SWISSPROT	ΤN	Į.
Top Hit Acessian No.	5.7E-01 AA194201.1 5.7E-01 AL111440.1	P00373	5.7E-01 AJ251835.1	5.7E-01 AL161532.2	5.7E-01 AL161532.2	5.7E-01 BF540962.1	5.7E-01 BE715051.1	5.7E-01 BE959722.2	5.6E-01 AB018283.2	5.6E-01 AB018283.2	5.6E-01 AL161501.2	5.6E-01 D83135.1	5.6E-01 AV684703.1	5.6E-01 AV684703.1	5.6E-01 AB038782.1	5.6E-01 BE888280.1	5.6E-01 AA493535.1	5.6E-01 AL161501.2		5.6E-01 BF573829.1	8393912		P03341	5902085 NT	5.5E-01 H46219.1	5.5E-01 AF227240.1	P48755	5.5E-01 AF063866.1	5.5E-01 U69097.1
Most Similar (Top) Hit BLAST E Value	5.7E-01	5.7E-01 P00373	5.7E-01	5.7E-01	5.7E-01	5.7E-01	5.7E-01	5.7E-01	5.6E-01	5.6E-01	5.6E-01	5.6E-01	5.6E-01	5.6E-01	5.6E-01	5.6E-01	5.6E-01	5.6E-01	5.6E-01 P50505	5.6E-01	5.5E-01	5.5E-01 P03341	5.5E-01 P03341	5.5E-01	5.5E-01	5.5E-01	5.5E-01 P48755	5.6E-01	5.5E-01
Expression Signal	0.92	1.88	0.55	1.13	1.13	0.91	1.29	1.31	1.1	1.1	0.59	0.77	4.11	4.11	1.13	7.84	1.39	2.38	2.56	3.64	6.04	6	9,3	1.17	1.57	2.93	1.34	1	1.01
ORF SEQ ID NO:	33412	34501			36835	37461			29635	29636	30152	30476	35625	32626	36285		38362	30152			27459	28990	. 28991	29178		29501	29951		31356
Exon SEQ ID NO:	20003	<u> </u>			23042			25675	16617	1991		17497	22082	22082	22717	25123	25204	ı	25460	L	14397	15881		1	1	L.,			18388
Probe SEQ ID NO:	6850	7941	8157	10004	10004	10803	12255	13025	3449	3449	3989	4354	9003	8003	9575	12153	12272	12661	12690	13167	1238	2766	2766	2985	3134	3306	3783	6249	5269

MITOCHONDRIAL TRIFUNCTIONAL ENZYME ALPHA SUBUNIT PRECURSOR (TP-ALPHA) INCLUDES: LONG-CHAIN ENOYL-COA HYDRATASE; LONG CHAIN 3-HYDROXYACYL-COA

S.cerevistae RIB3 gene encoding DBP synthase

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Z21619.1

5.4E-01

19492

7490

15461

5774

2173

598 8 2329 6320

598

LAMININ ALPHA-2 CHAIN PRECURSÓR (LAMININ M CHAIN) (MEROSIN HEAVY CHAIN) LAMININ ALPHA-2 CHAIN PRECURSOR (LAMININ M CHAIN) (MEROSIN HEAVY CHAIN)

302076545F1 NIH\_MGC\_62 Homo capienc cDNA clone IMAGE:4243690 5

NITRATE REDUCTASE [NADPH] (NR)

SWISSPROT SWISSPROT SWISSPROT EST\_HUMAN

Q60675 Q60675

5.4E-01 5.4E-01 5.4E-01

38046 38607 38608

24906 24906

24397

DEHYDROGENASE

SWISSPROT

5.4E-01 BF572536.

Q64428

5.4E-01

2.69 2.68 2.76

34039

20567

10195 11334 11920 11920

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Single Exon Probes Expressed in Placenta

SEQ ID NO:

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Probe SEQ ID

20483

7405

20483 21758 23008

505 7439

Norch4, PBX2, RAGE, lysophatidic acid acyl transferase-alpha, palmitoyl-protein thloesterase 2 (PPT2), Mus musculus major histocompatibility locus class III region;butyrophilin-like protein gene, partial cds; Notch4, PBX2, RAGE, tysophatidic acid acyl transferase-alpha, palmitoyi-protein thioesterase 2 (PPT2), Pseudomonas syringae pv. tomato strain DC3000 AvrE (avrE), HrpW (hrpW), and GstA (gstA) genes, Pseudomonas syringae pv. tomato strain DC3000 AvrE (avrE), HrpW (hrpW), and GstA (gstA) genes, Homo sapiens KIAA0929 protein Msx2 interacting nuclear target (MINT) homolog (KIAA0929), mRNA iamo sapiens KIAA0929 protein Msx2 interacting nuclear target (MINT) homolog (KIAA0929), mRNA Mus musculus major histocompatibility locus class III region:butyrophilin-like protein gene, partial cds; Crimean-Congo hemorrhagic fever virus strain SPU 415/85 nucleoprotein gene, complete cds EST02935 Fetal brain, Stratagene (cat#936206) Homo sapiens cDNA clone HFBCQ35 Drosophila melanogaster mRNA for 15,15' beta carotene dioxygenase (beta-diox gene) Raftus norvegicus gene for TIS11, complete cds 601660276R1 NIH\_MGC\_71 Homo sapiens cDNA clone IMAGE:3906090 3 601811077R1 NIH MGC 48 Homo sapiens cDNA clone IMAGE:4054003 3' Chlamydophila pneumoniae AR39, section 74 of 94 of the complete genome Carassius auratus gene for gonadotropin II beta subunit, complete cds **Fop Hit Descriptor** 1V4-NN0040-070400-160-c04 NN0040 Homo sapiens cDNA PM2-CN0030-030200-003-c10 CN0030 Homo sapiens cDNA QV3-HT0458-170200-090-b05 HT0458 Homo sapiens cDNA CREB-RP, and tenascin X (TNX) genes, complex CREB-RP, and tenascin X (TNX) genes, complex cerevisiae RIB3 gene encoding DBP synthase complete cds; and unknown genes complete cds; and unknown genes NT EST\_HUMAN EST HUMAN EST\_HUMAN HUMAN EST HUMAN EST\_HUMAN Top Hit Database Source EST 눋 눋 7657266 NT Þ F 눋 7657266 Top Hit Acesslon BE966592.2 Z21619.1 AE002247.2 AF030001.1 5.5E-01 AF030001.1 5.5E-01 BE163243.1 5.4E-01 AF232006.1 5.4E-01 AJ276682.1 AF232006.1 5.4E-01 AW896087. AW842327. ģ 5.5E-01 U88415.1 5.4E-01/ 5.4E-01/ 5.4E-01/ 5.5E-01 5.5E-01 5.5E-01 5.5E-01 5.4E-01 5.4E-01 5.4E-01 6.4E-01 5.4E-01 Vost Similar (Top) Hit BLAST E Value 0.59 0.59 0.56 2.8 2.82 0.83 0.47 8.1 8.11 5 2 1.64 وَ Expression Signal 28594 32269 32850 33746 34035 26405 26808 33950 37230 26404 26809 ORF SEQ ID NO: 38132 33951 35291

13372 13372 13788 13788 14456 15308

147 147

24467

11406

99869 10588

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wi37g04.x1 NCI_CGAP_Utt Homo saplens cDNA clone IMAGE:2427126 3' similar to gb:M13452 LAMIN A (HUMAN);  Homo saplens HLA class III region containing tenascin X (banascin-X) gene, partial cds; cytochrome P450 21-Motro saplens LAC class III region containing tenascin X (banascin-X) gene, partial cds; cytochrome P450 21-Motro saplens LAC class III region containing tenascin X (banascin-X) gene, partial cds; cytochrome P450 21-Motro saplens protein tyrosine phosphatase, receptor-type, zata polypeptide 1 (PTPRZ1) mRNA Homo saplens protein tyrosine phosphatase, receptor-type, zata polypeptide 1 (PTPRZ1) mRNA Homo saplens secreted C-type lectin precursor (LSLC) genes. Homo saplens secreted C-type lectin precursor (LSLC) genes complete gardine Eud2h12.y5 Scares ovary turnor NbHOT Homo saplens cDNA clone IMAGE:740711 5' Zu42h12.y5 Scares ovary turnor NbHOT Homo saplens cDNA clone IMAGE:7806112 5' Zu42h12.y5 Scares ovary turnor NbHOT Homo saplens cDNA clone IMAGE:3288118 3' similar to gb:J02783 PROTEIN DISULFIDE ISOMERASE PRECURSOR (HUMAN); Zu42h12.y5 Scares ovary turnor nbHOT Homo saplens cDNA clone IMAGE:3288118 3' similar to gb:J02783 PROTEIN DISULFIDE ISOMERASE PRECURSOR (HUMAN); Rordale gargonist radiose 1,5-bisphosphate carboxylase (rbcL) gene, partial cds; chloroplast gene for repetitive element; Tq71c12.x1 NCI_CGAP_P128 Homo saplens cDNA clone IMAGE:3288118 3' similar to gb:J02611 APOLI PORTOTEIN DISULEDE ISOMERASE PRECURSOR; (HUMAN); Tq71c12.x1 NCI_CGAP_LU24 Homo saplens cDNA clone IMAGE:351275 3' similar to gb:J02611 APOLI PORTOTEIN D PRECURSOR (HUMAN); Tq71c12.x1 NCI_CGAP_LU24 Homo saplens cDNA clone IMAGE:2551275 3' similar to gb:J02611 APOLI PORTOTEIN D PRECURSOR (HUMAN); Tq0133867F1 NIH_MGC_53 Homo saplens cDNA clone IMAGE:2551275 3' similar to gb:J02611 APOLI PORTOTEIN D PRECURSOR (HUMAN); Td0133867F1 NIH_MGC_53 Homo saplens cDNA clone IMAGE:2682168 5' Tq0133867F1 NIH_MGC_53 Homo saplens cDNA clone IMAGE:2682168 5' Tq0133867F1 NIH_MGC_54 Depter INTANESCRIPTION PACTOR NFAT5) (REL_DOMAIN-CONTAINING TRANSCRIP	T HUMAN T HUMAN T HUMAN T HUMAN T HUMAN T HUMAN T HUMAN T HUMAN T HUMAN T HUMAN	1 -   -   -   -   -   -   -   -   -   -			32850 29055 29065 29066 29066 29506 31813 31813 31813 32257 32257 35779 35779 35779 35770 35770	19492 25168 13722 13722 16957 16968 18770 18770 18954 18954 18954 22234 22234 22234 22234 22234 22234 14952 14952	12039 12217 12217 12217 12217 12217 12217 12217 12217 5574 5671 5671 5671 5671 5762 5762 5774 5671 5762 5774 5774 5774 5774 5774 5774 5774 577
Homo sapiens phospholipid scramblase 1 gene, complete cds Homo sapiens chromosome 21 sagment HS21C085	TN TN	5.2E-01 AF224492.1	R) A	3.05	27438	14379	1218
omo sapiens phospholipid scramblase 1 gene, complete cds					L	ı	125
JOLEAR FACTOR OF ACTIVALED I CELLS 5 (1 CELL IRANSCRIPTION FACTOR NEALS) EL DOMAIN-CONTAINING TRANSCRIPTION FACTOR NEATS)				7.57			1190
osophila melanogaster helix-loop-helix mRNA, complete cds			5.				839
POLIPOPROTEIN D PRECURSOR (HUMAN);	$\neg$	3.1	Ġ	1.73			45
30e05.s1 NCI_CGAP_Br7 Homo saplens cDNA clone IMAGE:1441376 3' similar to gb:J02611	Ī				L	┺	1
r1339867F1 NIH_MGC_53 Homo sapiens cDNA clone IMACE:3682168 5'	Г					L	6
W:COXA_HUMAN P20674 CYTOCHROME C OXIDASE POLYPEPTIDE VA PRECURSOR;							16
64b02.x1 NCI CGAP Met15 Homo sapiens cDNA clone IMAGE:2551275 3' similar to	2					ı	Γ
petitive element;			ις				26
71c12.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE: 3' similar to contains element MER29	Г						Г
betitive element;							56
71c12.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE: 3' similar to contains element MER29							Γ
laraplast product			'n	1.59			9
oridula gergonias ribulose 1,5-bisphosphate carboxylase (rbcL) gene, partial cds; chloroplast gene for							·
ROTEIN DISULFIDE ISOMERASE PRECURSOR (HUMAN);			ຜ				62
73c12.x1 NCI_CGAP_Pr28 Homo sapiens cDNA done IMAGE:3288118 3' similar to gb:J02783	7						Γ
(OTEIN DISULFIDE ISOMERASE PRECURSOR (HUMAN);			5.3	2.32		_	62
73c12.x1 NCI_CGAP_Pr28 Homo sapiens cDNA clone IMAGE:3288118 3' similar to gb:J02783	4						Γ
12g09.r1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:666112 5	Г		5.	0.95		L	E
12g09.r1 Scares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:866112.5	_			0.95		l_	7
42h12 y5 Soares ovary tumor NbHOT Homo sapiens cDNA clone IMAGE:740711 5'							74
42h12.y5 Soares ovary tumor NbHOT Homo sapiens cDNA clone IMAGE:740711 5'							74
coplasma genitalium section 9 of 51 of the complete genome				1.2			27
rno sapiens secreted C-type lectin precursor (LSLCL) gena, complete cds							15
mo sapiens protein tyrosine phosphatase, receptor-type, zeta polypeptide 1 (PTPRZ1) mRNA		4506328					5
rno sapiens protein tyrosine phosphatase, receptor-type, zeta potypeptide 1 (PTPRZ1) mRNA		4506328					43
f), and complement component C2 (C2) genes,>							29
rno sapens nun ciass in region contraming tenascenty (carascenty) gare, parta cass, cytochronien and allowates Inoxidase (CYP21B), complement component C4 (C4B) G11, helicase (SKI2W), RD, complement factor B	<u> </u>						
111 A 1- 111 A 1- 111 A 1- 111 A 1- 111 A 1- 11 A 11- 11 A 11- 11 A 11- 11 A 11- 11 A 11- 11 A 11- 11 A 11- 11	T	Ī				ı	:
37go4.x1 NCI_CGAP_Ut1 Homo saplens cDNA clone IMAGE:24271263' similar to gb.M13452 LAMINA			5.4E-01	2.41			17
				o.1	ı		3
thus norvegiculs gene for TIS11, complete cds			Value				7
Rattus norvegicus gene for TIS11, complete cds	Source	ď	1 N N N	Bubio			
Top Hit Descriptor Itus norvegicus gene for 71811, complete cds	Top Hit Database Source	Top Hit Acession No.	Most Similar (Top) Hit BLAST E	Expression Signal	ORF SEQ ID NO:	Exon SEQ ID NO:	Probe SEQ ID NO:

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Table 4
Single Exon Probes Expressed in Placenta

Moet Similar	Most Similar	Most Similar				
ORF SEQ Expression (Top) Hit Signal Signal BLAST E Value	E 6 9 >	(Top) H (Top) H BLAST Value	<u>.</u> ≅ ± ₪	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
2.85 5	2.85 5		ρ	.2E-01 AB018283.2	TN	Homo sapiens mRNA for KIAA0740 protein, partial cds
9	2.1 5	5.2	9	.2E-01 U65942.1	TN	Chlamydophila abortus strain S25/3 POMP91A and POMP90A precursor, genes, complete cds
1.05 5	1.05 5	5.2	Ş	.2E-01 D73443.1	TN	Azotobacter vinelandii icd gene for isocitrate dehydrogenase, complete cds
2	2	5.2E	þ	.2E-01 AL116780.1	NT	Botrytis cinerea strain T4 cDNA library under conditions of nitrogen deprivation
29708 2.01 5.2E	2		٥	.2E-01 AA984165.1	EST_HUMAN	am77g05.s1 Stratagene schizo brain S11 Homo sapiens cDNA clone IMAGE:1016504 3'
0.77 5.2E-	5		۶	.2E-01 AF020269.1	, FX	Medicago sativa chloropiast malate dehydrogenase precursor (p1mdh) mRNA, nuclear gene encoding chloropiast protein, complete cds
			1			Homo sapiens chromosome Xq28 melanoma antigan family A2a (MAGEA2A), melanoma antigan family A12 (MAGEA12), melanoma antigan family A3 (MAGEA3), caltractin (MAGEA12), melanoma antigan family A3 (MAGEA3), caltractin
0.87	വ	5.2E-0	_	2E-01 U82671.2	NT	(CALT), NAD(P)H dehydrogenasc-ilke protain (NSDHL), and Li>
19.0		5.2E-0	-	6752947 NT	INT	Mus musculus acetylcholine receptor beta (Acrb), mRNA
32283 0.92 5.2E-0		5.2E-0	·	5.2E-01 AA284261.1	EST_HUMAN	zc44d09.T7 Soares_senescent_fibrablasts_NbHSF Homo sapiens cDNA clone IMAGE:325169 3'
0.87		5.2E-01		5.2E-01 X02218.1	NT	Chicken duplicated genes for histone H2A, H4 and a histone H3 gene
0.87	2	5.2E-0	-		NT	Chicken duplicated genes for histone H2A, H4 and a histone H3 gene
0.49 5	2	2			EST_HUMAN	zq05b09.r1 Stratagene muscle 937.209 Homo sapiens cDNA clone IMAGE:028793 5'
1.32 5	2	2		2E-01 AF143952.2	본	Homo sapiens PELOTA (PELOTA) gene, complete cds
4.83			. =	5.2E-01 P18516	SWISSPROT	RETINOIC ACID RECEPTOR GAMMA (RAR-GAMMA) (RETINOIC ACID RECEPTOR DELTA) (RAR- DELTA)
. 2.5		. 5.1E-0		5.1E-01 M58509.1	LN	Human adrenodoxin reductase gene, exons 3 to 12
	L	5.1E-0	ıΨ	5.1E-01 AJ233944.1	TN	Polyangium vitallinum (strain PI vt1) 16S rRNA gene
4.57		5.1E-0	IΣ	5.1E-01 AJ233944.1	TN	Polyanglum vitellinum (strain PI vt1) 16S rRNA gene
1.02		5.1E-0	T	5.1E-01 X87885.1	NT	R.norvegicus mRNA for mammalian fusca protein
		5.1E-	91	5.1E-01 Al858495.1	EST_HUMAN	w39b12x1 NCI_CGAP_Ut1 Homo sapiens cDNA clone IMAGE:2427263 3'
30432 2.89 5.1E-		5.1E-	Įδ	5.1E-01 P96380	SWISSPROT	TRANSCRIPTION-REPAIR COUPLING FACTOR (TRCF)
0.6 5.1E-			2	BE091796.1	EST_HUMAN	IL2-BT0731-250400-077-G08 BT0731 Hamo saplens cDNA
32879 1 5.1E-4	1 5.1E-(	5.1E-(	12	5.1E-01 BE541068.1	EST HUMAN	601063606F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3450000 5'
6.0			I٣Ì	5.1E-01 AV712326.1	EST_HUMAN	AV712326 DCA Homo sapiens cDNA clone DCAAUF07 5'
1.35	1.35		7	5.1E-01 R80873.1	EST_HUMAN	y94a09.s1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:146872 3'
0.84	0.84		2	5.1E-01 AW806881.1	EST_HUMAN	QV4-ST0023-160400-172-a01 ST0023 Homo sapiens cDNA
35390 0.84 5.1E-	0.84		12	5.1E-01 AW808881.1	EST HUMAN	QV4-ST0023-160400-172-e01 ST0023 Homo capiens cDNA
4.65	4.65		힏	5.1E-01 J05412.1	NT	Human regenerating protein (reg) gene, complete cds
2	3.95	2	힏	.1E-01 W22302.1	EST_HUMAN	65B1 Human retina cDNA Tsp509I-cleaved sublibrary Homo sapiens cDNA not directional
66.0	66.0		티		Ę	Human carboxyl ester lipase (CEL) gene, complete cds
3.49 5.1E			티	5.1E-01 BF030207.1	EST HUMAN	601558883F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:3826767 5

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					0		
Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Тор Hit Descriptor
12634	25427		1,31	5.1E-01	5.1E-01 BF439982.1	EST_HUMAN	nac51f10x1 NCI_CGAP_Brn23 Homo saplens cDNA done IMAGE:3406218 3' similar to contains element TAR1 repetitive element ;
2203	_	28464			4885552	Ā	Homo sapiens postmeiotic segregation increased 2-like 9 (PMS2L9), mRNA
2203	ı				4885552 NT	L'N	Homo saplens postmetotic segregation Increased 2-like 9 (PMS2L9), mRNA
2211	15345	28472	2.09		5.0E-01 AF008210.1	TN	Buchnera aphidicola genomic fragment containing (chaperone Hsp60) groEL, DNA biosynthesis initiating protein (dnaA), ATP operon (stpCDGAHFEB), and putative chromosome replication protein (gidA) genes, complete cds; and termination factor Rho (rho) gene>
							Buchræra aphidicola genomic fragment containing (chaperone Hsp60) groEL, DNA biosynthesis initiating protein (dnaA), ATP operon (stp.CDGAHFEB), and putative chromosome replication protein (gidA) genes,
211	15345	28473	2.09		5.0E-01 AF008210.1	NT	complete cds; and termination factor Rho (rho) gene>
2231	15365		1.56	5.0E-01	5.0E-01 AL161533.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 33
3842	17001	30004	0.85	5.0E-01		TN	Mus musculus anti-DNA immunoglobulin light chain IgM mRNA, antibody 363p.138, partial cds
3934	17093	30091	0.93	5.0E-01		NT	Rattus norvegicus jagged protein mRNA, complete cds
3977	1	30137	2.67	5.0E-01		NT	Homo sapiens mRNA for KIAA1184 protein, partial ods
6782			0.82	5.0E-01		EST_HUMAN	602132642F1 NIH_MGC_81 Hamo sapiens cDNA clone IMAGE:4271939 5'
7842				5.0E-01		NT	Arabidopsis thaliana DNA ctromosome 4, contig fragment No. 49
7842	20897	34399	<b>78</b> 0	5.0E-01	.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 49
8727	21807		1.63		5.0E-01 M92304.1	IN	Xenceus laevis smooth muscle beta-tropomyosin mRNA, complete cds
8870	21949	35484	99'0		5.0E-01 BF107848.1	EST_HUMAN	601823850R1 NIH_MGC_79 Homo sapiens cDNA clone IMAGE:4043485 31
9657	21100	34613	2.13		5.0E-01 BF317212.1	EST_HUMAN	601903871F1 NIH_MGC_19 Hamo saptens cDNA clone IMAGE:41368325'
9824	22864	36445	1.47		5.0E-01 P35573	SWISSPROT	GLYCOGEN DEBRANCHING ENZYME (GLYCOGEN DEBRANCHER) [INCLUDES: 4-ALPHA- GLUCANOTRANSFERASE (OLIGO-1,4-1,4-GLUCANTRANSFERASE); AMYLO-1,6-GLUCOSIDASE (DEXTRIN 6-ALPHA-D-GLUCOSIDASE)]
							GLYCOGEN DEBRANCHING ENZYME (GLYCOGEN DEBRANCHER) [INCLUDES: 4-ALPHA-
0824	22864	36446	1 47		4 OF -01 P38573	TORGSPINS	GLUCANOTRANSFERASE (OLÍGO-1,4-1,4-GLUCANTRANSFERASE); AMYLO-1,6-GLUCOSIDASE (DEXTRIN 6-ALPHA-D-GLUCOSIDASEI)
10602	$\perp$				18.1	EST HUMAN	601445024F1 NIH MGC 65 Homo sapiens cDNA clone IMAGE:3849436 5'
12307	1		3.64			NT	Mus musculus MRC OX-2 antigen hamolog gene, exons 2-5, and complete cds
13093			2.25		02.2	Ŋ	Homo sapiens chromosome 21 segment HS21C102
13109	25724		4.71		5.0E-01 O13961	SWISSPROT	NUCLEAR ENVELOPE PROTEIN CUT11
812	13991	27045	1.83		4.9E-01 BF571462.1	EST_HUMAN ·	602076649F1 NIH_MGC_62 Hamo sepiens cDNA clane IMAGE:4243860 5'
1692			1.08		4.9E-01 AJ243955.1	NT	Xencpus faevis mRNA for c-Jun protein, 1978 BP
1955	15098		1.34		1.	NT	Cavia porcellus pulmonary surfactant protein A (SP-a) mRNA, complete cds
2252	18719	31735	1.17		4.9E-01 Q61554	SWISSPROT	FIBRILLIN 1 PRECURSOR

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Top Hit Descriptor	Homo sapiens diacylglycerol kinase 3 (DAGK3) gene, exon 10	Homo sapiens diacylglycerol kinase 3 (DAGK3) gene, excn 10	Oryza sativa subsp. Japonica mEF-G mRNA for mitochondrial elongation factor G, complete cds	PUTATIVE UNDECAPRENYL-PHOSPHATE ALPHA-N-ACETYLGLUCOSAMINYLTRANSFERASE	PUTATIVE UNDECAPRENYL-PHOSPHATE ALPHA-N-ACETYLGLUCOSAMINYLTRANSFERASE	601874964F1 NIH_MGC_54 Hamo sapiens cDNA clone IMAGE:4102503 5'	he90c02.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2907266 3' similar to TR:095714 O95714 HERC2.	Mus musculus unc13 homolog (C. elegans) 1 (Unc13h1), mRNA	Mus musculus adenylyl cyclase 1 (Adcy1) cDNA, partial cds	Homo sapiens neurotrophin-1/B-cell stimulating factor-3 gene, complete cds	ng22e11.s1 NCI_CGAP_Co10 Homo saplens cDNA clone IMAGE:1144652 3'	Homo sapiens chromosome 21 segment HS21C101	Homo saplens eukaryotic translation initiation factor 4 gamma, 1 (EIF4G1), mRNA	Homo sapiens potassium channel, subfamily K, member 5 (TASK-2) (KCNK5) mRNA, and translated	products	Saccharomyces cerevisiae) sporulation protein (SPO11) gene required for melotic recombination, complete	cds	Mus musculus siow skeletal muscle troponin T (Trint1) gene, complete cds	nu85f09.s1 NCI_CGAP_AM Homo sapiens cDNA done IMAGE:1217513	Homo sapiens reproduction 8 (D8S2298E) mRNA	Homo saplens chromosome 21 segment HS21C009	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 4	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 4	y7710, 55 Scares breast 2NbHBst Homo saplens cDNA done IMAGE:154795 5' similar to contains element	MEK6 repetitive element;	PM:1-HT0350-201299-004-b04 HT0350 Homo capiens cDNA	602184267F1 NIH_MGC_42 Homo saplens cDNA clone IMAGE:4300048 5	S.cerevisiae ORFs from chromosome X	Hano sapiens chromosame 21 segment HS21C027	Trypanosoma cruzi transposon VIP II SIRE ropoat region	Fells catus feline leukemia virus subgroup C receptor (FLVCR1) mRNA, complete cds	601883880F1 NIH_MGC_57 Homo saplens cDNA clone IMAGE:4096387 6	q72a09.x1 Soeres_testis_NHT Homo sepiens cDNA clone IMAGE:1755544.3/
Top Hit Database Source	L	NT	NT	SWISSPROT	SWISSPROT	EST_HUMAN	EST HUMAN	10946863 NT	Z	FN	EST_HUMAN	L	F		LN T		Z.	NT	EST_HUMAN	LN	INT	. IN	NT		EST_HUMAN	EST_HUMAN	EST_HUMAN	NT	F	NT		EST_HUMAN	EST HUMAN
Top Hit Acession No.	9E-01 AF020931.1	.9E-01 AF020931.1	.9E-01 AB040051.1	.9E-01 Q10606	.9E-01 Q10606	.9E-01 BF209791.1	9E-01 AW339905.1	10946863	.9E-01 AF053980.1	.9E-01 AF176912.1	.9E-01 AA613582.1	.9E-01 AL163301.2	11431438 NT		4504850 NT		.8E-01 J02987.1	4.8E-01 U92882.1	4.8E-01 AA659878.1	5031650 NT	4.8E-01 AL163209.2	AL161492.2	4.8E-01 AL161492.2		4.8E-01 AI820744.1	4.8E-01 BE155148.1	4.8E-01 BF568633.1	4.8E-01 X83502.1	4.8E-01 AL163227.2	.8E-01 AF227565.1	4.7E-01 AF192387.1	4.7E-01 BF217173.1	4.7E-01 AI204374.1
Most Similar (Top) Hit BLAST E Value	4.9E-01	4.9E-01	4.9E-01	4.9E-01	4.9E-01	4.9E-01	4.9E-01	4.9E-01	4.9E-01	4.9E-01	4.9E-01	4.9E-01	4.9E-01		4.8E-01		4.8E-01	4.8E-01	4.8E-01	4.8E-01	4.8E-01	4.8E-01	4.8E-01		4.8E-01	4.8E-01	4.8E-01	4.8E-01	4.8E-01	4.8E-01	4.7E-01	4.7E-01	4.7E-01
Expression Signal	2.67	2.67	1.61	0.86	0.86	1.96	96.0	22	1.05	2.61	4.94	1.69	1.27		0.59		9.66	69.0	4.18	1.83	1.06	3.59	3.59		1.81	1.05	0.55	1.9	1.56	5.78	0.59	8.07	0.84
ORF SEQ ID NO:	32682	32683	34156	34439	34440		36028		37166	l		31939			_			33378			34403	34497	34498		34686								33461
Exon SEQ ID NO:	19337	19337	20680	l	Į	22268	22484	L		L	L	L	25768		17592	1	18818	19970	19980	20544	20900	20988	20988	l		22562	23248	1	ı	25918	16318		20051
Probe SEQ ID NO:	6161	6161	7610	7882	7882	9190	9389	9496	10524	12197	13085	13094	13181		4462		5624	6817	6827	7469	7845	7938	7938		8089	9446	10212	10966	12279	12509	3142	6644	7186

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Probe SEQ ID	_ 0	ORF SEQ	Expression	Most Similar (Top) Hit	Top Hit Acession	Top Hit Database	Top Hit Descriptor
ö	Ö		S S	Value	ĝ	Source	
8049	21132	34652	0.75		4.7E-01 T11414.1	EST_HUMAN	hbc811 Human pancreatic islet Homo sapiens oDNA clone hbc811 Send
8049	21132		92'0	4.7E-01	4.7E-01 T11414.1	EST_HUMAN	hbc811 Human pancreatic islet Homo sapiens cDNA clone hbc311 5'end
9276	22352	35904	0.61	4.7E-01	LN 1051869	TN	Rattus norvegicus Spermine binding protein (Sbp), mRNA
11084	24158		4.37	4.7E-01	4.7E-01 AF102673.1	TN	Influenza A virus Isolate hk51697 hemagglutinin (HA) gene, partial cds
11340	24403		1.94	4.7E-01	4.7E-01 U41069.1	NT	Human collagen alphaz(XI) (COL11A2) gene, exons 6 through 16, and partial cds
11658	24737	38428	1.45	4.7E-01	4.7E-01 AW889448.1	EST_HUMAN	RC6-NT0029-240400-011-E08 NT0029 Hamo saplens cDNA
12401	25281		1.84	4.7E-01	4.7E-01 BE887763.1	EST_HUMAN	601511333F1 NIH_MGC_71 Hcmo sapiens cDNA clone IMAGE:3912488 5'
12529	25361		1.25	4.7E-01	4.7E-01 AW341561.1	EST_HUMAN	hd11c08.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2909198 3'
3837	16997			4.6E-01	4.6E-01 BF693300.1	EST_HUMAN	602081103F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4245481 5'
3837	16997	30000		4.6E-01	4.6E-01 BF693300.1	EST_HUMAN	602081103F1 NIH_MGC_81 Homo sapiens oDNA clone IMAGE:4245481 5'
5535	18732			,	4.6E-01 BF313593.1	EST_HUMAN	601900234F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4129472 5'
5535	18732	31748	26'0		4.6E-01 BF313593.1	EST_HUMAN	801900234F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4129472 51
2588	18783				4.6E-01 Q90643	SWISSPROT	INTERFERON REGULATORY FACTOR 3 (IRF-3)
5588	18783	31829			4,6E-01 Q90643	SWISSPROT	INTERFERON REGULATORY FACTOR 3 (IRF-3)
5993	18857	32140		4.8E-01	4.8E-01 BE734781.1	EST_HUMAN	601568755F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3843637 5'
						100	qh59h02.x1 Soeres_fetal_liver_spleen_1NFLS_S1 Homo saplens cDNA done IMAGE:1849011 3' similar to
2877	188/1	32157	3.62		4.6E-01 AI24/6/9.1	ES HUMAN	IR.O 19836 DO 1 TROPTILIN.
5677	18871		3.62		4.6E-01 AI247679.1	EST_HUMAN	qh59h02.x1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1849011 3' similar to TR:01s338 01s338 BUTYROPHILIN.;
5685	18879	32189			4.6E-01 P20050	SWISSPROT	MEIOSIS SPECIFIC PROTEIN HOP1
6763	18955		0.85		4.6E-01 AF212124.1	TN	Anolis schwartzi cytochrome b gene, partial cds; mitochondrial gene for mitochondrial product
2820	19040		6.0		4.6E-01 BE817247.1	EST_HUMAN	PM0-BN0260-120600-001-F07 BN0260 Homo sapiens cDNA
							Methanobacterium thermoautotrophicum from bases 1165751 to 1176238 (section 100 of 148) of the
6386	19555	32914	0.82		4.6E-01 AE000894.1	M	complete genome
						!	Emericella nidulans NEMPA (nempA) gene, mitochondrial gene encoding putative mitochondrial protein,
9069	20221	33649	2.39		4.6E-01 U6Z332.1	Z	complete cas
9009	2002	33650			4 6F-01 (U62332 1	L	Emericella nidulans NEMPA (nempA) gene, mitochondrial gene encocling putative mitochondrial protein, complete ods
27.57	25843		99'0		4.6E-01 L07320.1	LN	Murine cytomegalowirus e1 protein gene, complete cds
							nh04h05.s1 NCI CCAP Thy1 Home sepiens cDNA clone IMACE:943363 cimilar to contains Alu repetitive
7906	20958		0.78			EST_HUMAN	element;contains element L1 repetitive element;
8515	ı	35131			4.6E-01 BF697399.1	EST_HUMAN	602130953F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4287828 5
8946	1	İ			_	EST_HUMAN	0076b08.s1 NCI_CGAP_Kid5 Homo sapiens cDNA clone IMAGE:1572087 3' similar to gb:M36341 ADP-RIBOSYLATION FACTOR 4 (HUMAN);

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Top Hit Descriptor	oo76b08.s1 NCI_CGAP_Kid5 Homo sapiens cDNA done IMAGE:1572087 3' similar to gb:M36341 ADP-RIBOSYLATION FACTOR 4 (HUMAN);	ATRIAL NATRIURETIC PEPTIDE RECEPTOR B PRECURSOR (ANP-B) (ANPRB) (GC-B) (GUANYLATE CYCLASE)	ATRIAL NATRIURETIC PEPTIDE RECEPTOR B PRECURSOR (ANP-B) (ANPRB) (GC-B) (GUANYLATE CYCLASE)	Glycine max acetyl-CoA carboxylase (accB-1) gene, complete cds; nuclear gene for chloroplast product	Glycine max acetyl-CoA carboxylass (accB-1) gene, complete cds; nuclear gene for chloroplast product	wg73e12.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo saplens cDNA clone IMAGE:2370766 3'	wg73e12.x1 Scares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:23707663'	PUTATIVE VITELLOGENIN RECEPTOR PRECURSOR (%)	IL5-HT0730-100500-075-g05 HT0730 Hamo sepiens cDNA	IL5-HT0730-100500-075-g05 HT0730 Homo saplens cDNA	Human thiopurine methyltransferase (TPMT) gene, excn 10 and complete cds	Human thiopurine methytransferase (TPMT) gene, exon 10 and complete cds	Deinococcus radiodurans R1 section 68 of 229 of the complete chromosome 1	Deinococcus radiodurans R1 section 68 of 229 of the complete chromosome 1	455d02.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sepiens cDNA clone IMAGE:4541793'	xc25c06.x1 NCI_CGAPCo19 Homo saplens cDNA clone IMAGE:2585290 3' similar to gb:L07807 DYNAMIN-1 (HUMAN):	xc25c06.x1 NCI_CGAP_Co19 Hamo sapiens cDNA clone IMAGE:2585290 3' similar to gb1.07807	DYNAMIN-1 (HUMAN);	BASEMENT MEMBRANE-SPECIFIC HEPARAN SULFATE PROTEOGLYCAN CORE PROTEIN	PRECURSOR (HSPG) (PERLECAN) (PLC)	Mus musculus DNA polymerase epsilon catalytic subunit (Pole) gene, exons 2 through 12	COLLAGEN ALPHA 5(IV) CHAIN	as96e09.x1 Barstead aorta HPLRB6 Homo sapiens cDNA clone IMAGE:2353480 3'	ho60g02.x1 Soares_NFL_T_GBC_S1 Hama sapiens cDNA clane IMAGE:3041810 31	601657225R1 NIH_MGC_67 Hamo septens cDNA clone IMAGE:3866023 31	QV2-PT0012-140100-031-c09 PT0012 Homo saplens cDNA	COAT PROTEIN	Rat nucleolar proteins B23.1 and B23.2
Top Hit Database Source	EST_HUMAN	SWISSPROT	SWISSPROT	TN	TN	П		SWISSPROT	EST HUMAN	EST_HUMAN	NT	NT	NT		EST_HUMAN	FST HIMAN		EST_HUMAN		SWISSPROT	Ę	SWISSPROT	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	SWISSPROT	N
Top Hit Acession No.	6E-01 AA932237.1	6E-01 P55202	6E-01 P55202	6E-01 AF162283.1	.6E-01 AF162283.1	1.6E-01 AI915634.1	.6E-01 Al915634.1	.6E-01 P98163	.6E-01 BE185449.1	.6E-01 BE185449.1	.6E-01 AF019369.1	.6E-01 AF019369.1	.5E-01 AE001931.1	.5E-01 AE001931.1	.5E-01 AA677086.1	EE-04 AW083761 4		.5E-01 AW083761.1		.5E-01 Q05793	78.1	.6E-01 Q28247	.5E-01 AI708908.1	.5E-01 AW873495.1	.5E-01 BE963445.2	.5E-01 AW608814.1	.5E-01 Q00956	.5E-01 M37038.1
Most Similar (Top) Hit BLAST E Value	4	4	4.6E-01	4.6E-01	4.6E-01	4.6E-01	4.6E-01	4.6E-01	4.6E-01	4	4.6E-01	4.6E-01	4.5E-01	7	4.5E-01	*		4		4	4	4	4	4.5E-01	4	4.5E-01	4	4
Expression Signal	0.54	0.93	0.93	0.52	0.52	1.15	1.15	2.31	5.06	5.06	4.3	4.3	1.15	1.15	4.83	89.0	3	0.66		4.46	1.51	1.18	1.02	4.71	1.18	1.57	1.38	0.91
ORF SEQ ID NO:	35568			36490	36491		36810		37956		37573	37574	28203	28204	29124			29568			29651		30329		31161			34120
Exon SEQ ID NO:	22025	1		l		23218	23218	L	24317	Į.	23946	L	15103	15103		16860		16552		16563	l	١.	17336	18478	18186	L	l	20843
Probe SEQ ID NO:	8946	9501	9501	9866	9866	10181	10181	11238	11248	11248	11760	11760	1960	1960	2933	0000	9000	3380		3393	3465	4139	4186	4282	5058	9999	6740	7571

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				Most Similar			
Probe SEQ (D NO:	SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	(Top) HII BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
7785	20841	34333	2.39	4.5E-01	.5E-01 AI858849.1	EST_HUMAN	wi32e02.x1 NCI_CGAP_Ut1 Homo septiens cDNA clone IMAGE:2426618 3' similar to TR:Q92923 Q92923 SW/SNF COMPLEX 170 KDA SUBUNIT.;
8502			1.11	4.5E-01	.5E-01 M32661.1	ΙN	D.melanogaster Shaw2 protein mRNA, complete cds
8538	21679	35217	2.87	4.5E-01	.5E-01 AI648596.1	EST_HUMAN	[z56g11.x1 NCI_CGAP_0v35 Hamo sepiens cDNA clone IMAGE:2292644 3'
				į		TOGGGGIMA	POLY-BETA-HYDROXYBUTYRATE POLYMERASE (POLY(3-HYDROXYBUTYRATE) POLYMERASE) (PHB POLYMERASE) (PHB SYNTHASE) (POLY(3-HYDROXYALKANOATE) POLYMERASE) (PHA PON SAEDASES (PHA SYNTHASE) (PON YHYDROXYALKANOIC ACID SYNTHASE)
8/20	212	323/0	0.00	4.55-01	32-01 Q32/20 3w	MT	Homo seriens hypothetical profelin DKFZ0547G183 (DKFZ0547G183), mRNA
080		1000	00.3		2000	1	Eschadebia will K.13 MC16E5 sertion 108 of 400 of the complete name
9200	22278	71805	0.00		5E-01 AE000216.1	z EZ	Bombwc mon nuclear polyhedrosis yfuts, complete genome
10742		27252	25.50		MRGOOF,	EST HIMAN	EST02531 Fetal brain. Stratagene (cat#936206) Homo sablens cDNA clone HFBCY17
10713	1_	37353	25.59		.5E-01 M86006.1	EST HUMAN	EST02531 Fetal brain, Stratagene (cat#936206) Homo sapiens cDNA clone HFBCY17
11104		37812	:	4	5E-01 AW591271.1	EST HUMAN	xo14h01.x1 NCI_CGAP_UB Homo sapiens cDNA clone IMAGE:2703985 3' similar to SW:INT9_MOUSE EST_HUMAN \ Q64252 VIRAL INTEGRATION SITE PROTEIN INT-6. [1];
11225		37835		4	11430799 NT	NT	Homo saplens cadherin 3, P-cadherin (placental) (CDH3), mRNA
11530	L.		1.3	4	.5E-01 AV719382.1	EST_HUMAN	AV719382 GLC Homo sapiens cDNA clone GLCCED12 6
12164			5.58		4.5E-01 BE871461.1	EST_HUMAN	601449201F1 NIH_MGC_65 Homo saplens cDNA clone IMAGE:3852961 5'
12895			1.2	4	.5E-01 BF337531.1	EST_HUMAN	602035275F1 NCI_CGAP_Brn64 Homo sapiens cDNA clone IMAGE:4183290 5'
12970	25630		12.42	4.5E-01	11422099 NT	NT	Homo saplens testis-specific kinase 2 (TESK2), mRNA
2094	15234		1.11	4.4E-01	6680503 NT	ΙN	Mus musculus integral membrane-associated protein 1 (Imap1), mRNA
2462	, 10 10 10 10 10 10 10 10 10 10 10 10 10	20745	416		4E-01 PA0785	TORGRENA	VASCULAR ENDOTHELIAL GROWTH FACTOR B PRECURSOR (VEGF-B) (VEGF RELATED FACTOR)
3390	1	29575		`	4.4E-01 AF058790.1	N-	Rattus norvegicus SynGAP-b mRNA, complete cds
3390	1	29576			4.4E-01 AF058790.1	N.	Rattus norvegicus SynGAP-b mRNA, complete cds
3395	1	29580		[	4.4E-01 BF056726:1	EST_HUMAN	7)91402.y1 NCI_CGAP_Br16 Homo sapiens cDNA clone IMAGE:3393795 5'
4349	ı				4.4E-01 BE378707.1	EST_HUMAN	601237139F1 NIH_MGC_44 Homo saplens cDNA clone IMAGE:3609383 5
5536	18733	31749	1.31	ļ	4.4E-01 P04929	SWISSPROT	HISTIDINE-RICH GLYCOPROTEIN PRECURSOR
5536	l_		1.31	Ĺ	4.4E-01 P04929	SWISSPROT	HISTIDINE-RICH GLYCOPROTEIN PRECURSOR
5805	18995	Ì	1.58		4.4E-01 S65019.1	TN	mucin [rate, Sprague-Dawley, sulfur-dioxide-treated tracheal epithelium, mRNA Partial, 390 nt]
5823	19013		1.81		4.4E-01 AV720408.1	EST_HUMAN	AV720408 GLC Homo sepiens cDNA clone GLCCSC12 5'
6074	1	32584	1.12		4.4E-01 AI198413.1	EST_HUMAN	qi62h11.x1 NCI_CGAP_Brn25 Hamo sapiens cDNA clone IMAGE:1861125 3' similar to TR:Q29168 Q29168 UNKNOWN PROTEIN;

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Probe SEQ ID NO:	SEO D NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
6074	19256	32585	1.12	4	4E-01 AI198413.1	EST_HUMAN	q62h11.x1 NCI_CGAP_Brr25 Homo sapiens dDNA clone IMAGE:1861125 3' similar to TR:Q29168 Q29168 UNKNOWN PROTEIN:
6370	19539	32899	1.67	4	.4E-01 AW080795.1	EST HUMAN	xa27e08.x1 NC _CGAP_Co18 Home sapiens oDNA clone IMAGE:2585510 3' similar to TR:095164 095154 AFLATOXIN B1-ALDEHYDE REDUCTASE. ;
6458	19625		1.05	4	4E-01 AA776132.1	EST_HUMAN	ae85d11.s1 Stratagene schizo brain S11 Homo sapiens cDNA clone IMAGE.970965 3' similar to gb:M16038 TYROSINE-PROTEIN KINASE LYN (HUMAN);
7667	20629	34104	1.14		4.4E-01 AE000571.1	LN	Helicobacter pylori 26695 section 49 of 134 of the complete genome
8024	21107		12.3		4.4E-01 Z11679.1	NT	S.tuberosum mRNA for induced stolon tip protein (partial)
8962	22041	35584	1.11	4.4E-01		EST HUMAN	zl69a03.s1 Stratagene colon (#937204) Homo sapiens cDNA clone IMAGE:509836 3'
9352	22427	35985	0.78	4	4E-01 AF112540.1	NT.	HIV-1 isolate 08107v6 from USA, envelope glycoprotein (env) gene, partial cds
9385	22460	36023	0.62	4	4E-01 AW612578.1	EST_HUMAN	hho5c08.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2954222 3' similar to SW:WSH6_HUMAN P52701 DNA MISMATCH REPAIR PROTEIN MSH6:
9490	22547	36110	1.13	4	.4E-01 062836	SWISSPROT	ZINC FINGER X-CHROMOSOMAL PROTEIN
10167	23204	36798	1.95	4	4E-01 AI268650.1	EST_HUMAN	qo38f09,x1 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1910921 3'
10168	23205		2.09	4	.4E-01 P28922	SWISSPROT	GLYCOPROTEIN B PRECURSOR (GLYCOPROTEIN 14)
10302	23337	36942	4.94	4		SWISSPROT	TYROSINE-PROTEIN KINASE RECEPTOR TIE-1 PRECURSOR
10585	23620	L		4	4E-01 S76404.1	L L	beta -HKA=H,K-ATPase beta-surbunit [rats, Genomic, 8983 nt, segment 2 of 2]
10585	23620	3,7227	1.76	4	.4E-01 S76404.1	TN	beta -HKA=H,K-ATPase beta-subunit [rats, Genomic, 8983 nt, segment 2 of 2]
10829	23862	37485		4	4E-01 P02716	SWISSPROT	ACETYLCHOLINE RECEPTOR PROTEIN, DELTA CHAIN PRECURSOR
11522	24578	38256	1.64	4.4E-01	6691408 NT	NT	Terebratulina refusa mitochondrion, complete genome
12435	25308		4.23	4	0677874 NT	TN	Mus musculus sodium channel, type X, alpha polypeptide (Scn10a), mRNA
12447	26084		13.47	4	.4E-01 AL163282.2	NT	Homo sapiens chromosome 21 segment HS21C082
13051	25689		1.41	4.4E-01	.4E-01 P54725	SWISSPROT	UV EXCISION REPAIR PROTEIN PROTEIN RAD23 HOMOLOG A (HHR23A)
424	13619	26859	2.42	4	3E-01 AF155218.1	LN	Callitritx jacchus MW/LW opsin gene, upstream flanking region
424	13619		2.42	4	.3E-01 AF155218.1	TN	Cellithrix jacchus MW/LW opsin gene, upstream flanking région
1633	14785	27871		4	4.3E-01 AW866550.1	EST_HUMAN	QV4-SN0024-200400-183-b01 SN0024 Homo sapiens cDNA
2935	16112	L	1.34	4	.3E-01 AW935269.1	EST_HUMAN	CM2-DT0003-010200-077-c01 DT0003 Homo saplens cDNA
3127	16303	29316	0.95	4	.3E-01 AW999477.1	EST_HUMAN	MR0-BN0070-270300-008-g04 BN0070 Homo sapiens cDNA
4526	13619		1.27	4	.3E-01 AF155218.1	Z.	Cellithrix jacchus MW/LW opsin gene, upstream flanking region
4526	13619		1.27	4	.3E-01 AF155218.1	Ι	Callithrix jacchus MW/LW opsin gene, upstream flanking region
5071	18199		1.04		4.3E-01 AL161502.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 14
6220	18342		0.94		9635250 NT	NT	Xestia c-nigrum granulovirus, complete genome
5480	18679				4.3E-01 P48634	SWISSPROT	LARGE PROLINE-RICH PROTEIN BAT2 (HLA-B-ASSOCIATED TRANSCRIPT 2)
5480	18679	31694	0.95	╛	4.3E-01 P48634	SWISSPROT	LARGE PROLINE-RICH PROTEIN BAT2 (HLA-B-ASSOCIATED TRANSCRIPT 2)

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2011104	Top Hit Database Source	ΤΝ	FZ	NT	EST_HUMAN	EST_HUMAN	NT	<b>EST_HUMAN</b>	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST HUMAN	INT	NT	TN	EST_HUMAN	EST_HUMAN	EST_HUMAN	TN	EST_HUMAN	EST_HUMAN	EST_HUMAN	INT	FZ	EST_HUMAN	닐		뒫	TN	EST_HUMAN	SWISSPROT	SWISSPROT	EST_HUMAN
810	Top Hit Acession No.	4758039 NT	J57431.1	4.2E-01 U57431.1	4.2E-01 AA705007.1	4.2E-01 AW863666.1	4.2E-01 AB023489.1	4.2E-01 BE966485.2	4.1E-01 AI905481.1	4.1E-01 AV705243.1	4.1E-01 AV705243.1	4.1E-01 Al905949.1	7705283	4.1E-01 AL1615362	4.1E-01 AL161536.2	4.1E-01 AA906344.1	4.1E-01 AW961292.1	4.1E-01 AW961292.1	4.1E-01 AJ249207.1	4.1E-01 AA909257.1	4.1E-01 AV747880.1	4.1E-01 BF681393.1	J02298.1	J67535.1	4.1E-01 BF574604.1	6755521 NT		4.1E-01 AF160597.1	4.1E-01 AL139076.2	4.1E-01 AV649579.1	718584	<b>⊃1858</b> 4	4.1E-01 BF349382.1
	Most Similar (Top) Hit BLAST E Value	4.2E-01	4.2E-01 U57431.1	4.2E-01	4.2E-01	4.2E-01	4.2E-01	4.2E-01	4.1E-01	4.1E-01	4.1E-01	4.1E-01	4.1E-01	4.1E-01	4.1E-01	4.1E-01	4.1E-01	4.1E-01	4.1E-01	4.1E-01	4.1E-01	4.1E-01	4.1E-01 U02298.1	4.1E-01 U67535.1	4.1E-01	4.1E.01		4.1E-01	4.1E-01	4.1E-01	4.1E-01 P18584	4.1E-01 P18584	4.1E-01
	Expression Signal	0.72	0.51	0.51	0.81	1.44	1.43	1.87	211	1.46	1.46	1.77	1.46	2.12	2.12	99.0	0.73	0.73	3.78	0.99	1.36	4.84	99.0	2,48	1.36	1.51		0.75	1.58	1.15	0.68	0.68	1.14
	ORF SEQ ID NO:	35010		36142		37354	38005	38368	27338	27347	27348	27877	29001	29202	29203	29561	30028	30029	30513		30912	32626		34137	34827	35918				37266			
	SEQ ID NO:	21482	22576	22576	23212	23747	24364	24678	14283	14292	14292	14792	15890	16181	16181	16547	17030	17030	17532	17563	17924	19291	20010	20661	21307	22368		22762	23505	23656	23758	23758	23839
	Probe SEQ ID NO:	8401	9511	9511	10175	10714	11298	11679	1118	1127	1127	1640	2775	3006	3006	3375	3871	3871	4389	4422	4789	6111	6857	7590	8225	9292		9765	10470	10622	10725	10725	10806

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26116 1.38 4.0E-01 Z49301.1 NT 26036 1.21 4.0E-01 BF432020.1 EST HUMAN		27286 27286 27286 28317 28402 29532 30089 33108 6 34714 6 35827 6 35827 6 35827 6 35827 6 35827 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6	>	4.1E.01 X58700.1 NT 4.1E.01 X58700.1 NT 4.1E.01 Q09470 SW 4.1E.01 Q09470 SW 4.1E.01 Q09470 SW 4.1E.01 Q09470 SW 4.1E.01 Q09470 SW 4.1E.01 Q09470 NT 4.0E.01 AF203478.1 NT 4.0E.01 AF203480.1 NT 4.0E.01 AF20380.2 NT 4.0E.01 AF20380.2 NT 4.0E.01 AF20380.1 NT 4.0E.01 AF20380.1 NT 4.0E.01 AF20380.1 NT 4.0E.01 AF20380.1 SW 4.0E.01 AF20380.1 ES 4.0E.01 AF20380.1 ES 4.0E.01 AF2030.1 ES 4.0E.01 AF2030.1 ES 4.0E.01 AF2030.1 SW 4.0E.01 AF2030.1 SW 4.0E.01 AF2030.1 ES 4.0E.01 AF2030.1 ES 4.0E.01 AF2030.1 ES 4.0E.01 AF2030.1 ES 4.0E.01 AF2030.1 ES	Detabase Source NT SWISSPROT NT NT NT NT NT NT NT NT NT NT NT NT NT	Top Hit Descriptor  Zea mays. ZMPMS2 gene for 19 kDa zein protein  VOLTAGE-GATED POTASSIUM CHANNEL PROTEIN KV1.1 (HUKI) (HEK1)  Homo saplens DNA for amyloid precursor protein, compiete cds  Homo saplens SCL gene locus  Lequeus unbellus mitochrondron, complete genome  Diosophila melanogasster Dalimatian (dmt) mRNA, complete cds  Mus musculus platielet derived growth factor receptor, beta polypeptide (Pdgfrb), mRNA  Ascobolus immeraus mass2 gene  Ascobolus immeraus mass2 gene  Ascobolus immeraus mass2 gene  Ascobolus immeraus mass2 gene  Ascobolus immeraus mass2 gene  Ascobolus immeraus mass2 gene  Mus musculus biquilbn-protein ligeas e3 componen n-recognin (Ubr1), mRNA  Ascobolus immeraus mass2 gene  Mus musculus biquilbn-protein ligeas e3 componen n-recognin (Ubr1), mRNA  Homo saplens chromosome 21 segment HS21CO80  Homo saplens chromosome 21 segment HS21CO80  Homo saplens chromosome 21 segment HS21CO80  Strespicocous preumoniae YIIC (yilC), YIID (yilD), panicillin-binding protein 2x (pbp2x), and undecaprenty  Homo saplens chromosome 21 segment HS21CO80  Ovis arise partial JD2 gene for T cell receptor delta chain (TCRD21), excn 1  Ovis arise partial JD2 gene for T cell receptor delta chain (TCRD21), excn 1  Solvis arise partial JD2 gene for T cell receptor delta chain (TCRD21), excn 1  SON sa rise partial JD2 gene for T cell receptor delta chain (TCRD21), excn 1  SON Sa rise partial JD2 gene for T cell receptor delta chain (TCRD21), excn 1  SON Sa rise partial JD2 gene for T cell receptor delta chain (TCRD21), excn 1  SON Sa rise partial JD2 gene for T cell receptor delta chain (TCRD21), excn 1  SON Sa rise partial JD2 gene for T cell receptor delta chain (TCRD21), excn 1  SON Sa rise partial JD2 gene for T cell receptor delta chain (TCRD21), excn 1  SON Sa rise partial JD2 gene for T cell receptor delta chain (TCRD21), excn 1  SON Sa rise partial JD2 gene for T cell receptor delta chain (TCRD21), excn 1  SON Sa rise partial JD2 gene for T cell receptor delta chain (TCRD21)  SON Sa rise partial JD2 gene for T c
75507.1 1.84 3.9E-01 AF206618.1 NT				AF206618.1	N	Gorilla gorilla carboxyt-ester lipase (CEL) gene, complete cds
15825 28940 3.34 3.9E-01 AB0330(9.1 NT	L			AB033019.1	N-	Homo sapiens mRNA for KIAA1193 protein, partial cds
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3086	П.			3.8E-01	3.8E-01 AJ251057.1	TN	Human immunodeficiency virus type 1 complete genome (isolate 98SE-MP1213) Pleuronectes ametrantis aminonepitidase N (ambN) dene, partial cds
3113	l L	29305		3.8E-01			rieuroreus amarcanus aminopepudase n (ampri) perior por acus Arabidosis thraibana DNA chromosomae 4, condigitagement No. 2 2014/2014 Societa NET TOPC S1 Jours projets CNNA chois IMAGE 2347855 3'
3628	8 16792		1.09	3.8E-01	3.8E-01 AI807219.1	EST_HUMAN	wf38b12.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA done IMAGE:2357855 3

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Probe SEQ ID NO:	Exan SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Тор Hit Descriptor
3643	16792		26.0	3.8E-01	3.8E-01 Al807219.1	EST_HUMAN	wf38b12.x1 Scares_NFL_T_GBC_S1 Homo saplens cDNA clone IMAGE:2357855 3'
3852	17012	30012	1.07	3.8E-01	3.8E-01 BE154080.1	EST_HUMAN	PM0-HT0339-200400-010-G01 HT0339 Homo sapiens cDNA
4027	17183	30192	90.0	3.8E-01	1N 58045 NT	IN	Mus musculus general transcription factor II I (Gtf2i), mRNA
5727	18920		1.11	3.8E-01	3.8E-01 Q04888	SWISSPROT	TRANSCRIPTION FACTOR SOX-10
6469	19836		0.63	3.8E-01	\$46825.1	LN	prion protein [mink, Genomic, 2446 nt]
6761	19917	33312		3.8E-01	3.8E-01 BE072399.1	EST_HUMAN	QV3-BT0537-271299-049-e02 BT0537 Homo sapiens cDNA
	Ι.,						ta54f11,x1 Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:2047917 3' similar to
6899	20214	33644	4.39	3.8E-01	3.8E-01 AI374601.1	EST_HUMAN	contains Alu repetitive element;
7079	20132	33549	1.38	3.8E-01	3.8E-01 AL161513.2	NT	Arabidopsis thallana DNA chromosome 4, contig fragment No. 25
7685	20750		427	3.8E-01	3.8E-01 X61597.1	LN	M.musculus gene for kallikreir-binding protein
8493	21574	35111	0.54	3.8E-01	3.8E-01 M81385.1	, LN	Mouse liver receptor hamologous protein (LRH-1) mRNA, complete cds
8754	21833	35373	2.04	3.8E-01	3.8E-01 AB046851.1	INT	Homo saplens mRNA for KIAA1631 protein, partial cds
8826		35444	1.08	3.8E-01	11441264 NT	. LN	Homo saplens FOS-like antigen-1 (FOSL1), mRNA
9017	22096		1.29	3.8E-01	3.8E-01 AL163279.2	IN	Homo sapiens chromosome 21 segment HS210079
			-				ye43h06,r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone iMAGE:120539 5' similar to contains
9761		,	4.35		3.8E-01 T95413.1	EST_HUMAN	Alu repetitive element; contains PTR5 repetitive element;
11034	24113		1.38		3.8E-01 AV755814.1	EST_HUMAN	AV755814 BM Homo sapiens aDNA clone BMFBCE07 5
							Homo sapiens chromosome Xq28 melanoma antigen family A2a (MAGEA2A), melanoma antigen family A12
							(MAGEA12), metanoma antigen femily A2b (MAGEA2B), metanoma antigen family A3 (MAGEA3), caltractin
11699	24696	38388	1.57	3.8E-01	3.8E-01 U82671.2	NT	((CALT), NAD(P)H dehydrogenase-like protein (NSDHL), and Ll>
11824	24813		2.87	3.8E-01	3.8E-01 BE719219.1	EST_HUMAN	RC0-HT0841-040800-032-b12 HT0841 Homo sapiens cDNA
11992	24977	38681			3.8E-01 R42550.1	EST_HUMAN	yr92h11.s1 Soares Infant brain 1NIB Homo sapiens cDNA clone IMAGE:30289 3'
11992	24977		. 2.5		3.8E-01 R42550.1	EST_HUMAN	yf92h11,s1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:30289 3'
12438	25309	]	2.61	3.8E-01	3.8E-01 AE001124.1	LΝ	Borrella burgdorferi (section 10 of 70) of the complete genome
12569	26082		2	3.8E-01	3.8E-01 U94788.1	. LN	Human p53 (TP53) gene, complete cds
12695	25463		1.71	3.8E-01	3.8E-01 BE829256.1	EST_HUMAN	QV3-ET0063-190700-271-a05 ET0063 Homo sapiens cDNA
13105	l		1.48		3.8E-01 U78031.1	N	Mus muscultus epoptosis inhibitor bci-x (bci-x) gene, exon 3 and complete cds
13188	3 25772	31933			3.8E-01 AF194972.1	N	Mus musculus developmental control protein mRNA, partial cds
2551	15676	3 28799		L	3.7E-01 AB037831.1	NT	Homo sepiens mRNA for KIAA1410 protein, partial cds
3549		1 29726	10.67		3.7E-01 AF056336.1	NT	Danio rerio bone morphogenetic protein 4 precursor (BMP4) gene, complete cds
3974	17131	30135			3.7E-01 AA319482.1	EST_HUMAN	EST21715 Adrenal gland tumor Homo sapiens cDNA 5' end
4344						EST_HUMAN	ok39c07.x1 Scares_NSF_F8_9W_OT_PA_P_S1 Homo septens cDNA clone IMAGE:1510188 3'
4440						EST HUMAN	MR3-0T0007-080300-104-b02 OT0007 Homo sapiens cDNA
4509	17648	30636	2.91		3.7E-01 AE002408.1	LN L	Neisseria meningitidis serogroup B strain MC58 section 50 of 206 of the complete genome

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	Top Hit Descriptor	A033R Heart Homo sapiens cDNA clone A033	A033R Heart Homo sapiens cDNA done A033	Homo sapiens Interferon-induced protein p78 (MX1) gene, compiete cds	Horno saplens chromosome 21 segment HS21C078	Chicken (White leghorn) delta-1 and delta-2 crystallin genes, complete cds	Mus saxicola haptoglobin mRNA, complete cds	Homo sapiens tumor endothelial marker 7 precursor (TEM7), mRNA	ya50a07.r3 Soares fetal liver spleen 1NFLS Homo saplens cDNA clone IMAGE:66324 5'	Homo seplens chromosome 12 open reading frame 4 (C12ORF4), mRNA	Homo sapiens chromosome 12 open reading frame 4 (C12ORF4), mRNA	ok43b11.s1 NCi_CGAP_Lei2 Homo sapiens cDNA clone IMAGE:1516701 3'	Gallus gallus mRNA for beta-carotene 15,15-dioxygenase (bCDO gene)	mause ig germline alpha membrane exons region	qt46b07x1 Soares_fetal_lung_NbHL19W Homo sapiens cDNA clone IMAGE:1950997.3'	HIV-1 RU107B from Russia, gp120 V3-V5 region (env) gene, partial cds	HIV-1 RU107B from Russia, gp120 V3-V5 region (env) gene, partial cds	Rabbit mRNA for fast skeletal muscle myosin heavy chain (MHC)	Homo sapiens partial LIMD1 gene for LIM domains containing protein 1 and KIAA0851 gene	Homo sapiens partial LIMD1 gene for LIM domains containing protein 1 and KIAA0851 gene	Bovine mRNA for terminal decognucleotidyltransferase (TdT) (EC 2.7.7.31)	0046d03.s1 NCI_CGAP_Lu5 Homo septens cDNA clone IMAGE:1569221.3' similar to gb:M77698 TRANSCRIPTIONAL REPRESSOR PROTEIN YY1 (HUMAN):	Mus musculus retinoblestome 1 (Rb1), mRNA	Human heart/skeletal muscle ATP/ADP translocator (ANT1) gene, complete cds	Chlamydophila psittaci partial cmp1 gene for outer membrane protein 1	Human mRNA for KIAA0223 gene, partial ods	DKFZp762K075_r1 762 (synonym: hmel2) Homo saplens cDNA done DKFZp762K075 5'	Homo sapiens NF2 gene	Brassica napus mRNA for MAP4K alpha2 protein	Human mibp gene, partial cds	yd03e05.r1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:24443 5'	yd03e05.r1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:24443 5	hg33f02x1 NCI_CGAP_GC6 Homo saplens cDNA clone IMAGE:2947419 3'	hg33f02x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE;2947419 3'
	Top Hit Database Source	EST_HUMAN A	EST_HUMAN A	T		NT C	NΤ		T HUMAN			T_HUMAN		NΤ			NT IN	NT R		H IN	8. - LN	EST HIMAN T		Î	NT C	Ξ Σ	EST_HUMAN D	ī	NT B	H	EST_HUMAN N	EST_HUMAN N		EST_HUMAN h
	Top Hit Acession No.	3.7E-01 T12298.1	3.7E-01 T12298.1	3.7E-01 AF135187.1	3.7E-01 AL163278.2	3.7E-01 M10806.1		11525843 NT		11436739 NT	11436739 NT	3.7E-01 AA9029121	3.7E-01 AJ271386.1	3.7E-01 K00691.1	1		3.7E-01 U08361.1	3.7E-01 X05958.1	3.7E-01 AJ297357.1	3.7E-01 AJ297357.1		3 7E-01 A 4973540 1	7,678		3.7E-01 AJ243525.1	3.7E-01 D86976.1	3.7E-01 AL121154.1		3.6E-01 AJ009609.1	U89241.1	T80255.1	T80255.1	3.6E-01 AW 590184.1	3.6E-01 AW590184.1
Most Similar	(Top) Hit BLAST E Value	3.7E-01	3.7E-01	3.7E-01	3.7E-01	3.7E-01	3.7E-01	3.7E-01	3.7E-01 T66802.1	3.7E-01	3.7E-01	3.7E-01	3.7E-01	3.7E-01	3.7E-01	3.7E-01	3.7E-01	3.7E-01	3.7E-01	3.7E-01	3.7E-01	3.7E-04	3.7E-01	3.7E-01 J04982.1	3.7E-01	3.7E-01	3.7E-01	3.7E-01	3.6E-01	3.6E-01	3.6E-01	3.6E-01 T80255.1	3.6E-01	3.6E-01
	Expression Signal	0.74	0.74	1.27	1.25	0.7	0.8	3.48	0.69	1.96	1.96	99.0	1.34	9.0	4.21	0.46	0.48	1.8	2.02	2.02	2.73	1.40	3.5	1.17	3.94	1.82	2.94	6.99	0.77	9.07	3.97	3.97	6.55	6.55
	ORF SEQ ID NO:	31368	31369					33832		35143	35144	35180			37054	37437	37438		37989	37990							<del> </del>	31971	26520		27570		28209	
	SEC ID	18399	18339	19072	19253	19798	19819	20375	ı		21605	ı	22476	23408	23449	23816	23816	24170	24351	24351	23940	24080	1	١.	25229	25289	l _	25597	13489	14191	14498	١.		15109
	Probe SEQ ID NO:	5280	5280	5883	6071	6639	0999	7283	7965	8524	8524	8560	9402	10373	10414	10783	10783	11097	11285	11285	11754	12004	12066	12137	12314	12410	12821	12902	271	1020	1342	1342	1966	1966

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Top Hit Descriptor	Mus musculus ribosomal protein S19 (Rps19) gene, complete cds	Rattus norvegicus repeat element associated with the Rasgrf1 gene	Human mRNA for KJAA0323 gene, partial cds	P.irregulare (P3804) gene for actin	RC5-ST0171-181099-011-007 ST0171 Homo saplens cDNA	PROTEIN-LISOASPARTATE O-METHYLTRANSFERASE (PROTEIN BETA-ASPARTATE METHYLTRANSFERASE) (PIMT) (PROTEIN L-ISOASPARTYL METHYLTRANSFERASE) (L- ISOASPARTYL PROTEIN CARBOXYL METHYLTRANSFERASE)	Drosophila melanogaster sugar transporter 3 (sut3) mRNA, complete cds	H. sepiens serotonin transporter gene, exons 9 and 10	H.sapiens serotonin transporter gene, exons 9 and 10	RC1-HT0545-150600-014-b12 HT0545 Homo sapiens cDNA	Brassica napus mRNA for MAP4K alpha2 protein	ha02g04.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2872566 3'	MR4-BT0358-270300-005-c10 BT0359 Homo caplens cDNA	Homo seplens lipe gene Infron 5	FORMATE HYDROGENLYASE SUBUNIT 5 PRECURSOR (FHL SUBUNIT 5) (HYDROGENASE-3 COMPONENT E)	Homo sapiens PHEX gene	yi74a06.r1 Soares fetal liver spleen 1NFLS Homo capiens cDNA clone IMAGE:275987 5'	wt72cf0.x1 Soares_thymus_NHFTh Homo sapiens cDNA clone IMAGE:2513010 3' similar to TR:O15117 O15117 PYN BINDING PROTEIN [1];	SCO-SPONDIN	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 79	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RoRet gene, and sodium phosphate transporter (NPT3) gene, complete cds	Human hereditary haemochromatosis region, histona 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RoRet gene, and sodium phosphate transporter (NPT3) gene, complete ods	Homo sapiens lysosomal-associated membrane protein 2 (LAMP2), transcript variant LAMP2A, mRNA	Homo sapiens lysosomal-associated membrane protein 2 (LAMP2), transcript variant LAMP2A, mRNA
Top Hit Database Source	Z	TN	LN LN	Į,	EST_HUMAN F	SWISSPROT	T		Ę	EST_HUMAN	۲	EST HUMAN	EST_HUMAN	Т		- L	1		SWISSPROT		IN	NT		
Tap Hit Acessian No.	3.6E-01 AF216207.1	3.6E-01 AF056927.1	3.6E-01 AB002321.1	3.6E-01 X76725.1	3.6E-01 AW812033.1	P24206	35.1		3.6E-01 X76758.1	3.6E-01 BE707883.1	3.6E-01 AJ009609.1	3.6E-01 AW339393.1	3.6E-01 BE067699.1	3.6E-01 AJ006565.1				3.6E-01 AW027174.1	ĺ	3.6E-01 AL161583.2	3.6E-01 U91328.1	3.6E-01 U91328.1	4504956 NT	4504956 NT
Most Similar (Top) Hit BLAST E Value	3.6E-01	3.6E-01	3.6E-01	3.6E-01	3.6E-01	3.6E-01 P24206	3.6E-01	3.6E-01	3.6E-01	3.6E-01	3.6E-01	3.6E-01	3.6E-01	3.6E-01	3.6E-01 P16431	3.6E-01	3.6E-01	3.6E-01	3.6E-01 P98167	3.6E-01	3.6E-01	3.6E-01	3.6E-01	3.6E-01
Expression Signal	5.7	1.15	2.33	2.8	2.66	1.69	8.47	1.98	1.98	1.2	9.0	3.18	0.92	0.64	96.0	1.63	3.85	1.52	0.75	16.45	0.48	0.48	3.04	3.04
ORF SEQ ID NO:	28253				28806	28929		29738		30652	30981	31215		31713	32735				35032		35799	35800	35820	35821
Exon SEQ ID NO:	15147	15251	15474	1	ı	15814	ľ	Ĺ	1	17665	17993	18249	l	18697	19386	19767			21500		72257	22257	22281	22281
Probe SEQ ID NO:	2007	2113	2343	2463	2556	2694	2964	3558	3558	4528	4863	5123	5209	5498	6211	9607	7298	7435	8419	8474	9179	9179	9203	9203

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	iplor				n containing bent DNA fragment	AG PROTEIN Y4TS	IAGE:3958997 5'		5 to 714311 (section 62 of 148) of the complete			пріете депотів		(trithorax (Drosophila) homolog); translocated to,	AAGE:2679116 3' similar to gb:K00558 TUBULIN				77			/AGE:4053951 3'	ectivating protein mRNA, complete cds	mo saplens cDNA clone IMAGE:650872 31	4AGE:4076680 5'		ភាភ	Vo. 36		į		<b>∀</b>
Single Exultriones Expressed in Flacenta	Top Hit Descriptor	Homo sapiens chromosome 21 segment HS21C004	D. melanogaster singed gene, exons 3, 4, 5 & 6	D. melanogaster singed gene, exons 3, 4, 5 & 6	C.perfringens plc gene for phospholipace C upstroam region containing bent DNA fragment	PROBABLE PEPTIDE ABC TRANSPORTER ATP-BINDING PROTEIN Y4TS	601676418F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3958997 5	Arabidopsis theliana mRNA for SigB, complete cds	Methanobacterium thermoautotrophicum from bases 702375 to 714311 (section 62 of 148) of the complete	genome	Homo sapiens https gene for hair keratin, exons 1 to 9	Escherichia coli K-12 MG1655 section 225 of 400 of the complete genome	Mus musculus Emr1 mRNA, complete cds	Homo sapiens myeloid/iymphoid or mixed-lineage leukemia (trithorax (Drosophila) homolog); translocated to, 10 (AF10), mRNA	x80e11 x1 NCI_CGAP_Pan1 Home sapiens cDNA clone IMAGE:2679116 3' similar to gb:K00558 TUBULIN	ALPHA-1 CHAIN (HUMAN);	Pyrococcus sp. pol gene	Mus musculus mannose receptor, C type 2 (Mrc2), mRNA	Arabidopsis thallana DNA chromosome 4, contig fragment No. 77	Homo sapiens GAP-like protein (LOC51306), mRNA	Homo sapiens GAP-like protein (LOC51306), mRNA	001811060R1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4053951 3	Rettus norvegicus ADP-ribosylation factor-directed GTP ase activating protein mRNA, complete cds	zr08a09.s1 Stratagene NT2 neuronal precursor 937230 Homo sapiens cDNA done IMAGE:650872 3	601845470F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4076680 5	Danio rerio homeobox protein (hoxb5b) gene, complete cds	Rat leukocyte common antigen (L-CA) gene, exons 1 through 5	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 36	EARLY E2A DNA-BINDING PROTEIN	EARLY E2A DNA-BINDING PROTEIN	Human mRNA for KIAA0086 gene, complete cds	PM4-SN0012-030400-001-a11 SN0012 Homo sapiens cDNA
	Top Hit Database Source	TN	NT	IN	LN	SWISSPROT	EST_HUMAN	NT	ļ	Z !	L <sub>Z</sub>	LN	N.	·		EST HUMAN	N	TN	NT	NT.	IN	EST_HUMAN	NT	EST HUMAN	EST_HUMAN	LN	TN	TN	SWISSPROT	SWISSPROT	NT	EST_HUMAN
ig.iic	Top Hit Acession No.	3.6E-01 AL163204.2	K17550.1	K17550.1	X62825.1	253194	3.6E-01 BE902390.1	3.6E-01 AB004293.1		3.6E-01 AE000856.1	Y19210.1	3.6E-01 AE000335.1	J66888.1	11432598 NT		3.6E-01 AW 190229.1	3.6E-01 Z54173.1	6678933 NT	3.5E-01 AL161581.2	7706136 NT	7706136 NT	3.5E-01 BF129796.1	3.5E-01 U35776.1	3.5E-01 AA223252.1	3.5E-01 BF214381.1	3.5E-01 AF071253.1	3.5E-01 M18349.1	3.5E-01 AL161536.2	Q96687	Q96687	3.5E-01 D42045.1	3.5E-01 AW863916.1
	Most Similar (Top) Hit BLAST E Vatue	3.6E-01	3.6E-01 X17550.1	3.6E-01 X17550.1	3.6E-01 X62825.1	3.6E-01 Q53194	3.6E-01	3.6E-01		3.65-01	3.6E-01 Y19210.1	3.6E-01	3.6E-01 U66888.1	3.65-01		3.6E-01	3.6E-01	3.5E-01	3.5E-01	3.5E-01	3.5E-01	3.5E-01	3.5E-01	3.5E-01	3.5E-01	3.5E-01	3.5E-01	3.5E-01	3.5E-01 Q96687	3.5E-01 Q96687	3.5E-01	3.5E-01
	Expression Signal	1.23	1.13	1.13	0.58	16.64	2.42	3.27		4.44	3.16	7.87	3.63	88		1.4	1.38	3.71	1.03	1.53	1.53	4.66	1.28	1.34	0.73	2.62	4.34	9.0	1.1	1.1	1.29	F
	ORF SEQ ID NO:	36032	36225	36226		36708	37891	38088		37540								26467				27033	27905	28908		30501		26376	31627	31628	32146	
	Exan SEQ ID NO:	22468	22654	22654		23105	24256	24431	1	- 1	26205	25197	25297	25552		26141	25745	L.		ı	1_	13981	14822	16068	ı	<u>l_</u>	18176	13349	18649	18649	$\lfloor  \rfloor$	19537
	Probe SEQ ID NO:	9393	9599	9599	6996	10067	11187	11370		11729	12173	12261	12420	1282R		13130	13146	214	992	743	743	804	1670	2671	3795	4378	5048	5323	5449	5449	2995	6367

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Top Hit Descriptor	Homo sapians chromosome 21 segment HS21C010	Homo sapiens chromosome 21 segment HS21C010	Synechocystis sp. PCC6803 complete genome, 11/27, 1311235-1430418	Canis familiaris rod photoreceptor cGNP-gated channel alpha-subunit (CNGC1) mRNA, complete cds	Homo sapiens pulmonary surfactant protein D, promoter region and exon 1	Methylovorus sp. strain SS1 putative GrpE (grpE), DnaK (dnaK), and putative DnaJ (dnaJ) genes, complete cds	7n94a01 x1 NCI_CGAP_Ov18 Homo sapiens cDNA clone IMAGE:3572232 3' similar to TR:Q9UJ15	Q9UJ15 DJ18C9.1 ;	no11b10.s1 NOL_CGAP_Phe1 Homo sapiens cDNA clone IMAGE:1100347 3'	MR4-BT0403-230200-202-c01 BT0403 Homo sapiens cDNA	qi95c05,x1 NCI_CGAP_Kid3 Homo sepiens cDNA clone IMAGE:1867208 3' cimilar to contains Alu repotitive element:	Arabidopsis thallana DNA chromosome 4, contig fragment No. 90	zn12d11.s1 Stratagene hNT neuron (#937233) Homo sapiens cDNA clone IMAGE:547221 3'	Echovirus 22 1AB, 1C, 1D, 2A, 2B, 2C, 3A, 3B, 3C, 3D proteins RNA, complete mature peptides and cds	60157181171 NIH_MGC_55 Hamo sepiens cDNA clone IMAGE:3838826 3'	UI-HBI1-ael-e-12-0-UI.s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone (MAGE:2719582 3'	DKFZp761A249_r1 761 (synonym; hamy2) Homo sapiens cDNA clone DKFZp761A249 5'	zb53e12.s1 Soares_fetal_lung_NbHL19W Homo sapiens cDNA clone IMAGE:3073423'	tm63g05.x1 NCI_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2162840 3' similar to gb:S37431 LAMININ RECEPTOR (HUMAN);	602085283F1 NIH_MGC_83 Homo saplens cDNA clone IMAGE:4249365 5'	Escherichia coli K-12 MG1655 section 383 of 400 of the complete genome	Homo sapiens TCRAV28 gene, allele A4, partial	EST41765 Endometrial fumor Homo sapiens cDNA 5' end	Oricetulus griseus cholesterol 7-alpha-hydroxylase gene, complete cds	Bovine enterovirus strain K2577, complete genome	INTEGRIN BETA-8 PRECURSOR	INTEGRIN BETA-8 PRECURSOR	Ephydatia fluviatilis mRNA for PLC-gammaS, complete cds	Saccharomyces cerevisiae Mar1p (WAF1) gene, complete cds
Top Hit Database Source			NT	٠		<u>L</u>		EST_HUMAN (	EST_HUWAN I	EST_HUMAN N	EST HUMAN	Т	T_HUMAN		EST_HUMAN	Г		EST_HUMAN   1		T_HUMAN		LN	EST_HUMAN E			ISSPROT		П	<u>x</u>
Top Hit Acession No.			3.4E-01 D90909.1	U83905.1	3.4E-01 AF034862.1	3.4E-01 AF106835.1		3.4E-01 BF449010.1	3.4E-01 AA584196.1	3.4E-01 BE069912.1	3 4F-01   41240973 1	3 4E-01 AL161594.2	3.4E-01 AA085313.1	3.4E-01 L02971.1	3.4E-01 BE748912.1	3.4E-01 AW 204505.1	3.4E-01 AL120544.1	3.4E-01 N95225.1	3.4E-01 AI468082.1	3.4E-01 BF678702.1	3.4E-01 AE000493.1	3.4E-01 Y14930.1	3.4E-01 AA337063.1	3.4E-01 L04690.1	9633624 NT			7.1	3.4E-01 U19492.1
Most Similar (Top) Hit BLAST E Value	3.4E-01	3.4E-01	3.4E-01	3.4E-01 U83905.1	3.4E-01	3.4E-01		3.4E-01	3.4E-01	3.4E-01	3.4E-01	3.4E-01	3.4E-01	3.4E-01	3.4E-01	3.4E-01	3.4E-01	3.4E-01	3.4E-01	3.4E-01	3.4E-01	3.4E-01	3.4E-01	3.4E-01	3.4E-01	3.4E-01 P26013	3.4E-01 P26013	3.4E-01	3.4E-01
Expression Signal	78.0	78.0	1.09	6.1	0.78	4.47		1.89	1.48	1.79	43	264	4.92	217	96.0	1.8	1.71	1.39	1.07	9.0	0.48	0.68	1.38	0.71	1.87	4.12	4.12	0.57	4.68
ORF SEQ ID NO:	29261	29262	29403	29416	29608	29800				30884		32295		_	32676				33604	33480		35044		35380		L			34602
SEQ ID NO:	16241	١.	16392	16404		L	1	17049	17313	17902	18194			L	19330	L		20034	20180			21513	21764	21839	Ì		ł	22676	21088
Probe SEQ ID NO:	3065	3085	3218	3230	3424	3620		3890	4163	4767	2088	5802	5932	6130	6154	6234	6364	6882	7086	7205	8090	8432	8684	8760	8023	9413	9413	9621	9645

WO 01/57272 PCT/US01/00663

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Top Hit Descriptor	Saccharomyces cerevisiae Maf1p (MAF1) gene, complete cds	Glycine max putative transcription factor SCOF-1 (scof-1) mRNA, complete cds	Homo sepiens FAA gene, exon 16, 17 and 18	Vibrio cholerae chromosome I, section 4 of 251 of the complete chromosome	Methanobacterium thermoautotrophicum from bases 1018444 to 1029212 (section 87 of 148) of the complete genome	PROBABLE E4 PROTEIN	Rufilus arcasii cytochrome b (cytb) gene, mitochondrial gene encoding mitochondrial protein, partial cds	Human von Willebrand factor gene, exons 36 and 37	Human von Willebrand factor gene, exons 38 and 37	Rattus norvegicus mRNA for s-gicerin/MUC18, complete cds	Arabidopsis thallana DNA chromosome 4, contig fragment No. 27	7kGd12.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:3480646 3'	INOSINE-URIDINE PREFERRING NUCLEOSIDE HYDROLASE (IU-NUCLEOSIDE HYDROLASE)	(PURINE NUCLEOSIDASE)	Citrus variegation virus putative replicase gene, partial cds	S.cerevisiae RIB5 gene encoding Ribdilavin synthase	Schizosaccharomyces pambe Cwf8p (cwf8) gene, complete cds	Human autoantigen mRNA, complete cds	hwdzho8.x1 NCI_CGAP_Lu24 Homo seplens cDNA clone IMAGE:3176127 3' similar to contains PTR5.t3	PTR5 repetitive element;	Beta vulgaris mitochondrion, complete genome	Mus musculus SIL, MAP_17, CYP_a, SQL & CYP_b genes	Clostridium cellulolyticum partial spolVB gene and spoOA gene, strain ATCC 35319	Homo sapiens HLA class III region containing tenascin X (tenascin-X) gene, partial cds, cytochrome P450 21-	hydroxylase (GYP21B), complement component C4 (G4B) G11, helicase (SKI2W), RD, complement factor B	(Bf), and complement component C2 (C2) genes,>	Rhizobium leguminosarum sym plasmid pRL5JI nodX gene	Rhizobium leguminosarum eym plasmid pRL5JI nodX gene	Arebidopsis thaliana DNA chromosome 4, contig fragment No. 45	Homo saplens KIAA1100 protein (KIAA1100), mRNA	PROLINE-RICH PROTEIN LAS17	602184016T1 NIH_MGC_42 Homo sapiens cDNA clone IMAGE;4300251 3'
Top Hit Database Source	NT	NT	NT	NT	F	SWISSPROT	Ę	NT	. IN	뉟	F	EST_HUMAN		SWISSPROT	뒫	NT	IN	뒫		EST_HUMAN	N	ΙN	Ŀ			LΝ	된	Þ	Z	LZ LZ	SWISSPROT	EST_HUMAN
Top Hit Acesslon No.	U19492.1	3.4E-01 U68763.1	3.4E-01 AJ225084.1	3.4E-01 AE004096.1	3.4E-01 AE000881.1	P06925	3.4E-01 AF045981.1	3.4E-01 M25856.1	3.4E-01 M25856.1	3.4E-01 AB035507.1	3.4E-01 AL161515.2	3.4E-01 BF081948.1		Q27546	3.4E-01 U93604.1	3.4E-01 Z21621.1	3.4E-01 AF254351.1	3.4E-01 L26339.1	:	3.4E-01 BE218652.1	9838361 NT	3.4E-01 AJ297131.1	3.4E-01 AJ288948.1			3.4E-01 AF019413.1	3.3E-01 X07890.1	3.3E-01 X07990.1	3.3E-01 AL161545.2	7662485 NT	Q12446	3,3E-01 BF568880.1
Most Similar (Top) Hit BLAST E Value	3.4E-01 U19492.1	3.4E-01	3.4E-01	3.4E-01	3.4E-01	3.4E-01 P06925	3.4E-01	3.4E-01	3.4E-01	3.4E-01	3.4E-01	3.4E-01	!	3.4E-01 Q27546	3.4E-01	3.4E-01	3.4E-01	3.4E-01		3.4E-01	3.4E-01	3.4E-01	3.4E-01			3.4E-01	3.3E-01	3.3E-01	3.3E-01	3.3E-01	3.3E-01 Q12446	3.3E-01
Expression Signal	4.68	0.86	2.44	6.73	3.26	2.1	1.86	1.91	1.91	1.68	3.23	1.59		1.65	2.03	1.55	1.16	10.71		2.38	1.79	1.36	1.96			2.26	6.72	3.19	1.41	1.97	2.57	3.39
ORF SEQ ID NO:	34603	36522	36735			38014		38295	38296	38478		l		38793								32023								l		27562
Exon SEQ ID NO:	21088		L			L	L	24616	24616	24781	24806					25198	25912	_		25944		1	26160			25691	13253	13253	13656		_	14492
Probe SEQ ID NO:	9645	2897	10093	10695	.11267	11307	11350	11561	11561	11791	11817	12078		12110	12150	12264	12367	12489		12517	12579	12700	12954		_	13055	15	108	461	929	1227	1335

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	Top Hit Descriptor	Mus musculus disintegrin 5 (Dtgn5), mRNA	Mus musculus kappa B and Rss recognition component (Krc), mRNA	EST36722 Embryo, 8 week I Hamp sapiens cDNA 5' end	Homo segiens uridine monophosphate synthetase (orotate phosphoribosyl transferase and orotidino-5- decarboxylase) (UMPS) mRNA	Bacteriophage phi-YeO3-12 complete genome	INTERLEUKIN-12 ALPHA CHAIN PRECURSOR (IL-12A) (CYTOTOXIC LYMPHOCYTE MATURATION FACTOR 35 KD SUBUNT) (CLMF P35)	Streptomyces argillaceus mithramycin biosynthetic genes	Homo sapiens MTA1-L1 gene, complete cds	EXODEOXYRIBONUCLEASE V BETA CHAIN	GENOME POLYPROTEIN (CONTAINS: N-TERMINAL PROTEIN (P1); HELPER COMPONENT PROTEINASE (HC-PRO); PROTEIN P3]	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 10	Hypoxylon fragiforme chitin synthase gene, partial cds	Rattus norvegicus DNA for regucalcin, partiel cds	ф78b12.x1 NO_CGAP_Uß Homo sapiens dNA clone IMAGE:2205407 3' similar to gb:X57522 ANTIGEN PEPTIDE TRANSPORTER 1 (HUMAN);	Human pulmonary surfactant-associated protein SP-B (SFTP3) mRNA, complete cds	Synechocystis sp. PCC6803 complete genome, 22/27, 2755703-2868766	Rnarvegicus mRNA for 3'UTR of ubiquitin-like protein	R.narvegicus mRNA for 3'UTR of ublquiltin-like protein	601848090F1 NIH_MGC_55 Homo saplens cDNA clone IMAGE:4078823 5'	601472768T1 NIH_MGC_68 Hamp sapiens cDNA clone IMAGE:3875753 3'	601472768T1 NIH_MGC_68 Hamo sapiens cDNA clone IMAGE:3875753 3'	CIRCUMSPOROZOITE PROTEIN (CS)	Flexibacter litoralis gyrB gene for DNA gyrase B subunit, partial cds	Flexibacter litoralis gyrB gene for DNA gyrase B subunit, partial cds	ty84h01x1 NCI_CGAP_Kld11 Homo sapiens cDNA clone IMAGE:2285809 3' similar to contains Alu repetitive element;contains element L1 repetitive element ;	ty84h01 x1 NO_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2285809 3' similar to contains Alu repetitive element,contains element 1.1 repetitive element;	J2498F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA chone J2498 6' similar to TEGT
	Top Hit Database Source			EST_HUMAN E			SWISSPROT FA	Г	Ĭ	SWISSPROT	SWISSPROT PI		Ĭ	NT N	EST_HUMAN P			Z Z	NT R	EST_HUMAN 6	EST_HUMAN 6			H . LN	NT FI	EST HUMAN		
26	Top Hit Acession No.	6753685 NT	6754477 NT	3.3E-01 AA332734.1	4507834 NT	3.3E-01 AJ251805.1		32.2				3.3E-01 AL161498.2	3.3E-01 AF200446.1	3.3E-01 D31662.1	3.3E-01 AI539114.1				3.3E-01 X89819.1	3.3E-01 BF213873.1	3.3E-01 BE619650.1	3.3E-01 BE619650.1	P05691	3.3E-01 AB034233.1	3.3E-01 AB034233.1	3.3E-01 AIB28131.1	3.3E-01 AI628131.1	3.3E-01 N85146.1
	Most Similar (Top) Hit BLAST E Value	3.3E-01	3.3E-01	3.3E-01	3.35-01	3.3E-01	3.3E-01,002743	3.35-01	3.3E-01	3.3E-01 O84645	3.3E-01 P22602	3.3E-01	3.3E-01	3.3E-01	3.3E-01	3.3E-01	3.3E-01	3.3E-01	3.3E-01	3.3E-01	3.3E-01	3.3E-01	3.3E-01 P05691	3.3E-01	3.3E-01	3.3F-01	3.3E-01	3.3E-01
	Expression Signal	1.26	1.43	1.02	623	1.61	1,09	0.78	1.04	2.72	0.82	1.19	1.81	2.37	1.91	1.02	1.14	2.55	2.55	0.68	1.37	1.37	1.29	0.59	0.59	4 63	4.83	1.9
-	ORF SEQ ID NO:	27873				29215		29311			30076					30966				32411		32577		33680		33586		
	SEQ ID NO:	14788	14826	14926	15604	16190	1	1	16749	17070	17080	ı	1			1	18089	18639		1_	L	19249	1_		<u></u>	20165		<u> </u>
	Probe SEO ID NO:	1836	1674	1777	2477	3014	3080	3121	3584	3911	3927	4072	4108	4487	4812	4843	4960	6439	5439	5907	2909	2909	6162	6932	6932	2020	7029	7961

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Top Hit Descriptor	602;40372F1 NIH_MGC_46 Hcmo sapiens cDNA clone IMAGE:4301800 5'	601873281F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4097180 5'	MITOGEN-ACTIVATED PROTEIN KINASE KINASE KINASE 1 (MAPKÆRK KINASE KINASE 1) (MEK KINASE 1) MÆRK 1)	CM3-ET0041-180500-187-d10 ET0041 Homo statens cDNA	CM3-ET0041-180500-187-d10 ET0041 Homo sapiens cDNA	za67h01.s1 Soares_fetal_lung_NbHL19W Homo sepiens cDNA clone IMAGE:297649 3'	RC4-TN0077-250800-011-904 TN0077 Homo sapiens cDNA	Homo sapiens high-mobility group phosphoprobin (HMGI-C) gene, exons 1-3, complete cds	Helicobacter pylori 26695 section 109 of 134 of the complete genome	D.mauritana Adh gene	D.maunitana Adh gane	602070802F1 NCI_CGAP_Bm64 Homo capieno oDNA clone IMAGE:4213585 5'	hv51g02.x1 NCI_CGAP_Lu24 Hcmo sapiens cDNA clone IMAGE:3176978 3'	GALECTIN-3 (GALACTOSE-SPECIFIC LECTIN 3) (MAC-2 ANTIGEN) (IGE-BINDING PROTEIN) (35 KD ECTIN) (CABBOHYDRATE BINDING PROTEIN 35) (OBP 35) (I AMININ-BINDING PROTEIN) (LECTIN	L-29) (CBP30)	ob71g02.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1336850 3'	Rhizabium leguminosarum sym plasmid pRL5JI nodX gene	Homo sapiens aldehyde oxidase 1 (AOX1), mRNA	Pyrococcus horikoshii 073 genomic DNA, 287001-544000 nt. position (2/7)	Raftus norvegicus EH domain binding protein Epsin mRNA, complete cds	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 61	Fusarium poae virus 1 RNA2 putative RNA dependent RNA polymerase gene, complete cds	P.vulgaris arc5-1 gene	LACTOSE PERMEASE (LACTOSE-PROTON SYMPORT) (LACTOSE TRANSPORT PROTEIN)	Arabidopsis thallana cultivar Columbia RPP13 (RPP13) gene, complete cds	S.cerevisiae chromosome II reading frame ORF YBR172c	EST369264 MAGE resequences, MAGD Homo saplens cDNA	EST369264 MAGE resequences, MAGD Homo sapiens cDNA	Bctrytis cinerea strain T4 cDNA library under conditions of rutogen deprivation	601868804F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4111512 5'	Mus musculus Pbx/knotted 1 hamecbox (Pknox1), mRNA	Homo sapiens promyelocytic leukamia zho finger protein (PLZF) gene, complete cds
Top Hit Database Source	EST_HUMAN 6	EST_HUMAN 6	N TORGOSIWS	Т	T	П	Г	Г	NT TN	J L	NT	EST_HUMAN	EST_HUMAN I		SWISSPROT	EST_HUMAN	Г		LN	LN LN	/ IN	IN IN	J.N.	SWISSPROT	ĮN		EST_HUMAN	EST_HUMAN E		EST_HUMAN (		IN
Top Hit Acession No.	3.3E-01 BF683954.1	3.3E-01 BF210322.1	OROGOR	3.3E-01 BE828461.1	3.3E-01 BE828461.1	3.3E-01 N69866.1	3.3E-01 BF376745.1	L41044.1	3.3E-01 AE000631.1		X63953.1	3,3E-01 BF526499,1	3.3E-01 BE219351.1		P47953	3,3E-01 AA806621.1	3.3E-01 X07990.1	6598319 NT	3.3E-01 AP000002.1	3.2E-01 AF018261.1	3.2E-01 AL161561.2	3.2E-01 AF047013.1	3.2E-01 Z50202.1	Q48624	3.2E-01 AF209730.1	Z36041.1	3.2E-01 AW957194.1	3.2E-01 AW957194.1	3.2E-01 AL111655.1	3.2E-01 BF203817.1	7710079 NT	3.2E-01 AF060568.1
Most Similar (Top) Hit BLAST E Vatue	3.3E-01	3.3E-01	3 3E-01 OB2928	3.3E-01	3,3E-01	3,3E-01	3.3E-01	3.3E-01 L41044.1	3.3E-01	3.3E-01 X63953.1	3,3E-01 X63953.1	3.3E-01	3.3E-01		3.3E-01 P47953	3.3E-01	3.3E-01	3.3E-01	3.3E-01	3.2E-01	3.2E-01	3.2E-01	3.2E-01	3.2E-01 Q48624	3.2E-01	3.2E-01	3.2E-01	3.2E-01	3.2E-01	3.2E-01	3.2E-01	3.2E-01
Expression Signal	23.1	0.73	0.83	1.16	1.16	2.9	2.81	2.08	0.74	3,35	3.35	2.1	9.35		3.7	2.8	2.33	1.85	22.03	2.5	92'0	23.03	1.48	6.74	-	1.3	6.42	6.42	1.25	3.22	2.83	1.23
ORF SEQ ID NO:	35379	35544	35041	36280	36290	36330	36260		37520	37675	37676		38242		38389		26253	38357	L			27408	27535	27648			28069		28142			29000
Exon SEQ ID NO:	21839	22005	22300	22720	22720	22760	22690	ı	23897	24041	24041	1	24565		24706	L	13253	ı	25685	13664	13918	14350	14467	14575	14815	14964	14974	14974	15035	15361	15729	15889
Probe SEQ ID NO:	8759	8926	8	9578	9228	9711	9752	10196	10865	10960	10960	11279	11507		11626	12018	12036	12250	13044	469	736	1188	1311	1421	1663	1815	1825	1825	1891	2227	2606	2774

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	_	_	Т-		-1		$\overline{}$	_					$\neg$	_	Т		_	$\neg$	_		_	Т	Т	$\neg$	_			$\neg$	Т	$\neg$
Top Hit Descriptor	Humam h NAT allele 3-2 gene for anylamine N-scetyttansferase	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 46	Rabbit beta-like globin gene duster encoding the epsilon, gamma, delta (pseudogene) and beta globin	polypeptides, complete cds	HYPOTHETICAL 81.7 KD PROTEIN C13G7.04C IN CHROMOSOME I PRECURSOR	602081972F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4246505 5'	CM0-HT0569-060300-269-110 HT0569 Homo sapiens cDNA	Giardia intestinalis pyruvaterflavodoxin oxidoreductase and flanking genes	Fugu rubripes gamme-aminobutyric acid receptor beta subunit gene, partial cds; 55kd erythrocyte membrane	protein (150), syrightic residents sociation integrational protein (170), proteingen or proteinted enhancer protein (PCOLCE) genes, complete c>	AV718037 FHTA Homo saplens cDNA clone FHTAABH01 5'	Human mRNA for KIAA0361 gene, KIAA0361 protein	Homo sapiens partial LMO1 gene for LIM domain only 1 protein, exon 1	Rat ISO-atrial natriuretic factor gene, complete cds	Rattus norvegicus repeat, map NOS-D12W ox1	H.saplens gene fragment for acety/choline receptor (AChR) alpha subunit exons 8, 9 and 3' flanking region	601897107F1 NIH_MGC_19 Homo sapiens cDNA clane IMAGE:4126633 5'	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 70	601855580F1 NIH_MGC_57 Homo saptens cDNA clone IMAGE:4075627 51	60/855580F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4075627 5'	Deinococcus radiodurans R1 section 152 of 229 of the complete chromosome 1	Oryctolagus cuniculus Ig H-chain pseudogene, V-region (VH6-a2) gene, partial cds	Onyciclagus cuniculus lg H-chain pseudogene, V-region (VH6·a2) gene, partial cds	Homo sapiens chromosome 21 segment HS21C004	Human monocyte antigen CD14 (CD14) mRNA, complete cds	Homo sapiens 6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase (PF2K) gene, exons 12 and 13	Home sapiens 6-phosphofructo-2-kinase/fructoso-2,6-bisphosphatase (PF2K) gene, exons 12 and 13	Borrelia burgdorferi plasmid cp32-2, erpC and erpD genes, complete cds; and unknown genes	hve9605.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3181569 3'	Homo sapiens gene for AF-6, complete cds
Top Hit Database Source	LZ	Į.		뉟	SWISSPROT	EST_HUMAN	EST_HUMAN	NT		F	T HUMAN	LN	N	LΝ	NT	TN	EST_HUMAN	LΝ	EST_HUMAN	EST_HUMAN	NT	NT	NT	NT	NT	NT	LN.	LN	T HUMAN	LN
Top Hit Acession No.	210879 1	3 2F-01 AI 161546 2		3.2E-01 M18818.1	210268	17.1	3.2E-01 BE173964.1			3.2E-01 AF018494.1	3.2E-01 AV718037.1	3.2E-01 AB002359.1	3.2E-01 AJ277661.1	3.2E-01 M60266.1	3.2E-01 AJ231001.1	3.2E-01 X02508.1	3.2E-01 BF311635.1	3.2E-01 AL161574.2	3.2E-01 BF246771.1	3.2E-01 BF246771.1	3.2E-01 AE002015.1	3.2E-01 U51026.1	3.2E-01 U51026.1	3.2E-01 AL163204.2	3.2E-01 M86511.1	3.2E-01 AF041829.1	3.2E-01 AF041829.1	3.2E-01 U44914.1	3.2E-01 BE326230.1	3.2E-01 AB011399.1
Most Similar (Top) Hit BLAST E Value	9 2F_01	3.2E-01		3.2E-01	3.2E-01 Q10268	3.2E-01	3.2E-01	3.2E-01 L27221.1		3.2E-01	3.2E-01	3.2E-01	3.2E-01	3.2E-01	3.2E-01	3.2E-01	3.2E-01	3.2E-01	3.2E-01	3.2E-01	3.2E-01	3.2E-01	3.2E-01	3.2E-01	3.2E-01	3.2E-01	3.2E-01	3.2E-01	3.2E-01	3.2E-01
Expression Signal	92.0	0 83		1.37	1.35	66.9	2.93	1.08		0.73	0.65	1.17	0.52	1.5	79.0	15.01	14.52	1.24	0.69	69.0	1.14	98.0	0.86	0.67	2.54	0.61	0.61	4.33	0.62	3.94
ORF SEQ ID NO:				30641	30740		31560	32589		32965	33277		34643	34969	L		35187		36310	35311	35391	35485	35486	35895		35983	35984	36824		Ц
Exon SEQ ID NO:	16857			17653	_	17993	ı	19260		19601		L	١.	21446	1	21643	1_	L	L		L	21950	21950	L	22354	22426	22426	23235	_	l l
Probe SEQ ID NO:	9096	200		4614	4621	4880	5386	8209		6433	6729	6872	8040	8365	8461	8562	8565	8656	8698	8698	8771	8871	8871	9267	9278	9351	9351	10198	10402	10518

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	Top Hit Descriptor	EST04702 Fetal brain, Stratagene (cat#936206) Homo sapiens cDNA clone HFBDZ21	Drosophila melanogaster laminin A (Lam-A) mRNA, complete cds	ELONGATION FACTOR TU (EF-TU)	Bos faurus inositol 1,4,5-trisphosphate receptor type I mRNA, complete cds	Homo sapiens deoxycytidylate deaminase gene, complete cds	601275480F1 NIH_MGC_20 Homo sapiens cDNA done IMAGE:3616746 5'	ye90h06.r1 Soares fetal liver coleen 1NFLS Homo sapiens cDNA clone IMAGE:125051 5' similar to de:M64241 QM PROTEIN (HUMAN);	Homo sapiens KIAA0174 gene product (KIAA0174), mRNA	Homo sapiens KIAA0174 gene product (KIAA0174), mRNA	h46h08.x1 Soares_NFL_T_GBC_S1 Homo saplens cDNA done IMAGE:2975391 3'	Mus musculus gene for Ser/Thr khase KKIAMRE, exon 6	Daucus oarota mRNA for transcription factor E2F (E2F gene)	Xylella fastidiosa, section 130 of 229 of the complete genome	Homo sapiens hepatocyte nuclear factor-3 alpha (HNF3A) gene, exon 1	HYPOTHETICAL PROTEIN H11236	S.cerevisiae chromosome XV reeding frame ORF YOL141w	Mus musculus mRNA for polycystin	Homo sapiens filamin 2 (FLN2) gene, exons 10 through 22	RC3-HN0001-310300-011-b04 HN0001 Homo sapiens cDNA	ql39d01.x1 NCI_CGAP_Co8 Homo sapiens cDNA clone IMAGE:1874589 3'	H.saplens gene for immunoglobulin kappa light chain variable region A8 and A9	MR2-CT0222-281099-005-h05 CT0222 Homo sapiens cDNA	601306121F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3640420 5'	Homo sapiens hyaluronan synthase 2 (HAS2), mRNA	yg46f01.s1 Soares Infant brain 1NIB Homo sapiens cDNA clone IMAGE:35639 3'	Mus musculus phosphatidylinositd-4-phosphate 5-kinase, type 1 gamma (Pip5k1 c), mRNA	602124743F1 NIH_MGC_56 Homo septens cDNA clone IMAGE:4281611 5'	602124743F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4281611 5'	qi61e11.x1 NCI_CGAP_Kld3 Homo seplens cDNA clone IMAGE:1863980 3' similar to gb:S55700 HYDROXYMETHYLGLUTARYI-COA LYASE PRECURSOR (HUMAN);	yb47708.s1 Stratagene fetal spieen (#837205) Homo sapiens cDNA clone IMACE:74367 3' similar to similar FST HI IMAN I to de:M91036 ma2 HEMOGLOBIN GAMMA-A AND GAMMA-G CHAINS (HUMAN)	
	Top Hit Database Source	T_HUMAN	N D	SWISSPROT EL	NT Bo	NT TA	EST_HUMAN 60	ye EST HUMAN 96			EST_HUMAN hiv	NT				SWISSPROT H		IM IN		EST HUMAN R	T_HUMAN		HUMAN	T_HUMAN		EST_HUMAN y			Г		MAN TO TO	EST LICINIFIA
2.6	Top Hit Acession No.	3.2E-01 T06813.1			3.2E-01 AF157625.1	L39874.1	3.2E-01 BE385776.1	3.1E-01 R18051.1	7661971	7661971 NT	3.1E-01 AW629036.1	3.1E-01 AB029069.1	3.1E-01 AJ251586.1	3.1E-01 AE003984.1	3.1E-01 AF176111.1		3.1E-01 Z74883.1	3.1E-01 Y13278.1	3.1E-01 AF184122.1	3.1E-01 AW983549.1	3.1E-01 AI264458.1	3.1E-01 X71887.1	3.1E-01 AW377354.1	3.1E-01 BE737392.1	4885390 NT	3.1E-01 R45318.1	6679322 NT	3.1E-01 BF696639.1	3.1E-01 BF696539.1	3.1E-01 AI244001.1	3 1F.01 T55325 1	3.15-01 133223.1
	Most Stmilar (Top) Hit BLAST E Value	3.2E-01	3.2E-01 L07288.1	3.2E-01 083217	3.2E-01	3.2E-01	3.2E-01	3.15-01	3.1E-01	3.1E-01	3.1E-01	3.1E-01	3.1E-01	3.1E-01	3.1E-01	3.1E-01 P44132	3.1E-01	3.1E-01	3.1E-01	3.1E-01	3.1E-01	3.1E-01	3.1E-01	3.1E-01	3.1E-01	3.1E-01	3.1E-01	3.1E-01	3.1E-01	3.1E-01	3 1E.01	٠. الترد
	Expression Signal	3.05	3.11	3.26	22	2.07	1.24	339	3.77	3.77	1.28	3.51	0.94	2.0	9.24	2.0	0.75	0.83	2.65	1.3	96.0	62.0	0.69	2.32	0.7	0.84	0.68	1.04	1.04	1.68	800	0.30
	ORF SEQ ID NO:	37620					31545	28967	28985	28986			30181	31177	31838	32205	32206		32390	33141	33200	33382		31491	34416	35467	36742			36979		
	Exon SEQ ID NO:	23988	l	25572	25891	25669	<u> </u>	15853	Į.	ł	16098	16416	17173		18790	18910	18911	18922	19080	19755	19822	19974	20220			21928	23144					ı
	Probe SEG ID NO:	10905	12289	12861	12969	13018	13089	2736	2762	2762	2920	3242	4016	5077	5699	5717	5718	5729	5892	6595	6863	6821	6905	7109	7856	8849	10106	10272	10272	10334	10540	

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Probe SEQ ID		ORF SEQ	Expression	Most Similar (Top) Hit	1 %	Top Hit Database	Top Hit Descriptor
ë	ö		<u>.</u>	Value	<u> </u>	Source	
7270		33806	96.0	3.0E-01	3.0E-01 AL163206.2	LN	Homo sapiens chromosome 21 segment HS21C006
7481	20558	34028	4.3	3.0E-01	10947007 NT	LZ LZ	Mus musculus midnolin (Midn-pending), mRNA
7670	l	34214	1.61	3.0E-01	3.0E-01 AF071810.1	NT	Streptococcus pneumoniae strain DBL5 PspA (pspA) gene, partial cds
8111	l	34713	1.34	3.0E-01	3.0E-01 AE001755.1	NT	Thermotoga maritima section 67 of 136 of the complete genome
8568	21649		3.1	3.0E-01	9910161	Ł	Mus musculus C-type (calcium dependent, carbohydrate recognition domain) lectin, superfamily member 9 (Cleosf9), mRNA
8658	ı	35279	0.48	3.0E-01	3.0E-01 Z70200.1	LN	H.sapiens gene for U5 snRNP-specific 200kD protein
8671	ı	35288	1.23	3.0E-01	83.1	EST_HUMAN	601339079F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3681594 5'
9029	ı	35649	69.0	3.0E-01	3.0E-01 AF141676.1	NT	Streptomyces sulfonofaciens isopenicillin N synthase (pcbC) gene, partial cds
9072	22151		0.82	3.0E-01	7681685 NT	NT	Homo saplens DKFZP586M0122 protein (DKFZP586M0122), mRNA
	l		,			!	Anabaena PCC7120 cytosine-specific DNA methyltransferase (dmnB) gene, complete cds, putative
9419	22493	36059	1.09		3.0E-01 AF220507.1	SWISSPROT	andramiade prosprionocypuariserase gene, peruarcus, and unandern gene HYPOTHETICAL 59.5 KD PROTEIN IN WZA-ASMA INTERGENIC REGION
9927			0.46			LN	Synechocystis sp. PCC6803 complete genome, 6/27, 630555-781448
10173	<u> </u>	36803	0.84		-2	EST_HUMAN	602133271F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4288336 5'
							Actinobacillus actinomycelemcomitans TadA (tadA), TadB (tadB), TadC (tadC), TadD (tadD), TadE (tadE),
10346	23381	36992	0.45	3.0E-01	3.0E-01 AF152598.3	NT	ladF (tadF), and TadG (tadG) genes, complete cds
40348	19000	36003	0.45	0.0	2 OE 04 AE143508 2		Actinobacillus actinomycetemcomitans TadA (tadA), TadB (tadB), TadC (tadC), TadD (tadD), TadE (tadE). TadE (tadE) and TadG (tadG) canes: complete cds
10606	1	37248	0.6	3.0E-01		T HUMAN	xe03d10.x1 Soares NFL T GBC S1 Homo sapiens cDNA clone IMAGE:2606035 3'
10608		37250	2.51	3.0E-01		П	Aspergillus oryzae bipA gene for ER chaperone BiP, complete cds
10629	23663	37271	0.76	3.0E-01	3.0E-01 BF683841.1	EST_HUMAN	602140133F1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4301097 5'
10629			0.76	3.0E-01	3.0E-01 BF683841.1	EST_HUMAN	602140133F1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4301097 5'
12067		38755	2.16		3.0E-01 H51029.1	EST_HUMAN	yp84b10.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:194107 5'
12067	25048		2.16		3.0E-01 H51029.1	EST_HUMAN	yp84b10.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:194107 5'
12470			1.3	3.0E-01		SWISSPROT	PONTICULIN PRECURSOR
12731	_		1.88	3.0E-01	3.0E-01 AJ297631.1	NT	Rattus norvegicus mRNA for glyceraldehyde-3-phosphate dehydrogenase type 2 (gapdh-2 gene)
13061			4.49		TN 9977799	TN	Mus musculus ribose 5-phosphate isomerase A (Rpla), mRNA
							Mus musculus mas proto-oncogene and lgf2r gene for insulin-like growth factor type 2 and L41ps and Au76
1771			0.94		2.9E-01 AJ249895.1	NT	pseudogenec
1930	15073	28176	0.94		5174502 NT	N	Homo sapiens membrane component, chromosome 11, surface marker 1 (M11S1) mRNA
2080						ΝΤ	Aquifex aedicus section 68 of 109 of the complete genome
2322		28585				N	Chrysodidymus synuraideus mitochondrion, complete genome
3253	16427	29445	96.0		2.9E-01 AF078111.1	NT	Xenopus laevis transcription factor E2F mRNA, complete cds

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Top Hit Descriptor	Bos taurus partial stat5A gene, exons 5-19	Bos taurus partial stat5A gene, exons 5-19	601882570F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4095113 5	Buchnera aphidicala plasmid plueu isolata MI 2-isopropylmaltate synthase (leuA) gene, partial cds; 3- isopromytealiste debutronances fan R) nane, committe cds; and isopropylmaltate debudratase subunit (leuC)	isdatolyginalizate darijutogonace (toda) gena, compress darijutogonace (toda) and toda ciking and toda ciking and toda ciking and toda ciking and toda ciking and toda ciking and toda ciking and toda ciking and toda ciking and toda ciking and toda ciking and toda ciking and toda ciking and toda ciking and toda ciking and toda ciking and toda ciking and toda ciking and toda ciking and toda ciking and toda ciking and toda ciking and toda ciking and toda ciking and toda ciking and toda ciking and toda ciking and toda ciking and toda ciking and toda ciking and toda ciking and toda ciking and toda ciking and toda ciking and toda ciking and toda ciking and toda ciking and toda ciking and toda ciking and toda ciking and toda ciking and toda ciking and toda ciking and toda ciking and toda ciking and toda ciking and toda ciking and toda ciking and toda ciking and toda ciking and toda ciking and toda ciking and toda ciking and toda ciking and toda ciking and toda ciking and toda ciking and toda ciking and toda ciking and toda ciking and toda ciking and toda ciking and toda ciking and toda ciking and toda ciking and toda ciking and toda ciking and toda ciking and toda ciking and toda ciking and toda ciking and toda ciking and toda ciking and toda ciking and toda ciking and toda ciking and toda ciking and toda ciking and toda ciking and toda ciking and toda ciking and toda ciking and toda ciking and toda ciking and toda ciking and toda ciking and toda ciking and toda ciking and toda ciking and toda ciking and toda ciking and toda ciking and ciking and ciking and ciking and ciking and ciking and ciking and ciking and ciking and ciking and ciking and ciking and ciking and ciking and ciking and ciking and ciking and ciking and ciking and ciking and ciking and ciking and ciking and ciking and ciking and ciking and ciking and ciking and ciking and ciking and ciking and ciking and ciking and ciking and ciking and ciking and ciking and ciking and ciking and ciking and ciking and ciking and ciking and ciking and ciking and ciking a	AU150910 NT2RP2 Homo sapiens cDNA clone NT2RP2003901 3'	Arabidopsis thaliana sulfonylurea receptor-like protein mRNA, complete cds	Baboon lymphocyte homing/adheston receptor mRNA, complete cds	Pyrococcus abyesi complete genome; segment 5/6	Pyrococcus abyssi complete genome; segment 5/6	UI-H-BI2-ehg-b-02-0-UI.s1 NCI_CGAP_Sub4 Homo sapiens cDNA clone IMAGE:2726714 3'	UI-H-BI2-ang-b-02-0-UI.s1 NCI_CGAP_Sub4 Homo sapiens cDNA clone IMAGE:2725714 3'	Trypanosoma cruzi stage-specific surface glycoprotein gp82 (gp82) mRNA, partial cds	Torpedo californica mRNA encodirig acetylchollne receptor gamma subunit	Torpedo californica mRNA encoding acetylcholine receptor gamma subunit	ny35h02.s1 NCI_CGAP_Pr12 Homo sapiens cDNA clone IMAGE:1273779 similar to contains LTR8.t2 LTR8	repetitive element	Campylobacter jejuni NCTC11168 complete genome; segment 3/6	Rattus norvegious activin receptor-like kinase 7 (ALK7) mRNA, complete cds	Rattus norvegicus activin receptor-like kinase 7 (ALK7) mRNA, complete cds	wz88t05.x1 NCI_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2565921 3' similar to contains element. M/FR20 recetifiue element	D. melanogaster: part of the 44D cuticle gene cluster encoding cuticle gene i	Homo sapiens TNF-a-inducible RNA binding protein (TIRP) gene, complete cds	Chlamydomonas reinhardtii mRNA for nitrite reductase structural locus	Chlamydomonas reinhardtii mRNA for nitrite reductase structural locus	Callinectes sapidus cadmlum-inducible metallothionein CdMT-I mRNA, complete cds	Raftus norvegicus A-kinase anchoring protein AKAP150 mRNA, complete cds	Prune dwarf virus movement protein, complete cds; coat protein, complete cds	Guira guira occyte maturation factor Mos (c-mos) gene, partial cds	801148733F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3163888 5	801148733F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3163688 5	Human mRNA for serine/threonine protein kinase, complete cos
Top Hit Database Source	ΤN	N	EST_HUMAN		<del>L</del> Z	EST HUMAN	NT	LN	IN	NT	EST_HUMAN	EST_HUMAN	ΙΝ	NT	N		EST_HUMAN	Ę	LΝ	LN	NAMILI TOD		LN	L	Į.	N	TN	N FN	۲	EST_HUMAN	EST_HUMAN	Ā
Top Hit Acession No.		2.9E-01 AJ237937.1	3F217743.1		2 DE-04   AF197456.1	2.9E-01 AU150910.1	2.9E-01 AF225908.1	M22452.1	1,1248287.1	2.9E-01 AJ248287.1	4W294100.1	.9E-01 AW 294100.1	.9E-01 AF128843.1	.9E-01 V01394.1	.9E-01 V01394.1			2	.9E-01 U35025.1	.9E-01 U35025.1	O D D A AND D E D A 4	2 05 04 1/00000 4	2 0F-01 AF092453 1	9F-01 Y08937.1	2 9E-01 Y08937.1	9E-01 AF200418.1	2.8E-01 U67136.1	128145.1	2.8E-01 AF168050.1	2.8E-01 BE313442.1	2.8E-01 BE313442.1	2.8E-01 D86550.1
Most Similar (Top) Hit BLAST E Value	2.9E-01	2.9E-01	2.9E-01		2 BE.041	2.9E-01	2.9E-01	2.9E-01	2.9E-01	2.9E-01	2.9E-01	2.9E-01	2.9E-01	2.9E-01	2.9E-01		2.9E-01	. 2.9E-01	2.9E-01	2.9E-01					ľ	7	2			"		
Expression Signal	0.64	0.64	0.75		- 53	0.82	1.09	0.81	96.0	96.0	0.46	0.46	1.94	1.79	1.79			3.12				60.00	50.0		1 24		``	1.96	3.34			
ORF SEQ ID NO:		34950	1				35747			L	L			l					38587			3201/	32004		l		ŀ		27331	L	L	5 27541
Exon SEQ ID NO:	21424	21424	21437		24645	21873	22204	22311	22563	22663	1	ì	I.,	L		1		24874	<u> </u>	L		70407		┸				L	L	L	L	Ш
Probe SEQ ID NO:	8343	8343	8356		9534	8794	9125	9233	9447	9447	10405	10405	11133	11433	11433		11881	11886	11900	11900		17071	40777	12108	12125	13204	582	587	1107	1306	1306	1319

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_		_		_	_	$\neg$			$\overline{}$	_		_		$\overline{}$	_	_	_	_	_	_	_							_	_	_			_	$\neg$
	Top Hit Descriptor	QV1-CT0364-120200-085-b05 CT0364 Homo sapiens cDNA	DKFZp586l2321_r1 586 (synonym: hute1) Homo sapiens cDNA clone DKFZp586l2321	hd44b03.x1 Soares_NFL_T_GBC_S1 Homo capiens cDNA clone IMAGE:2912333 3'	Escherichia coli K-12 MG1655 section 384 of 400 of the complete genome	Escherichla coli K-12 MG1655 section 384 of 400 of the complete genome	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 65	Arabidopsis thaliana mRNA for lipoytransferase, complete cds	Toxoplasma gondii 90kDa heat-shock protein (HSP90) mRNA, partial cds	B.taurus microsatellite (ETH121)	B.taurus microsatellite (ETH121)	Pyrococcus horikoshii OT3 genamic DNA, 777001-994000 nt. position (4/7)	Borrelia burgdorfert (section 66 of 70) of the complete genome	Pseudomonas aeruginosa PA01, section 11 of 529 of the complete genome	ov44g10x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1640226 3' similar to contains Alu	repetitive element; contains element MER22 repetitive element;	RNA POLYMERASE BETA SUBUNIT (LARGE STRUCTURAL PROTEIN) (L PROTEIN)	Hepatitis G virus isolate 60 (SZNAE12) polyprotein precursor, gene, partial cds	Bovine adenovirus 3 complete genome	602042601F1 NCI_CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4180129 5'	qt69c11.x1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:1876628 3' similar to contains Alu	repetitive element contains element LTR5 repetitive element;	Mouse Kv3.3 gene for potassium channel protein, exon 2	EST67072 Infant brain Homo sapiens cDNA 5' end	Hamo saplens OCTN2 gene, complete cds	CM1-BN0024-150200-118-g12 BN0024 Homo sapiens cDNA	oa01d06.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1303691 3' similar to gb:M34539 FK508-	BINDING PROTEIN (HUMAN);	244101.r1 Soares ovary tumor NbHOT Homo saplens cDNA clone IMAGE:724921 5' similar to contains Alu	repetitive element;	Bovine 680 bp repeated unit of 1,723 satellite DNA	Mesembryanthemum crystallinum fructose-biphosphate aldolase mRNA, complete cds	Mesembryanthemum crystallinum fructose-biphosphate aldolase mRNA, complete cds	UI-H-BI4-eoi-f-04-0-UI.s1 NCI_CGAP_Sub8 Homo sapiens cDNA clone IMAGE:3085182 3'
	Top Hit Database Source	EST_HUMAN	EST_HUMAN	EST_HUMAN	FZ	NT	TN	N	۲	LZ	TN	NT	Z	Z		EST_HUMAN	SWISSPROT	ΙΝ	NT	<b>EST_HUMAN</b>		EST_HUMAN	NT	EST HUMAN	N	EST_HUMAN		EST HUMAN		EST HUMAN	N	NT	NT	EST_HUMAN
	Top Hit Acession No.	2.8E-01 AW860020.1	2.8E-01 AL047620.1	2.8E-01 AW511195.1	2.8E-01 AE000494.1	2.8E-01 AE000494.1	2.8E-01 AL161565.2	2.8E-01 AB020975.1	2.8E-01 AF179480.1	2.8E-01 Z14037.1	2.8E-01 Z14037.1	2.8E-01 AP000004.1	2.8E-01 AE001180.1	2.8E-01 AE004450.1	i.	2.8E-01 A1090868.1	2.8E-01 P13615	2.8E-01 AF075238.1	2.8E-01 AF030154.1	2.8E-01 BF528188.1		2.8E-01 AI272669.1	2.8E-01 X60797.1	2.8E-01 AA349997.1	2.8E-01 AB016625.1	2.8E-01 AW992583.1		2.8E-01 AA765296.1		2.8E-01 AA404576.1	2.8E-01 M36668.1	2.8E-01 AF003124.1	2.8E-01 AF003124.1	2.8E-01 BF511215.1
	Most Similar (Top) Hit BLAST E Value	2.8E-01	2.8E-01	2.8E-01	2.8E-01	2.8E-01	2.8E-01	2.8E-01	2.8E-01	2.8E-01	2.8E-01					2.8E-01	2.8E-01	2.8E-01	2.8E-01	2.8E-01		2.8E-01	2.8E-01	2.8E-01	2.8E-01	2.8E-01		2.8E-01		2.8E-01	2.8E-01	2.8E-01	2.8E-01	2.8E-01
	Expression Signal	1.87	1.49	1.51	2.98	2.98	2.95	1.16	1.37	2.52	2.52	1.05	1.67	9.0		2.17	2	0.92	4.95	1.52		3.66	0.61	23.61	2.57	0.93		0.66		0.64	0.67	1.65	1.65	7.84
	ORF SEQ ID NO:		28326	i		L		28958			29235	Ŀ	30257							31090				31602	. 32211			32548				32874		
	Exon SEQ ID NO:	14915	15210		15667	15657	15736	15848	16211	16212	16212	16633	17257	17386		17458	17719	18074	18080	18113				25804	18916	19124		19225		19241	26212			2002
	Probe SEQ ID NO:	1766	2069	2200	2542	2542	2612	2730	3035	3036	3036	3466	4103	4240		4315	4582	4944	4950	4984		2006	5318	5428	5723	5938		6042		6020	6305	6347	6347	6870

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					·6		
Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
7145	20280	33721	0.64	7	.8E-01 U65300.1	LΝ	Orthogeomys heterodus cytochrome b (cytb) gene, mitochondrial gene encoding mitochondrial protein, complete cds
7599	20669		1.14	2	8E-01 U05633.1	LN	Marsilea quadrifdia ribulose-1,6-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, chloroplast gene encoding chloroplast protein, partial cds
8284	21366	34884	1.31	2.8E-01	8E-01 Al346126.1	EST_HUMAN	аравиот XI NCI_CGAP_Co8 Homo saplens cDNA clone IMAGE:1926289 3' similar to gb;X06323_cds1 MITOCHONDRIAL 60S RIBOSOMAL PROTEIN L3 (HUMAN);
8284	21386	34886		2.8E-01	Al346126.1	EST_HUMAN	qp48h01.x1 NCI_CGAP_Co8 Homo sapiens cDNA clone IMAGE:1926289 3' similar to gb:X06323_cds1 MITOCHONDRIAL 60S RIBOSOMAL PROTEIN L3 (HUMAN);
8404	21485			2.8E-01	2.8E-01 U51688.1	TN	Homo sapiens lanosterol 14 alpha demethylase cytochrome P450 (CYP51) gene, exon 5
8712		35328	9.0		2.8E-01 AA911629.1	EST_HUMAN	of02h05.s1 NCI_CGAP_Co12 Homo capiens cDNA clone IMAGE:1419983 3' similar to gb:M87789 IG GAMMA-1 CHAIN C REGION (HUMAN);
8789	21868		7.72		2.8E-01 BF347847.1	EST_HUMAN	602022987F1 NCI_CGAP_Brin67 Homo sapiens cDNA clone IMAGE:4158525 5'
9996	22628	36199	1.14		U17251.1	NT	Neurospora crassa negative regulator sulfur controller-2 (scon-2) gene, complete cds
9912	22952				L13654.1	LΝ	Lycopersicon esculentum peroxidase (TPX1) mRNA, complete cds
10092	23130	36733			AF132728.1	LN.	Escherichia coli translocated intimin receptor Tir (tir) gene, complete cds
10092	23130	36734			AF132728.1	NT	Escherichia coli translocated intimin receptor Tir (tir) gene, complete cds
10152	23189				AE001310.1	LN	Chlamydia trachomatis section 37 of 87 of the complete genome
	1						Rattus norvegicus glycerol-3-phosphate dehydrogenase gene, promoters A and B and exons 1a and 1b;
10156	- 1				2.8E-01 AF294393.1	Ę	nuclear gene for mitochondrial product
10265		36898	3.8		7706163 NT	NT NT	Homo septens hypothetical protein (LOC51319), mRNA
10519	1		1.1	2.8E-01	9626154	FN	Fujinami sarcoma virus, complete genome
10561	23596				2.8E-01 BE959727.2	EST_HUMAN	601654822R1 NIH_MGC_57 Homo sapiens cDNA clane IMAGE:3839765 3'
10982	24061	36928	1.88			EST_HUMAN	601880794F1 NIH_MGC_55 Hamo sapiens cDNA clone IMAGE:4109350 5
10982	24061	37696				EST_HUMAN	601880794F1 NIH_MGC_55 Hamo sapiens cDNA clone IMAGE:4109350 5
11011	24090	37727	3.01	2.8E-01	.8E-01 BF695970.1	EST_HUMAN	601852148F1 NIH_MGC_56 Hano sapiens cDNA clone IMAGE:4076026 5'
							Droscohila heteroneura fruitiess (fru) gene, alternative splice products, 5' flanking region, exons 1 through 7
11119	- 1	37823	1.53		2.8E-01 AF051662.1	LVI FOL	and complete cds sociated attailed MCC on Homo conjune CDNA Johns IMACE: 40739853 51
11556	- 1				BF6/4023.1	ES TOWAN	10/2/3/4 (of 1 Nit) MCC 63 Hours expens curva cidia invace 12/3000 0
11851		38533		2	.8E-01 AJ248285.1	본	Pyrococcus abyesi complete genome; segment 3/6
11861	24840			2	.8E-01 AJ248285.1	NT	Pyrococcus abyssi complete gename; segment 3/6
12715			12.79		2.8E-01 D83329.1	NT	Mus musculus DNA for prostaglandin D2 synthase, complete cds
12846	25562			Z	2.8E-01 BE178699.1	EST_HUMAN	PM4-HT0606-030400-001-a07 HT0606 Homo sapiens cDNA
12875	L	31996		7	BE9001	EST_HUMAN	601673020F1 NIH_MGC_21 Hamo sapiens cDNA clone IMAGE:3955996 5'
13052			1.59	2.8E-01	11433629 NT	NT	Homo sapiens CDC42-binding protein kinase beta (DMPK-like) (CDC42BPB), mRNA

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	_		_		_			_	_		_			_	_				٠.			_	_,			٠.,			_			_	_	_
Top Hit Descriptor	Rattus nonegicus CDK104 mRNA	z39b10.s1 Scares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:788827 3' similar to contains Alu repetitive element:	numera transmes transmessile element Tin100 nene for transmessia complete cde	Journal of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the contro	Subject gene	zd22h10.rl Soares_feta_heart_NbHH19W Homo sapiens cDNA clone IMAGE:341443 b	GAG POLYPROTEIN (CONTAINS; INNER COAT PROTEIN P12; CORE PROTEIN P15; CORE SHELL PROTEIN P20: NI ICI FOPROTEIN P10]	Delice and the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the s	Agins novegious vesicual morbannie agrispora type z, promota regulara exor.	EST175679 Infant brain, Bento Soares Homo sapiens cDNA clone UHIBO1R 5 end	EST175679 Infant brain, Bento Soares Homo sapiens cDNA clone UHIBO1R 5' end	Feline immunodeficiency virus env gene, isolate ITTO088PIU (M88), partial	ta43611.x2.NCI_CGAP_Lu25 Homo sapiens cDNA clone IMAGE:2046836 3' similar to contains element L1	epauve dedirent, 11.1. Transage Lies-seiter COMA	CM1-H 10875-J60900-385-e05 H 10675 Homo sapiens conva	Rattus norvegicus Insulin receptor (Insr), mRNA	wc92e11.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2462828 3'	Drosophija buzzatii alpha-esterase 6 (aE6) gene, partial cds	Drosophila buzzatii alpha-esterase 6 (aE6) gene, partial cds	Homo sapiens DiGeorge syndrome critical region, telomeric end	RC1-CT0286-230200-016-e03 CT0286 Homo sapiens cDNA	HOMEOBOX PROTEIN HOX-A4 (CHOX-1.4)	Astreopora myriophithalma mitochondrial cytb gene for cytochrome b, partial cds	LATENT TRANSFORMING GROWTH FACTOR BETA BINDING PROTEIN 1 PRECURSOR	(TRANSFORMING GROWTH FACTOR BETA-1 BINDING PROTEIN 1) (TGF-BETA1-BP-1)	(TRANSFORMING GROWTH FACTOR BETA-1 MASKING PROTEIN, LARGE SUBUNIT)	LATENT TRANSFORMING GROWTH FACTOR BETA BINDING PROTEIN 1 PRECURSOR	(TRANSFORMING GROWTH FACTOR BETA-1 BINDING PROTEIN 1) (TGF-BETA1-BP-1)	(TRANSFORMING GROWTH FACTOR BETA-1 MASKING PROTEIN, LARGE SUBUNIT)	Archaeoglobus fulgidus section 13 of 172 of the complete genome	Archaeoglobus fulgidus scotion 13 of 172 of the complete genome	FIBRILLIN 1 PRECURSOR	td08h08.x1 NCI_CGAP_CL11 Homo sapiens cDNA clone IMAGE:2075103 3	HYPOTHETICAL 20.9 KD PROTEIN B0563.3 IN CHROMOSOME X
Top Hit Database Source	ΙN	F. H. IMAN	Т	- L	٦	EST_HUMAN	TOGOSIMS	TOWN TOWN THE	T	j	EST_HUMAN	IN	1	ES HOMAN	EST_HUMAN		T_HUMAN	LN	N	IN	EST_HUMAN	SWISSPROT	N			SWISSPROT			SWISSPROT	N⊤	L	SWISSPROT	EST_HUMAN	SWISSPROT
Top Hit Acession No.	.7E-01 Y17324.1	2 7E-01 AA450061 1	2.7 C4 A D00 4006 4	-		2.7E-01 W58067.1	000044	1,000+1	2.7E-01 AF047575.1	.7E-01 AI372772.1	.7E-01 AI372772.1	.7E-01 Y13868.1		.7E-01 AI310858.1	2.7E-01 BF088284.1	8393620 NT	2.7E-01 Al928015.1	2.7E-01 AF216214.1	2.7E-01 AF216214.1	2.7E-01 L77569.1	2.7E-01 AW856131.1	2.7E-01 P17277	2.7E-01 AB033171.1			2.7E-01 Q00918	;		2.7E-01 Q00918	2.7E-01 AE001094.1	2.7E-01 AE001094.1	2.7E-01 Q61554	2.7E-01 AI540070.1	2.7E-01 Q11079
Most Similar (Top) Hit BLAST E Value	2.7E-01	2.75.01	27.7	Z./E-01	2./E-01	2.7E-01	0 7E 04 D03944	7. /E-01	2.7E-01	2.7E-01	2.7E-01	2.7E-01		2.7E-01	2.7E-01	2.7E-01	2.7E-01	2.7E-01	2.7E-01	2.7E-01	2.7E-01	2.7E-01	2.7E-01			2.7E-01			•					
Expression Signal	4.34	12 64	10.01	2.04	1.63	3.16	4	Q+.	3.1	0.94	0.94	70.7		4.36	0.99	99.0	1.94			2.39		1.98	1.31			0.86			0.86	1.05	1.05	1.74	0.77	0.92
ORF SEQ ID NO:	26717		l	71617		28012					28511	ļ_		28775								31452				32998	ŀ		32889	33293		33667		34058
Exon SEQ ID NO:	13683	13813	2	14445	14803	14917	1	14800	16057	15383	15383	15568	1	- 1	16225	16533	17272	l	ı	17292	18275	18583	18802			19639	ı		19639	19901	19901	20233	1	20585
Probe SEQ ID NO:	88	OC C	970	2887	1650	1768	1	181	2204	2250	2260	2440		2526	3049	3361	4118	4133	4133	4140	5153	5381	5607			6472			6472	6745	6745	6918	7197	7511

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Top Hit Descriptor	NITROGEN REGULATORY PROTEIN NUT1	NITROGEN REGULATORY PROTEIN NUT1	Boo taurus micromolar calcium activated neutral protesse 1 (CAPN1) gene, exons 11-20, and partial cds	Bos taurus micromolar calcium activated neutral protease 1 (CAPN1) gene, exons 11-20, and partial cds	EST58740 Infant brain Homo saplens cDNA 5' end similar to similar to myosin-binding protein H	EST58740 Infant brain Homo sapiens cDNA 5' end similar to similar to myosin-binding protein H	Oryctolagus cuniculus UDP-glucuronosyltransferase (UGT2B13) mRNA, complete cds	ze35b11.s1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE.360957 3' similar to contains Alu	Instruction actions, Instruction of the Section of the Section of the Instruction of the	vc91h06.s1 Soares infent brain 1NIB Homo sepiens cDNA clone IMAGE:23511.3	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 52	MAJOR VAULT PROTEIN (MVP) (LUNG RESISTANCE-RELATED PROTEIN)	THREONYL-TRNA SYNTHETASE (THREONINE-TRNA LIGASE) (THRRS)	THREONYL-TRNA SYNTHETASE (THREONINE-TRNA LIGASE) (THRRS)	FIMBRIAE W PROTEIN	Rettus norvegicus DNA for peroxisome assembly factor-2, exon 4, 5, 6, 7, 8, 9, 10, 11,12, 13, 14, 15, 16, 17 and complete cds	Oryctolagus cuniculus calgranulin C mRNA, partial cds	Mus musculus transcription factor NF-ATc isoform a (NF-ATca) mRNA, complete cds	Homo sapiens xeroderma pigmentosum complementation group C (XPC) gene, intron 9	Homo sapiens xeroderma pigmentosum complementation group C (XPC) gene, intron 9	Raftus norvegicus mRNA for class I beta-tubulin, complete cds	Homo sapiens neuropilin 2 (NRP2) gene, complete cds, alternatively spliced	Homo sapiens neuropilin 2 (NRP2) gene, complete cds, alternatively spliced	AV705043 ADB Hamo sapiens cDNA clane ADBCOD05 5'	AV705043 ADB Hamo saplens cDNA clane ADBCOD05 5	Home capiens caveolin-1/-2 locus, Contig1, D7S522, genes CAV2 (exons 1, 2a, and 2b), CAV1 (exons 1 and	2)	Arabidopsis thaliana mRNA for sulfate transporter, complete cds	Homo sapiens fragile 16D oxido reductase (FOR) gene, exon 6	IROQUOIS-CLASS HOMEODOMAIN PROTEIN IRX-2
Top Hit Database Source	SWISSPROT	SWISSPROT	ΤN	N.	EST_HUMAN	EST_HUMAN	Ν	TO L	EST HIMAN	FST HUMAN	LN LN	SWISSPROT	SWISSPROT	SWISSPROT	SWISSPROT	LN	Ł	L	Z	Į,	FZ	FN	NT	EST_HUMAN	EST_HUMAN	Ŀ	LN.	N L	LX	SWISSPROT
Top Hit Acession No.	Q01168	Q01168	2.7E-01 AF248054.1	2.7E-01 AF248054.1	2.7E-01 AA351121.1	2.7E-01 AA351121.1	2.7E-01 L01081.1	7 T O A A D C C C C C C C C C C C C C C C C C	2 7F-01 AW868503 1	2 7E-01 R39257 1	2.7E-01 AL161552.2	Q14764	083809	083809	P37928	2 7F-01 D89660 1	27E-01 AF091848.1	2.7E-01 AF087434.1	2.7E-01 AF156539.1	2.7E-01 AF156539.1	2.7E-01 AB011679.1	2.7E-01 AF281074.1	2.7E-01 AF281074.1	2.7E-01 AV705043.1	2.7E-01 AV705043.1	, 200001	2.7E-01 AJ133269.1	2.7E-01 AB008782.1	2.7E-01 AF217491.1	P78411
Most Similar (Top) Hit BLAST E Value	2.7E-01 Q01168	2.7E-01 Q01168	2.7E-01	2.7E-01	2.7E-01	2.7E-01	2.7E-01	0.45	27F.01	2.7E-01	2.7E-01	2.7E-01 Q14764	2.7E-01 O83809	2.7E-01 O83809	2.7E-01 P37928	2.7F-01	27E-01	2.7E-01	2.7E-01	2.7E-01	2.7E-01	2.7E-01	2.7E-01				2.7E-01	2.7E-01	2.7E-01	2.6E-01 P78411
Expression Signal	0.87	0.87	2.1	2.1	0.72	0.72	99'0	0	0.00	0 89	0.83	1.4	10.56	10.56	2.66	80	0.9	2.06	1.06	1.06	0.51	0.58	95.0	1.99	1.99		2.58	1.49	2.75	2.8
ORF SEQ ID NO:	34283	34284	34425	34428			34540	0.40			35104		ŀ			38636	36923		37099	37100					37762	į	37772			26710
Exan SEQ ID NO:	20795	20795	20919	20919		20968	21026	70,70	L	Ţ			1		<u> </u>	23043		$\mathbf{l}_{-}$		23490		23798	23798		24127				IJ	16013
Probe SEQ ID NO:	7734	7734	7895	7865	7917	7197	7976	5	8330	8380	8486	8959	9534	9534	9537	10005	10286	10323	10455	10455	10749	10765	10765	11050	11050	,	11061	12816	13034	482

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Top Hit Descriptor	Bos taurus mRNA for mb-1, complete cds	601510838F1 NIH_MGC_71 Hamo sapiens cDNA clone IMAGE:3912345 5'	Glycine max pseudogene for Bd 30K	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 2	Arabidopsis thallana DNA chromosome 4, contig fragment No. 2	bb04d10.x1 NIH_MGC_14 Homo sapiens cDNA clone IMAGE:2968451 3' similar to gb:M36072 60S RIBOSOMAL PROTEIN L7A (HUMAN); gb:M14689_cds1 Mouse surfeit locus surfeit 3 protein gene	(MOUSE);	Human prealbumin gene, complete cds	601126016F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:2990043 5'	EST386635 MAGE resequences, MAGM Homo saplens cDNA	Bacteriphage T2 DNA-(adenine-N6)methytransferase (dam) gene, complete cds	Homo sapiens acetylcholinesterase collagen-like tall subunit (COLQ) gene, exons 1A, 2, 3, 4, and 5	EST371580 MAGE resequences, MAGF Homo sapiens cDNA	QV1-BT0630-040400-132-e03 BT0630 Homo sapiens cDNA	Entercoccus faecium strain N97-330 vanD glycopeptide resistance gene cluster, complete cds; and unknown gene	Gallus gallus mRNA for skeletal myosin heavy chain, complete ods	Gallus gallus mRNA for skeletal myosin heavy chain, complete cds	aa89d07.r1 Stratagene fetal retina 937202 Homo saplens cDNA clone IMAGE:838477 5	Arabidopsis thaliana PSI type III chlorophyll a/b-binding protein (Lhca3*1) mRNA, complete cds	Ophrestia radicosa maturase-like protein (matk) gene, complete cds; chloroplast gene for chloroplast product	yj51e05.r1 Soares placenta NbZHP Homo sapiens cDNA clone IMAGE:152288 5'	am33b11.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1468605 31	Paramecium caudatum gene for PAP, complete cds	Acetobacter xylinum cellulose synthase (bcsA) gene, partial cds, CMCax and CcpAx genes, complete cds	td16g03.x1 NCI_CGAP_Co16 Homo sapiens cDNA clone IMAGE:2075788 3' similar to contains element MER35 repetitive element ;	Homo sapiens protein translocase, JM28 protein, UDP-galactose translocator, pim-2 protocnoogene homolog pim-2h, and shat-type potassium channel genes, complete cds; JM12 protein and transcription factor IGHM perhanear 3 menes, arenear partial cds; and unknown op	מוופוסמ ס ממוכס לאם ונוס ככל בין בין בין בין בין בין בין בין בין בין
Top Hit Database	TN	EST_HUMAN	NT	LN	LΝ		EST HUMAN	LN	EST_HUMAN	EST_HUMAN	: IN	LN	EST_HUMAN	EST_HUMAN	Ę	Ę	LN LN	EST_HUMAN	NT	LN	EST_HUMAN	EST_HUMAN	LN⊤	FN	EST_HUMAN	<u> </u>	12
Top Hit Acesslan No.	2.6E-01 D16459.1	2.6E-01 BE885087.1	2.6E-01 AB013290.1	2.6E-01 AL161472.2	2.6E-01 AL161472.2		2.6E-01 AW 733152.1	2.6E-01 M11844.1	2.6E-01 BE272440.1	2.6E-01 AW974531.1	2.6E-01 M22342.1	2.6E-01 AF229118.1	2.6E-01 AW959510.1	2,6E-01 BE080598.1	2.6E-01 AF175293.1	2.6E-01 AB021180.1	2.6E-01 AB02:180.1	2.6E-01 AA457617.1	2.6E-01 U01103.1	2.6E-01 AF142703.1	2.6E-01 H04858.1	2.6E-01 AA884625.1	2.6E-01 AB035972.1	2.6E-01 M96060.1	2.6E-01 AI862398.1	A C C C C C C C C C C C C C C C C C C C	Z.DE-UT AFZU/ SSU.1
Most Similar (Top) Hit BLAST E Value	2.6E-01	2.6E-01	2.6E-01 /	2.6E-01	2.6E-01		2.6E-01	2.6E-01	2.6E-01	2.6E-01	2.6E-01	2.6E-01	2.6E-01	2.6E-01	2.6E-01	2.6E-01	2.6E-01	2.6E-01	2.6E-01	2.6E-01	2.6E-01	2.6E-01	2.6E-01	2.6E-01	2.6E-01	c n	Z.0E-V.1
Expression Signal	1.94	1.77	1.09	69'2	7.69		10.39	1.13	11.66	1.11	0.84	1.67	0.79	16.93	1.71	0.69	0.69	1.14	2.25	1.15	3.63	0.61	1.29	0.67	0.84		0.04
ORF SEQ ID NO:		27651	27705	28188	28189		_	28485			29845	29899	30352			l	30736	ł		30958	Ŀ			31802	·		32394
Exon SEQ ID NO:	13688	14578	14622	15088	15088		15295	15354	15735	16336	16834	16894	17364	17415	17616	ı	17754	17805		17970	L	L	18657	L	1		19083
Probe SEQ ID NO:	84	1424	1468	1945	1946		2159	2220	2611	3161	3671	3733	4215	4270	4478	4817	4617	4670	4770	4837	5086	5155	5457	5565	5689		5895

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Porbage         Exm         ORF SEG         Expression         Monta Shmillar (Top)-HII Accession         Top-HII Accession         Accession Accession         Top-HII Accession         Top-HII Accession         Top-HII Accession         Accession Accession         Top-HII Accession         Top-HII Accession         Top-HII Accession         Accession Accession         Accession Accession         Accession Accession         Accession Accession         Accession Accession         Accession Accession         Accession Accession         Accession Accession         Accession Accession         Accession Accession         Accession Accession         Accession Accession         Accession Accession         Accession Accession         Accession Accession         Accession Accession         Accession Accession         Accession Accession         Accession Accession         Accession Accession         Accession Accession         Accession Accession         Accession Accession         A								
26271         2.57         2.6E-01         AE001811.1         NT           19601         32859         1.96         2.6E-01         AI582557.1         EST_HUMAN           19714         33090         0.98         2.6E-01         AL162757.2         NT           19861         33364         0.74         2.6E-01         AL162757.2         NT           19961         33364         0.74         2.6E-01         BE792052.1         EST_HUMAN           20621         34098         0.74         2.6E-01         BE792052.1         EST_HUMAN           20621         34098         0.7         2.6E-01         BE792052.1         EST_HUMAN           20699         34476         1.73         2.6E-01         BE782052.1         EST_HUMAN           21170         34685         1.3         2.6E-01         BE782052.1         EST_HUMAN           21170         34685         1.3         2.6E-01         BE783072.2         BT_HUMAN           21671         35548         2.97         2.6E-01         BE78333.1         EST_HUMAN           21670         35548         1.74         2.6E-01         BE7834588.1         BT_HUMAN           21670         35506         4.06	Probe SEO ID NO:		ORF SEQ ID NO:	Expression Signal		Top Hit Acessian No.	Top Hit Database Source	Top Hit Descriptor
19601         32856         1,96         2,6E-01         AI582557.1         EST_HUMAN           19714         33080         1,96         2,6E-01         AI582557.1         EST_HUMAN           19714         33080         0,98         2,6E-01         AI582557.2         NT           19861         33364         0,74         2,6E-01         BE792052.1         EST_HUMAN           20621         34086         0,74         2,6E-01         BE792052.1         EST_HUMAN           20846         3476         1,04         2,6E-01         BE792052.1         EST_HUMAN           20858         34476         1,73         2,6E-01         BE148961.1         EST_HUMAN           20859         34476         1,73         2,6E-01         BE148961.1         EST_HUMAN           2110         34834         1,18         2,6E-01         BE143961.1         EST_HUMAN           21669         34476         1,73         2,6E-01         BE143961.1         EST_HUMAN           21670         34685         1,3         2,6E-01         BE143961.1         EST_HUMAN           21871         35507         4,06         2,6E-01         BE143961.1         EST_HUMAN           22629         36200<	6196	1 1		2.57	2.6E-01		ĻΝ	Thermotoga maritima section 123 of 138 of the complete genome
19501 32860 1.96 2.6E-01 AI582557.1 EST_HUMAN 1961 33364 0.74 2.6E-01 BE792052.1 EST_HUMAN 1961 33364 0.74 2.6E-01 BE792052.1 EST_HUMAN 20051 34098 0.77 2.6E-01 BE792052.1 EST_HUMAN 2170 34698 0.77 2.6E-01 BE149901.1 EST_HUMAN 2170 34695 1.73 2.6E-01 AA196149.1 EST_HUMAN 21971 35506 4.06 2.6E-01 BE30339.1 EST_HUMAN 21971 35506 4.06 2.6E-01 BE30339.1 EST_HUMAN 22670 36270 0.92 2.6E-01 BE30339.1 EST_HUMAN 22671 35506 4.06 2.6E-01 BE30339.1 EST_HUMAN 22671 35506 4.06 2.6E-01 BE30339.1 EST_HUMAN 22670 36270 0.92 2.6E-01 A7057121.1 NT 22670 36270 0.92 2.6E-01 A7057121.1 NT 22670 36270 0.92 2.6E-01 A7057121.1 NT 22670 36270 0.92 2.6E-01 A7057121.1 NT 22670 36270 0.93 2.6E-01 A7057121.1 NT 22670 36270 0.48 2.6E-01 A7057121.1 NT 22670 0.48 2.6E-01 A70769.1 NT 22670 37740 0.48 2.6E-01 A70769.1 NT 22670 0.48 2.6E-01 A70769.1 NT 22670 0.48 2.6E-01 A70769.1 NT 22670 0.48 2.6E-01 A70769.1 NT 22770 0.48 2.6E-01 A70769.1 NT 22670 0.48 2.6E-01 A70769.1 NT 22670 0.48 2.6E-01 A70769.1 NT 22670 0.48 2.6E-01 A70769.1 NT 22670 0.48 2.6E-01 A70769.1 NT 22670 0.48 2.6E-01 A70769.1 NT 22670 0.48 2.6E-01 A70769.1 NT 22670 0.48 2.6E-01 A70769.1 NT 22670 0.48 2.6E-01 A70769.1 NT 22670 0.48 2.6E-01 A70769.1 NT 22670 0.48 2.6E-01 A70769.1 NT 22670 0.48 2.6E-01 A70769.1 NT 22670 0.48 2.6E-01 A70769.1 NT 22670 0.48 2.6E-01 A70769.1 NT 22670 0.48 2.6E-01 A70769.1 NT 22670 0.48 2.6E-01 A70769.1 NT 22670 0.48 2.6E-01 A70769.1 NT 22670 0.48 2.6E-01 A70769.1 NT 22670 0.48 2.6E-01 A70769.1 NT 22670 0.48 2.6E-01 A70769.1 NT 22670 0.48 2.6E-01 A70769.1 NT 22670 0.48 2.6E-01 A70769.1 NT 22670 0.48 2.6E-01 A70769.1 NT 22670 0.48 2.6E-01 A70769.1 NT 22670 0.48 2.6E-01 A70769.1 NT 22670 0.48 2.6E-01 A70769.1 NT 22670 0.48 2.6E-01 A70769.1 NT 22670 0.48 2.6E-01 A70769.1 NT 22670 0.48 2.6E-01 A70769.1 NT 22670 0.48 2.6E-01 A70769.1 NT 22670 0.48 2.6E-01 A70769.1 NT 22670 0.48 2.6E-01 A70769.1 NT 22670 0.48 2.6E-01 A70769.1 NT 22670 0.48 2.6E-01 A70769.1 NT 22670 0.48 2.6E-01 A70769.1 NT 22670 0.48 2.6E-01 A70769.1 NT 22670 0.48 2.6E-01 A70769.1 NT 22670 0	6830				,,	AI582557.1		ts02e12.x1 NCI_CGAP_Pan1 Homo septens cDNA clone IMAGE:2227438 3' similar to SW:NDF1_RAT QR4289 NEUROGENIC DIFFERENTIATION FACTOR 1 ;contains element LTR1 repetitive element;
19714         33090         0.98         2.6E-01         AL162757.2         NT           19961         33364         0.74         2.6E-01         BE792052.1         EST_HUMAN           20315         33765         0.74         2.6E-01         BE792052.1         EST_HUMAN           20527         34098         0.77         2.6E-01         BE19801.1         EST_HUMAN           20569         34476         1.73         2.6E-01         AL13907.2         NT           2110         34634         1.73         2.6E-01         AL196149.1         EST_HUMAN           2110         34634         1.73         2.6E-01         AL196149.1         EST_HUMAN           2110         34634         1.18         2.6E-01         AL196149.1         EST_HUMAN           2110         34634         1.18         2.6E-01         BE144331.1         EST_HUMAN           21600         35148         2.97         2.6E-01         BE74331.1         EST_HUMAN           21671         35507         4.06         2.6E-01         BE74331.1         EST_HUMAN           22629         35207         4.06         2.6E-01         BE714331.1         EST_HUMAN           22629         3.6200	6330			_		A1582557.1	EST HUMAN	te02e12.x1 NCI_CGAP_Pan1 Homo sepiens cDNA clone IMAGE:2227438 3' similar to SW:NDF1_RAT Q84289 NEUROGENIC DIFFERENTIATION FACTOR 1 ;contains element LTR1 repetitive element ;
19861         33364         0.74         2 6E-01         BE792052.1         EST_HUMAN           19861         33365         0.74         2 6E-01         BE792052.1         EST_HUMAN           20315         33768         1,04         2 6E-01         BE198901.1         EST_HUMAN           25848         0.77         2 6E-01         BE149901.1         EST_HUMAN           25848         0.78         2 6E-01         BA196149.1         EST_HUMAN           2110         34476         1.73         2 6E-01         RA196149.1         EST_HUMAN           21116         34634         1.18         2 6E-01         RA196149.1         EST_HUMAN           2116         34634         1.18         2 6E-01         RA196149.1         EST_HUMAN           21170         34685         1.3         2 6E-01         RA196149.1         EST_HUMAN           2160         35148         2.97         2 6E-01         BE134331.1         EST_HUMAN           2160         35248         1.74         2 6E-01         BE134331.1         EST_HUMAN           21671         35507         4.06         2 6E-01         BE134368.1         EST_HUMAN           22629         36200         0.92         2	6552					AL162757.2	N <sub>T</sub>	Neisseria meningitidis serogroup A strain Z2491 complete genome; segment 6/7
19861         33365         0.74         2.6E-01         BE792052.1         EST_HUMAN           20315         33768         1.04         2.6E-01         AI914380.1         EST_HUMAN           20821         34088         0.78         2.6E-01         BE149901.1         EST_HUMAN           20896         34476         1.73         2.6E-01         AI136077.2         NT           21116         34634         1.18         2.6E-01         RC2411.1         EST_HUMAN           21170         34686         1.3         2.6E-01         BE14331.1         EST_HUMAN           21170         34686         1.3         2.6E-01         BE144331.1         EST_HUMAN           21871         35507         4.06         2.6E-01         BE144331.1         EST_HUMAN           21871         35507         4.06         2.6E-01         BE830339.1         EST_HUMAN           22629         3620         0.02         2.6E-01         BE830339.1         EST_HUMAN           22670         4.06         2.6E-01         BE830339.1         EST_HUMAN           2310         35714         1.13         2.6E-01         AF057121.1         NT           22629         36200         0.62	6807	1			"	BE792052.1	EST_HUMAN	601581754F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3936156 5'
20915         33768         1,04         26E-01         Al914380.1         EST_HUMAN           20921         34098         0,7         26E-01 BE148961.1         EST_HUMAN           20926         34476         0,78         2.6E-01 AL138077.2         INT           2110         34834         1,18         2.6E-01 AL138077.2         INT           21170         34885         1,3         2.6E-01 AL13807.1         EST_HUMAN           21870         35148         2.97         2.6E-01 BE144331.1         EST_HUMAN           21871         35507         4.06         2.6E-01 BE34388.1         EST_HUMAN           21871         35507         4.06         2.6E-01 BE34338.1         EST_HUMAN           22629         3.6200         4.06         2.6E-01 BE34338.1         EST_HUMAN           22670         3.6507         4.06         2.6E-01 BE34338.1         EST_HUMAN           22670         3.6200         0.02         2.6E-01 BE34338.1         EST_HUMAN           22670         3.6200         0.02         2.6E-01 BE34333.1         EST_HUMAN           22670         3.6200         0.02         2.6E-01 BC34333.1         INT           23428         0.05         2.6E-01 AF057121.1         I	6807					BE792052.1	EST_HUMAN	601581754F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3938156 5
20621         34098         0.7         2.6E-01 BE143961.1         EST HUMAN           20596         2.6E-01 AL136077.2         NT           20698         34476         1.73         2.6E-01 AL136077.2         NT           20110         34634         1.73         2.6E-01 R10365.1         EST HUMAN           21110         34634         1.73         2.6E-01 R02411.1         EST HUMAN           21110         35148         2.97         2.6E-01 R02411.1         EST HUMAN           21971         35506         4.06         2.6E-01 BE30339.1         EST HUMAN           21971         35507         4.06         2.6E-01 BE830339.1         EST HUMAN           22629         4.06         2.6E-01 BE830339.1         EST HUMAN           22629         4.06         2.6E-01 BE830339.1         EST HUMAN           22629         4.06         2.6E-01 BE830339.1         EST HUMAN           2310         36507         4.06         2.6E-01 BE830339.1         EST HUMAN           23428         0.95         2.6E-01 AF057121.1         NT           23428         0.63         2.6E-01 AF057121.1         NT           23428         0.63         2.6E-01 AF057121.1         NT	7183	ļ		٠	,,,	AI914380.1	EST_HUMAN	wd48c04.x1 Soares_NFL_T_GBC_S1 Homo sapiens oDNA clone IMAGE:2331365 3' similar to gb:M37721 PEPTIDYL-GLYCINE ALPHA-AMIDATING MONOOXYGENASE PRECURSOR (HUMAN);
25848         0.96         2.6E-01         AL138077.2         NT           20696         34476         1.73         2.6E-01         AA196149.1         EST_HUMAN           21116         34634         1.73         2.6E-01         R10365.1         EST_HUMAN           21170         34685         1.3         2.6E-01         RC2411.1         EST_HUMAN           21170         34685         1.74         2.6E-01         BE144331.1         EST_HUMAN           21971         35506         4.06         2.6E-01         BE30339.1         EST_HUMAN           21971         35507         4.06         2.6E-01         BE830339.1         EST_HUMAN           22629         4.06         2.6E-01         BT-HUMAN           23410         36713         1.13         2.6E-01         SWISSPROT           23428         0.63         2.6E-01         BT-BSS480.1         NT           23429         0.648         2.6E-01	7549	i	l			BE148961.1	EST_HUMAN	CM0-HT0246-031199-085-f04 HT0245 Homo sapiens cDNA
20696         0.78         2.6E-01         AA196149.1         EST_HUMAN           20969         34476         1.73         2.6E-01         R10365.1         EST_HUMAN           21116         34634         1.18         2.6E-01         R702411.1         EST_HUMAN           21606         35048         1.3         2.6E-01         BF144331.1         EST_HUMAN           21671         35148         2.97         2.6E-01         BF143331.1         EST_HUMAN           21971         35506         4.06         2.6E-01         BF1830339.1         EST_HUMAN           21971         35507         4.06         2.6E-01         BE830339.1         EST_HUMAN           22629         36200         0.92         2.6E-01         BF1830339.1         EST_HUMAN           22679         4.06         2.6E-01         BF1830339.1         EST_HUMAN           22679         4.06         2.6E-01         AF057121.1         NT           23110         36713         1.13         2.6E-01         BF3366         SWISSPROT           23428         0.63         2.6E-01         BF3366         SWISSPROT           23420         0.64         2.6E-01         BF3366         SWISSPROT	7587	ı			,	AL139077.2	NT	Campylobacter jejuni NCTC11168 complete genome; segment 4/6
20969         34476         1.73         2.6E-01         R10365.1         EST_HUMAN           21116         34634         1.18         2.6E-01         ER14331.1         EST_HUMAN           21606         35148         2.97         2.6E-01         ER144331.1         EST_HUMAN           21671         35148         2.97         2.6E-01         ER144331.1         EST_HUMAN           21671         35506         4.06         2.6E-01         ER14331.1         EST_HUMAN           21671         35507         4.06         2.6E-01         BE830339.1         EST_HUMAN           22629         36200         0.92         2.6E-01         BE830339.1         EST_HUMAN           22679         3.620         0.92         2.6E-01         AF057121.1         NT           23110         36713         1.13         2.6E-01         AF057121.1         NT           23420         0.62         2.6E-01         AF057121.1         NT           23420         0.63         2.6E-01         AF057121.1         NT           23420         0.63         2.6E-01         AF057121.1         NT           23420         0.64         2.6E-01         AF057121.1         NT	7626			0.78	,	AA196149.1	EST_HUMAN	zp92e01.r1 Stratagene HeLa cell s3 937216 Homo sapiens cDNA clone IMAGE:627672 5'
2000         34476         1.73         2.6E-01         R01050.1         EST_HUMAN           21110         34634         1.18         2.6E-01         BE14433.1         EST_HUMAN           21170         34686         1.3         2.6E-01         BE14433.1         EST_HUMAN           21671         35506         4.06         2.6E-01         BE830339.1         EST_HUMAN           21971         35507         4.06         2.6E-01         BE830339.1         EST_HUMAN           22679         4.06         2.6E-01         BE830339.1         EST_HUMAN           22879         6.09         2.6E-01         X17604.1         NT           23110         36713         1.13         2.6E-01         X17604.1         NT           23110         36713         1.13         2.6E-01         X17604.1         NT           23110         36713         1.13         2.6E-01         X17604.1         NT           23110         36714         1.13         2.6E-01         X17604.1         NT           23428         0.63         2.6E-01         Y10190.1         NT           23429         0.48         2.6E-01         Y10190.1         NT           24804	1					D4000E 4	HOU HOU	y37a03.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:129004 3' striitar to कर्मस्य १८४१ । 14 SMAIT NI ICI FAR RIBONI ICI FOPROTFIN C (HUMAN):
2170         34885         1.3         26E-01 BE144331.1         EST_HUMAN           2160         35148         2.97         2.6E-01 BF343688.1         EST_HUMAN           21971         35506         4.06         2.6E-01 BE830339.1         EST_HUMAN           21971         35507         4.06         2.6E-01 BE830339.1         EST_HUMAN           22629         36200         0.92         2.6E-01 X77804.1         NT           22879         0.5         2.6E-01 X77804.1         NT           23110         36713         1.13         2.6E-01 P87366         SWISSPROT           2310         36714         1.13         2.6E-01 P87366         SWISSPROT           23428         0.63         2.6E-01 P87366         SWISSPROT           23780         0.63         2.6E-01 P87366         SWISSPROT           23780         0.63         2.6E-01 P87366         SWISSPROT           23873         0.48         2.6E-01 P87366         SWISSPROT           24804         31.14         2.6E-01 Y10190.1         NT           26070         4.14         2.6E-01 P87366         SWISSPROT           25365         32069         3.86         2.6E-01 P87366         SWISSPROT	8033	Т				R02411.1	EST HUMAN	ye82a07.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMACE:124212.5
21610         35148         2.97         2.6E-01         BF34368.1         EST_HUMAN           21871         35506         4.06         2.6E-01         BE830339.1         EST_HUMAN           21971         35507         4.06         2.6E-01         BE830339.1         EST_HUMAN           22629         36200         0.92         2.6E-01         X17604.1         NT           22879         0.5         2.6E-01         X17604.1         NT           23110         36713         1.13         2.6E-01         SWISSPROT           23110         36714         1.13         2.6E-01         SWISSPROT           23428         0.63         2.6E-01         Y10196.1         NT           23780         0.48         2.6E-01         Y10196.1         NT           23873         0.48         2.6E-01         Y10196.1         NT           24804         31.14         2.6E-01         X51755.1         NT           26070         4.14         2.6E-01         X51755.1         NT           25365         32069         3.86         2.6E-01         X51755.1         NT	808	L	L			BE144331.1	EST HUMAN	MR0-HT0166-181199-003-412 HT0166 Homo sapiens cDNA
21686         36223         1.74         26E-01 (010199         SWISSPROT           21971         35506         4.06         2.6E-01 BE830339.1         EST_HUMAN           22629         36200         0.92         2.6E-01 X17604.1         NT           22879         0.5         2.6E-01 X17604.1         NT           23110         36713         1.13         2.6E-01 P87366         SWISSPROT           23120         36713         1.13         2.6E-01 P87366         SWISSPROT           23428         0.63         2.6E-01 P87366         SWISSPROT           23428         0.63         2.6E-01 Q28236         SWISSPROT           23760         1.09         2.6E-01 Q28236         SWISSPROT           23873         0.48         2.6E-01 Q128236         SWISSPROT           24804         31.14         2.6E-01 X51755.1         NT           26070         4.14         2.6E-01 X51755.1         NT           25365         3.2069         3.86         2.6E-01 AF316896.1         NT	8529	ı				BF343588.1	EST_HUMAN	602014422F1 NCI_CGAP_Bnn64 Homo sapiens cDNA clane IMAGE:4150396 5
21971         3550e         4.0e         2.6E-01         BE830339.1         EST_HUMAN           22629         36200         0.92         2.6E-01         X17604.1         NT           22879         0.5         2.6E-01         X17604.1         NT           23110         36713         1.13         2.6E-01         P87366         SWISSPROT           23418         36714         1.13         2.6E-01         P87366         SWISSPROT           23428         0.63         2.6E-01         P87366         SWISSPROT           23429         0.63         2.6E-01         Y10196.1         NT           23420         0.48         2.6E-01         Y10196.1         NT           24804         31.14         2.6E-01         X51755.1         NT           26070         4.14         2.6E-01         X51755.1         NT           26070         3.2069         3.86         2.6E-01         X51755.1         NT	8605	١				Q10199	SWISSPROT	HYPOTHETICAL 75.2 KD PROTEIN C11C11.02 IN CHROMOSOME II
21971         35507         4.06         2.6E-01 BE830339.1         EST HUMAN           22629         36200         0.92         2.6E-01 X17604.1         NT           22879         0.5         2.6E-01 PS7366         SWISSPROT           23110         36714         1.13         2.6E-01 PS7366         SWISSPROT           23428         0.63         2.6E-01 PS7366         SWISSPROT           23760         1.09         2.6E-01 PV10198.1         NT           23873         0.48         2.6E-01 PV10198.1         NT           24804         31.14         2.6E-01 X51755.1         NT           26070         4.14         2.6E-01 PV10198.1         NT           25365         32069         3.86         2.6E-01 PV10198.1         NT	8892	1				BE830339.1	EST_HUMAN	RC5-ET0082-310500-021-F10 ET0082 Homo sapiens cDNA
22629         36200         0.92         2.6E-01         X17604.1         NT           23310         36713         1.13         2.6E-01         P87366         SWISSPROT           23428         0.63         2.6E-01         P87366         SWISSPROT           23750         0.63         2.6E-01         P87366         SWISSPROT           23750         1.09         2.6E-01         P710186.1         NT           23873         0.48         2.6E-01         Y15874.2         NT           24804         31.14         2.6E-01         X51755.1         NT           26070         4.14         2.6E-01         X51755.1         NT           26070         3.36         2.6E-01         X51755.1         NT	8892	L				BE830339.1	EST_HUMAN	RC5-ET0082-310500-021-F10 ET0082 Homo sapiens cDNA
22979         0.5         2.6E-01 AF057121.1         NT           23110         36713         1.13         2.6E-01 P87366         SWISSPROT           23128         0.63         2.6E-01 P87366         SWISSPROT           23428         0.63         2.6E-01 Q78296         SWISSPROT           23760         1.09         2.6E-01 Y10196.1         NT           23873         0.48         2.6E-01 Y15874.2         NT           24604         31.14         2.6E-01 X51756.1         NT           26070         4.14         2.6E-01 X51769.1         NT           25365         32069         3.86         2.6E-01 AF316896.1         NT	9667	l				X17604.1	LN	S. occidentalis INV gene for invertase (EC 3.2.1.26)
22979         0.5         2.6E-01 AF057121.1         NT           23110         36713         1.13         2.6E-01 P87366         SWISSPROT           23428         0.63         2.6E-01 P97366         SWISSPROT           23750         1.09         2.6E-01 Q28295         SWISSPROT           23873         0.48         2.6E-01 V10196.1         NT           24804         31.14         2.6E-01 X51755.1         NT           26070         4.14         2.6E-01 X51765.1         NT           25365         32069         3.86         2.6E-01 AF316896.1         NT								Lontra canadensis cytochrome b (cytb) gene, mitochondriai gene encoding mitochondrial protein, complete
23110         36713         1.13         2.6E-01         P87366         SWISSPROT           23140         36714         1.13         2.6E-01         P87366         SWISSPROT           23428         0.63         2.6E-01         Q28295         SWISSPROT           23760         1.09         2.6E-01         Y10186.1         NT           24804         31.14         2.6E-01         Y17186.1         NT           26070         4.14         2.6E-01         X57755.1         NT           25365         32069         3.86         2.6E-01         HF31686.1         NT	9940					AF057121.1	ΙNΤ	æ
2310         36714         1.13         2.6E-01         P87366         SWISSPROT           23428         0.63         2.6E-01         Q28296         SWISSPROT           23760         1.09         2.6E-01         Y10196.1         NT           23873         0.48         2.6E-01         Y15874.2         NT           24804         31.14         2.6E-01         X51756.1         NT           26070         4.14         2.6E-01         BE883491.1         EST HUMAN           25365         32069         3.86         2.6E-01         AF316896.1         NT	10072	l				P87366	SWISSPROT	GREEN-SENSITIVE OPSIN (GREEN CONE PHOTORECEPTOR PIGMENT) (KFH-G)
23428         0.63         2.6E-01         Q28296         SWISSPROT           23760         1.09         2.6E-01         Y10196.1         NT           23873         0.48         2.6E-01         Y15874.2         NT           24804         31.14         2.6E-01         X51755.1         NT           26070         4.14         2.6E-01         X51755.1         NT           25365         32069         3.86         2.6E-01         AF316896.1         NT	10072	ı				P87366	SWISSPROT	GREEN-SENSITIVE OPSIN (GREEN CONE PHOTORECEPTOR PIGMENT) (KFH-G)
237E0         1.09         2.6E-01 Y10196.1         NT           23873         0.48         2.6E-01 Y15874.2         NT           24804         31.14         2.6E-01 X51755.1         NT           26070         4.14         2.6E-01 BE88349.1         EST_HUMAN           25365         32069         3.86         2.6E-01 AF316896.1         NT	10393	l		0.63		028295	SWISSPROT	VON WILLEBRAND FACTOR PRECURSOR (VWF)
23873         0.48         2.6E-01 X15874.2         NT           24804         31.14         2.6E-01 X51755.1         NT           26070         4.14         2.6E-01 BE883491.1         EST_HUMAN           25365         32069         3.86         2.6E-01 AF316896.1         NT	10727	1_		1.09		Y10196.1	卜	Homo sapiens PHEX gene
24804         31.14         2.6E-01 X51755.1         NT           26070         4.14         2.6E-01 BE883491.1         EST_HUMAN           25365         3.2069         3.86         2.6E-01 AF316896.1         NT	10840			0.48		Y15874.2	LN	Danio rerio mRNA for RPTP-alpha protein
26070         4.14         2.6E-01 BE883491.1         EST_HUMAN           25365         3.2069         3.86         2.6E-01 AF316896.1         NT	11815	l		31.14		X51755.1	TN	Human lambda-immunoglobulin constant region complex (germline)
25365 32069 3.86 2.6E-01 AF316896.1 NT	12468					BE883491.1	EST_HUMAN	601511052F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3912612 5
	12535					AF316896.1	LN	Homo sapiens Na/K-ATPase gamma subunit (FXYDZ) gene, complete cds, atternatively spiloed

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Table 4
Single Exon Probes Expressed in Placenta

onige Exon Trobes Expressed II tracolita	Top Hit Descriptor	Cavia cobaya mRNA for serbre/threoine kinase, complete cds	Thermotoga maritima section 25 of 136 of the complete genome	Homo sapiens inosital polyphosphate 1-phosphatase (INPP1) gene, complete cds	601126016F1 NIH_MGC_9 Homo saplens cDNA clone IMAGE:2990043 5'	HYPOTHETICAL PROTEIN MG039	Arabidopsis thaliana floral homeotic (AP3) gene, promoter region and partial cds	Homo sapiens ATP synthese, H+ transporting, mitochondrial F1 complex, delta subunit (ATP6D), nuclear neres encoding mitochondrial protein mRNA	Homo saplens ATP synthase, H+ transporting, mitochondrial F1 complex, delta subunit (ATP5D), nuclear	gene encoding mitochondrial protein, mRNA	Starfish (P.ochraceus) cytoplasmic actin gene, complete cds	Mus musculus ICR/Swiss glyceraldehyde 3-phosphate dehydrogenase (Gapd-S) gene, complete cds	Ureaplasma urealyticum section 57 of 59 of the complete genome	ye11g07.r1 Stratagene lung (#937210) Homo sapiens cDNA clone IMAGE:117468 5'	Homo saplens hyperpolarization activated cyclic nucleotide gated potassium channel 4 (HCN4) mRNA	Aquifex aeolicus section 7 of 109 of the complete genome	Mus musculus protein-L-Isoaspertate (D-aspartate) O-methyltransferase 1 (Pcmt1), mRNA	zs11a12.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:684862 5'	B.taurus mRNA for D-aspartate oxidase	EST385464 MAGE resequences, MAGM Homo sapiens cDNA	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 29	wg11c07.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2364780 3'	wg11c07.xt Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2364780 3'	RHIBPROTEIN	Mus musculus neuronal apoptosis inhibitory protein 6 (Naip6) gene, complete cds, and Naip3 gene, exons 2-9	MOI TANHIRITING HORMONE PRECLIRSOR (MIH.)	model in the interest of the interest of the interest of the interest of the interest of the interest of the interest of the interest of the interest of the interest of the interest of the interest of the interest of the interest of the interest of the interest of the interest of the interest of the interest of the interest of the interest of the interest of the interest of the interest of the interest of the interest of the interest of the interest of the interest of the interest of the interest of the interest of the interest of the interest of the interest of the interest of the interest of the interest of the interest of the interest of the interest of the interest of the interest of the interest of the interest of the interest of the interest of the interest of the interest of the interest of the interest of the interest of the interest of the interest of the interest of the interest of the interest of the interest of the interest of the interest of the interest of the interest of the interest of the interest of the interest of the interest of the interest of the interest of the interest of the interest of the interest of the interest of the interest of the interest of the interest of the interest of the interest of the interest of the interest of the interest of the interest of the interest of the interest of the interest of the interest of the interest of the interest of the interest of the interest of the interest of the interest of the interest of the interest of the interest of the interest of the interest of the interest of the interest of the interest of the interest of the interest of the interest of the interest of the interest of the interest of the interest of the interest of the interest of the interest of the interest of the interest of the interest of the interest of the interest of the interest of the interest of the interest of the interest of the interest of the interest of the interest of the interest of the interest of the interest of the interest of the interest of the interest of the i	INTSWITCH UNITED REPORTS ESSOCIATION (CONTINUED CONTINUED  Vibrio chalerae chramosome II, section 73 of 93 of the complete chromosome	Mus musculus annexin V gene, intron 4 segment containing 5' LTR and gag portion of MuERV-L (murine endogenous retrovirus) element	601437468F1 NIH_MGC_72 Hcmo sapiens cDNA clone IMAGE:3922600 5'	
EXUIT FIUDES	Top Hit Database Source	D. TN	NT TN	TN TN	EST_HUMAN 6		Г				NT	_≥	D TN	EST_HUMAN y		NT		T_HUMAN	NT B	EST_HUMAN E	NT		_	SWISSPROT R	2 0	TOGGSSI	2		N LN		EST_HUMAN 6
Billic	Top Hit Acession No.	2.6E-01 D88425.1	2.6E-01 AE001713.1	2.6E-01 AF141325.2	2.6E-01 BE272440.1		2.6E-01 U30729.1	TN 982004	007001	4502296 NT	2.5E-01 M26501.1		3.1	2.5E-01 T89837.1	4885406 NT	2.5E-01 AE000675.1	6679216 NT	7.1			2.5E-01 AL161517.2	2.5E-01 AI741483.1	2.5E-01 AI741483.1	Q03314	2 EE 04 A E 24 24 24 4		,		2.5E-01 AE004416.1		2.5E-01 BE896785.1
]	Most Similar (Top) Hit BLAST E Value	2.6E-01	2.6E-01	2.6E-01	2.6E-01	2.6E-01 P47285	2.6E-01	2 KE_01	2.2.	2.5E-01	2,5E-01	2.5E-01	2.5E-01	2.5E-01	2.5E-01	2.5E-01	2.5E-01	2.5E-01	2.5E-01	2.5E-01	2.5E-01	2.5E-01	2.5E-01	2.5E-01 Q03314	2 55 04	2.3C-01 01 2424	2.35.01	Z.0E-V.	2.5E-01	2.5E-01	2.5E-01
	Expression Signal	2.04	1.78	2.36	1.43	2.04	2.4	1 87		1.7	2.51	1.23	1.75	5.45	4.53	11.21	1.22	1.02	1	3.34	7.18	1.25	1.25	0.88	20	1	2 2	3.68	2.3	3.54	0.8
	ORF SEQ ID NO:		_					26503		26503		27093		27367			28814		28936	_	29815		30106	-	30055	١			31023		31060
	Exen SEQ ID NO:		25663	25692	15735	l	25748	13472	7	13472	13484	14032	14251	14310	14916	15608	15688	15690	15820	16666	16803	17108	17108	17578	47077	10004	1		18034		18084
	Probe SEQ ID NO:	12922	13007	13057	13098	13107	13150		23	252	265	982	1085	1145	1767	2479	2563	2565	2702	3499	3639	3950	3950	4438	1227	10/1	Ç.	8/84	49Q4	4926	4954

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Top Hit Descriptor	Della brassica cytochrome oddase subunit II (COII) gene, partial cds; mitochondrial gene for mitochondrial product	on70d04.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1562023 3'	802:32442F1 NIH_MGC_81 Hamo sapiens cDNA clone IMAGE:4271578 5'	Homo sapiens KIAA0851 gene (partial), XT3 gene and LZTFL1 gene	Homo sapiens KIAA0851 gene (partial), XT3 gene and LZTFL1 gene	Homo sapiens FLI-1 gene, partiel	Mesembryanthemum crystallinum putative potassium channel protein Mkt1p mRNA, complete cds	Zaccys dhumnades fructose-1,6-bisphosphatase mRNA, complete cds	wg76d05.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo saplens cDNA clone IMAGE:2371017 3' similar to TR:060267 060267 KIAA0512 PROTEIN. ;	Homo sapiens serine palmitoy transferase, subunit II gene, complete cds; and unknown genes	IMMUNOGLOBULIN A1 PROTEASE PRECURSOR (IGA1 PROTEASE)	Aquifax aedicus section 12 of 109 of the complete genome	D. discoideum (Ax3-K) panA gene	S.pambe swi6 gene	Bovine adenovirus 3 complete genome	Oryza longistaminata receptor kinase-like protein, family member D, and retrofit (gag/pd) genes, complete cds	H.sapiens AGT gene, Pstl fragment of intron 4	Escherichia coli K-12 MG1655 section 202 of 400 of the complete genome	Rettus norvegicus mRNA for aphaB crystallin-related protein, complete cds	xb18e02.x1 NCI_CGAP_Kid13 Homo sapiens cDNA clone IMAGE:2576618 3'	xb18a02.x1 NCI_CGAP_Kid13 Homo sapiens cDNA clone IMAGE:2576618 3'	Becillus firmus hypothetical 34.0 kDa protein, hypothetical 8.9 kDa protein, hypothetical 10.1 kDa protein, hypothetical 21.0 kDa protein, putative thlosulfate sulfurtransferase, hypothetical 16.1 kDa transcriptional	regulator and hypothetical 18.2 kDa>	Homo sapiens gene for TU12B1-TY, exon 13	Homo sapiens gene for TU12B1-TY, exon 13	wc33d05.x1 NCI_CGAP_Gas4 Homo capiens cDNA clone IMAGE:2457129 3'	wc33d05x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2467129 3'	Glycine max mRNA for mitotic cyclin b1-type, complete cds	Mus musculus Wrn protein (Wrn) gene, complete cds	Mus musculus Wm protein (Wm) gene, complete cds
Top Hit Database Source		П	EST_HUMAN 6	H	H LN		ΝŢ	z IN	M NAMUH_TSE		SWISSPROT		N D	S LN	NT	O IN	IN	NT TN			EST HUMAN x	<u> </u>	<u>د</u>		TN.	EST_HUMAN M	LHUMAN			NT NT
Top Hit Acession No.	.5E-01 AF325363.1	2.4E-01 AA938316.1	4E-01 BF576124.1	.4E-01 AJ289880.1	.4E-01 AJ289880.1	.4E-01 Y17293.1	.4E-01 AF267753.1	4E-01 AF251708.1	2.4E-01 AI742958.1	2.4E-01 AF111168.2	P45384	.4E-01 AE000680.1	.4E-01 Z36534.1	.4E-01 X71783.1	4E-01 AF030154.1	.4E-01 U72726.1	.4E-01 X74209.1	2.4E-01 AE000312.1		.4E-01 AW078596.1	4E-01 AW078596.1		2.4E-01 U89914.1	2.4E-01 AB032785.1	2.4E-01 AB032785.1	.4E-01 A1925707.1	.4E-01 AI925707.1	.4E-01 D50871.1	.4E-01 AF091216.1	2.4E-01 AF091216.1
Most Similar (Top) Hit BLAST E Value	2.5E-01	2.4E-01	2.4E-01		2.4E-01	2.4E-01	2.4E-01	2.4E-01	2.4E-01	2.4E-01	2.4E-01 P45384	2.4E-01	2.4E-01	2.4E-01	2.4E-01	2.4E-01	2.4E-01	2.4E-01	2.4E-01	2.4E-01	2.4E-01		2.4E-01	2.4E-01	2.4E-01	2.4E-01	2.4E-01	2.4E-01	2.4E-01	2.4E-01
Expression Signal	12	1.41	4.4	16.83	16.83	16:0	29.78	1.43	1.64	1.17	1.25	2.29	3.13	2.22	6.27	3.03	1.51	76.0	0.65	0.65	99.0		1.89	1.46	1.46	6.0	6.0			12.86
ORF SEQ ID NO:		26783	27113	27557	27558	27642		28193	28353	28467		28602	28845	29045	29069		29402	30016		31266	31267		31415	31416	31417	31818		31847		
Exon SEQ ID NO:	25674	13759	14047	14489	14489	14569	ı	15092	15231	Ι.	15370	l	ł		l		16391	1	l	18303	18303		18447	l	l	18773		18797	18964	18964
Probe SEQ ID NO:	13024	292	871	1332	1332	1415	1808	1949	2091	2208	2237	2336	2602	2820	2846	3202	3217	3856	4141	5181	5181		5334	5335	5335	5578	5578	5802	5772	5772

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Top Hit Descriptor	Gallus gallus brain-derived neurotrophic factor (BDNF) gene, 5' end	Branchiostoma floridae mRNA for calmodulin Z (caMZ gene)	7154404.x1 NC_CGAP_B16 Homo sapiens cDNA clone IMAGE:3338503 3' simiter to SW:SFR4_HUMAN Q08170 SPLICING FAÇTOR, ARGININE/SERINE-RICH 4 ;contains element TAR1 TAR1 repetitive element		Drosophila melanogaster p38a MAP kinase gene, complete cds	Homo sapiens HSPC142 protein (HSPC142), mRNA				Bos taurus guanyly cyclase-activating protein 2 (guca2) mRNA, complete cds	Mus musculus DXImx48e protein (DXImx48e) mRNA, complete cds	M.musculus pah gene and promotor	M.musculus pah gene and promotor	Streptococcus pneumoniae rr08 and hk08 genes; two component system 08	Streptococcus pneumoniae rr08 and hk08 genes; two component system 08	Tetrahymena thermophila macronuclear gene encoding ribosomal protein L3, exons 1-2		Campylobacter Jejuni NCTC11168 complete genome; segment 4/6	Campylobacter Jejuni NCTC11168 complete gename; segment 4/6		IN MEKZZDI IAKI repetuve etementi;	┱	T		Arabidopsis thaliana DNA chromosome 4, contig fragment No. 6	Mus musculus type 1 sigma receptor gene, complete cds	IN 601176415F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3531843 5	NN 601176416F1 NIH_MGC_17 Homo caplens cDNA clone IMAGE:3531843 5'	P.asiatica mosaic virus genortic RNA	Homo saplens fragile 16D oxido reductase (FOR) gene, exon 6	Arabidopsis thaliana ethylene-insensitive3-like1 (EIL1) mRNA, complete cds	Mus musculus mRNA for putative mc7 protein (mc7 gene)
Top Hit Database Source	ΙΝ	LΝ		EST_HUMAN	ΙN	F	EST_HUMA	EST_HUMAN	EST_HUMAN	IN	F	ΙN	N⊤	ΙN	TN	LN L	EST_HUMAN	١	NT		EST HUMAN	<u> </u>	Z	SWISSPROT	NT	NT	EST_HUMAN	EST_HUMAN	ΝΤ	ΙΝ	N	N
Top Hit Acession No.	2.4E-01 M83377.1	2.4E-01 AJ133836.2		2.4E-01 BF592336.1	2.4E-01 AF035546.1	7661801 NT	2.4E-01 AV733787.1	24E-01 AA398672.1	2.4E-01 Al698989.1	L43001.1	2.4E-01 AF229644.1	2.4E-01 X97252.1	2,4E-01 X97252.1	2.4E-01 AJ006397.1	2.4E-01 AJ006387.1	2.4E-01 AJ012585.1	2.4E-01 BF242794.1	2.4E-01 AL139077.2	2.4E-01 AL139077.2		-	Ì	2.4E-01 AF2Z0067.1	2.4E-01 Q03692	2.4E-01 AL161494.2	2.4E-01 AF030199.1	2.4E-01 BE296917.1	2.4E-01 BE296917.1	2.4E-01 Z21647.1	2.4E-01 AF217491.1	2.4E-01 AF004213.1	2,4E-01 AJ278191.1
Most Similar (Top) Hit BLAST E Value	2.4E-01	2.4E-01		2.4E-01	2.4E-01	2.4E-01	2.4E-01	2.4E-01	2.4E-01	2.4E-01	2.4E-01	2.4E-01	2.4E-01	2.4E-01	2.4E-01	2.4E-01	2.4E-01	2.4E-01	2.4E-01		2.4E-01	2.4E-01	2,4E-01	2.4E-01	2.4E-01	2.4E-01	2.4E-01	2.4E-01	2.4E-01	2.4E-01	2.4E-01	2.4E-01
Expression Signal	0.7	0.97		2.54	2.47	2.49	0.94	0.87	1.59	7.79	99.0	0.5	0.5	1.48	1.48	1.28	1.18	0.58	0.58		8.30	00:00	0.56	1.8	2.15	1.96	1.8	1.8	8.04	1.75	1.35	1.62
ORF SEQ ID NO:				32517	32620	32738		33051	33212	34046	34461			34939	35000	35162	35416	L		<u> </u>	ł	1	Ì	37297	37722	37788	38174			38827		
Exon SEQ ID NO:	1 1	25815		19200	19286	19390	19443	1	19824	20573	20954	21353	21353	ı	1	21625	21877	ı	22408	ł	- 1	1	- (		24085	L		24508	24537	l	П	25258
Probe SEQ ID NO:	5800	6010		6016	9106	6215	6269	6516	6665	7498	7902	8271	8271	8392	8392	8544	8798	9332	9332		9783	coss	C086	10654	11006	11074	11447	11447	11478	12159	12289	12360

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Single Exon Probes Expressed in Placenta

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oligie Extil Flores Expressed III Flacella	Top Hit Descriptor	Gallus gene coding for a-actin	RC3-CT0413-100800-023-b06 CT0413 Homo sapiens cDNA	Hömo sepiens mRNA for bradykinin B1 receptor (B1BKR gene)	Homo sapiens chromosome 21 segment HS21C081	aromatase [Poephila guttata=zebra finches, ovary, mRNA, 3188 nt]	Mycoplasma genitalium section 35 of 51 of the complete genome	Methanococcus jannaschii section 138 of 150 of the complete genome	601142073F1 NIH_MGC_14 Hamo sapiens cDNA clone IMAGE:3505818 5	Brassica napus sig gene for S-tocus glycoprotein, cultivar T2	Mus musculus cdh5 gene, exon 1, partial	Homo sapiens partial infron 3 of the wild type AF-4/FEL gene	601175562F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3531015 5'	Human crythropoletin gene, complete cds	Marinilabilia agarovorans gyrB gene for DNA gyrase subunit B, partial cds, strain:IFO 14957	nof 6d06.s1 NCI_CGAP_Phet Home saplens cDNA clone IMAGE:1100843 3' similar to contains Alu repositive alement THR repositive element:	who that at Scares pleasants Nb2HP Hamp sapiens cDNA clane IMAGE:130357.3	1997/10.11 Soares fetal liver spleen INFLS Home sapiens cDNA clone IMAGE:213283 5	GSTA5=glutathione S-transferase Yc2 subunit (5' region, intron 1) [rats, Morris hepatoma cell line, Genomic,	2212 nt, segment 1 of 3]	Hσπο sapiens KIAA0450 gene product (KIAA0450), mRNA	y17f01.r1 Scares placenta Nb2HP Homo sapiens cDNA clone IMAGE: (49017 5'	Mus musculus renin (Ren-1c) gene, promoter region	Synechocystis sp. PCC6803 complete genome, 1/27, 1-133859	Horno sapiens mitogen-activated protein kinasa p38dalta (PRKM13) mRNA, complete cds	Homo sapiens nuclear transport factor 2 (placental protein 15) (PP15) mRNA	Mus musculus tulip 1 mRNA, complete cds	Human gamma-B-crystallin (gamma 1-2) and gamma-C-crystallin (gamma 2-1) genes, complete cds	602132210F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4271547 5	Homo sapiens mRNA for KIAA1512 protein, partial cds	7K30b06.X1 NCI_CGAP_OV18 Homo sapiens cDNA clone IMAGE:3476699 3' similar to SW:GAG_SMSAV PRO3330, CAG_POY YPROTEIN P12: CORE_PRO15: NNER COAT PROTEIN P12: CORE_PRO3330, CAG_POY YPROTEIN P12: CORE_PRO15: NNER COAT PROTEIN P12: CORE_PRO3330, CAG_POY YPROTEIN P13: NNER COAT PROTEIN P12: CORE_PRO3330, CAG_POY YPROTEIN P13: CORE_PRO3330, CAG_POY YPROTEIN P13: CORE_PRO3330, CAG_POY YPROTEIN P13: CAG_POY YPROTEIN P13: CAG_POY YPROTEIN P13: CAG_POY YPROTEIN P13: CAG_POY YPROTEIN P13: CAG_POY YPROTEIN P13: CAG_POY YPROTEIN P13: CAG_POY YPROTEIN P13: CAG_POY YPROTEIN P13: CAG_POY YPROTEIN P13: CAG_POY YPROTEIN P13: CAG_POY YPROTEIN P13: CAG_POY YPROTEIN P13: CAG_POY YPROTEIN P13: CAG_POY YPROTEIN P13: CAG_POY YPROTEIN P13: CAG_POY YPROTEIN P13: CAG_POY YPROTEIN P13: CAG_POY YPROTEIN P13: CAG_POY YPROTEIN P13: CAG_POY YPROTEIN P13: CAG_POY YPROTEIN P13: CAG_POY YPROTEIN P13: CAG_POY YPROTEIN P13: CAG_POY YPROTEIN P13: CAG_POY YPROTEIN P13: CAG_POY YPROTEIN P13: CAG_POY YPROTEIN P13: CAG_POY YPROTEIN P13: CAG_POY YPROTEIN P13: CAG_POY YPROTEIN P13: CAG_POY YPROTEIN P13: CAG_POY YPROTEIN P13: CAG_POY YPROTEIN P13: CAG_POY YPROTEIN P13: CAG_POY YPROTEIN P13: CAG_POY YPROTEIN P13: CAG_POY YPROTEIN P13: CAG_POY YPROTEIN P13: CAG_POY YPROTEIN P13: CAG_POY YPROTEIN P13: CAG_POY YPROTEIN P13: CAG_POY YPROTEIN P13: CAG_POY YPROTEIN P13: CAG_POY YPROTEIN P13: CAG_POY YPROTEIN P13: CAG_POY YPROTEIN P13: CAG_POY YPROTEIN P13: CAG_POY YPROTEIN P13: CAG_POY YPROTEIN P13: CAG_POY YPROTEIN P13: CAG_POY YPROTEIN P13: CAG_POY YPROTEIN P13: CAG_POY YPROTEIN P13: CAG_POY YPROTEIN P13: CAG_POY YPROTEIN P13: CAG_POY YPROTEIN P13: CAG_POY YPROTEIN P13: CAG_POY YPROTEIN P13: CAG_POY YPROTEIN P13: CAG_POY YPROTEIN P13: CAG_POY YPROTEIN P13: CAG_POY YPROTEIN P13: CAG_POY YPROTEIN P13: CAG_POY YPROTEIN P13: CAG_POY YPROTEIN P13: CAG_POY YPROTEIN P13: CAG_POY YPROTEIN P13: CAG_POY YPROTEIN P13: CAG_POY YPROTEIN P13: CAG_POY YPROTEIN P13: CAG_POY YPROTEIN P13: CAG_POY YPROTEIN P13: CAG_POY YPROTEIN P13: CAG_POY YPROTEIN P13: CAG_POY YPROTEIN P13: CA	SHELL PROTEIN P30, NUCLEOPROTEIN P10];
EVOIL LIONS	Top Hit Database Source	NT	EST_HUMAN	NT	L	NT	NT	NT	EST HUMAN	TN	TN		EST_HUMAN	IN	IN	EST HIMAN	EST HIMAN	EST HUMAN		LN	NT	EST_HUMAN	TN	TN	⊥N	FX	LN	LN	EST HUMAN	Į.		EST_HUMAN
Juli G	Top Hit Acession No.	2.4E-01 V01507.1	2.4E-01 BF229975.1	2.4E-01 AJ238044.1	2.4E-01 AL163281.2	2.3E-01 S75898.1	2.3E-01 U39713.1	2.3E-01 U67596.1	2.3E-01 BE311893.1	2.3E-01 AJ245480.1	2.3E-01 Y10887.2	2,3E-01 AJ235353.1	2.3E-01 BE297718.1	2.3E-01 M11319.1	2.3E-01 AB015033.1	23E.01 AA601370 1	2.3E-01 AA001010.	2.3E-01 H69836.1		2.3E-01 S82821.1	7662133 NT	2.3E-01 R82252.1	2.3E-01 L78789.1	2.3E-01 D90899.1	2.3E-01 AF092535.1	5031984 NT	2.3E-01 AB032400.1	2.3E-01 M19364.1	2.3E-01 BF574804.1	2.3E-01 AB040945.1		2.3E-01 BF058381.1
	Most Similar (Top) Hit BLAST E Value	2.4E-01	2.4E-01	2.4E-01	2.4E-01	2.3E-01	2.3E-01	2.3E-01	2.3E-01	2.3E-01	2.3E-01	2.3E-01	2.3E-01	2.3E-01	2.3E-01	10 G				2.3E-01	2.3E-01	2.3E-01	2.3E-01	2.3E-01	2.3E-01	2.3E-01	2.3E-01	2.3E-01	2.3E-01	2.3E-01	 - II	2.3E-01
	Expression Signal	1.95	1.37	1.4	4.16	1.39	5.53	29.31	3.57	1.11	1.72	1.78	1.85	86.0	1.5	90.1	200.7	1.32		0.98	5,15	98.0	1.91	1.12	2.76	5.65	0.87	1.03	0.63	2.47		2.03
	ORF SEQ ID NO:					26633					27898		28764	28945	27646	70000		29644		30100		30588			30728	30800	L		31345			31776
	Exon SEQ ID NO:	25914	26151	25701	25718	13597	13840	13869	14130	14786	14813	15242	15643	15835	14573	16704	46220	16623		17103	17202	17610	17659	17710	17748	17811	18281	18345	18379	18620		18742
	Probe SEQ ID NO:	12588	12839	13072	13102	400	654	684	857	1634	1661	2103	2517	2717	2885	ŝ	2452	3456		3944	4046	4470	4520	4573	4611	4676	6169	5223	9280	5419		5545

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Top Hit Descriptor	C,familiaris rom1 gene	Vittaforma corneum small subunit ribosomal RNA gene	23S rRNA [Leuconostoc camosum, Genomic, 2866 nt]	as27e12.x1 Barstead sorta HPLRB6 Homo sapiens cDNA clone IMAGE:2318446 3' similar to gb:X13238 CYTOCHROME C OXIDASE POLYPEPTIDE VIC PRECURSOR (HUMAN);		Oryctolagus auniculus cytochrome oxidase subunit VIa (coxVIa2) mRNA, complete ods; nuclear gene for mitochondrial product	as42f12.x1 Barstead aoria HPLRB6 Homo sepiens cDNA clone IMAGE:2319887 3' similar to contains Alu repettive element.	Т	Secale cereate amega secalin gene, complete cds	Glycine max resistance protein LM17 precursor RNA, partial cds	N AV719681 GLC Homo sapiens cDNA done GLCDGB08 5'	Γ	Mus museulus myosin XV (Myo15), mRNA		N za12e08.r1 Sogres fetal liver spleen 1NFLS Home sapiens cDNA done IMAGE:292358 5	Homo sapiens protocedherin alpha cluster (LOC63960), mRNA	Homo sapiens protocadherin alpha cluster (LOC63960), mRNA	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 58	Oxytricha nova macronuclear telomere-binding protein alpha subunit (tel-alpha alanine version) gene,	∞mplete cds	Mus musculus prosaposin (psap\SGP-1) gene, complete cds			Т	N EST84061 Rhabdomyosarcoma Homo sapiens cDNA 5' end similar to DnaJ homolog (GB:X63368)	Mus musculus phosphatidylinositol 3-kinase catalytic subunit delta (Pik3od), mRNA	N 601120110F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:2966739 5'	IN EST376533 MAGE resequences, MAGH Homo sapiens cDNA	Haemophilus influenzae genes for HinclI restriction-modification system (HinclI methyltransferase (EC 2.1.1.72) and HinclI endonuclease (EC 3.1.21.4))
Top Hit Database Source	Σ	<u>E</u>	<u>k</u>	EST HUMAN	EST HUMAN	ž	EST HUMAN	Ł	뉟	Ν	EST_HUMAN	EST_HUMAN	N	EST_HUMAN	EST_HUMAN	노	۲	۲		Ł	ΤN	EST_HUMAN	EST_HU	EST_HUMAN	EST_HUMAN	F	EST_HUMAN	EST_HUMAN	Ϋ́
Top Hit Acession No.	2.3E-01 XB6587.1	2.3E-01 L39112.1	2.3E-01 S60371.1	2.3E-01 Al708840.1	23E-01 AI708840.1	2.3E-01 AF198089.1	23E-01 AI718148.1	8923323 NT	2.3E-01 AF000227.1	2.3E-01 AF175389.1	2.3E-01 AV719681.1	2.3E-01 AV719681.1	6754779 NT	2.3E-01 BE888071.1	2.3E-01 N80983.1	11416821 NT	11416821 NT	2.3E-01 AL161558.2		2.3E-01 M68931.1	2.3E-01 U57999.1	2.3E-01 AW090541.1	2.3E-01 AW964460.1	2.3E-01 AA372164.1	2.3E-01 AA372164.1	6679318 NT	2.3E-01 BE277860.1	2.3E-01 AW964460.1	2.3E-01 X52124.1
Most Similar (Top) Hit BLAST E Value	2.3E-01	2.3E-01	2.3E-01	2.3E-01	23E-01	2.3E-01	2.3E-01	2.3E-01	2.3E-01	2.3E-01	2.3E-01	2.3E-01	2.3E-01	2.3E-01	2.3E-01	2.3E-01	2.3E-01	2.3E-01		2.3E-01	2.3E-01	2.3E-01	2.3E-01	2.3E-01	2.3E-01	2.3E-01	2.3E-01	2.3E-01	2.3E-01
Expression Signal	5.25	66.0	1.32	1.98	1.98	0.66	4 63	0.86	0.76	2.54	5.37	5.37	4.26	1.56	2.8	0.71	0.71	0.52		1.73	0.62	0.58	0.52	0.64	0.64	0.5			1.57
ORF SEQ ID NO:	32122		32367	32560	32570	33348	33573	33796	33989	34123	34125	34126		34338		34530				34788	35300	35594	35715	35970	35971	36398		36616	
Exen SEQ ID NO:	18841	18958	19060	19244	19244	19949	20153	20343	20517	20645	20648	20648	ı	1		21018	21018	21118		21265	21770	22051	22168	22417	22417	22820	22970	23024	i i
Probe SEQ ID NO:	5647	5766	5870	6062	6062	6794	7017	7260	7440	7573	7576	7576	7784	7789	7931	7968	7968	8036		8183	8690	8972	6806	9341	9341	9780	9930	9985	10037

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Top Hit Descriptor	Homo sapiens chromosome 21 segment HS21C085	Mus musculus ATP-binding cassette protein (Abcb8) mRNA, partial cds	Mus musculus breast/ovarian cancer susceptibility protein (BRCA1) mRNA, complete cds	Drosophila melanogaster UNC-119 (unc-119) gane, complete cds	Mus musculus mixed lineage kinase 3 (Mik3) and two pore domain K+ channel subunit (Kcnk6) genes,	complete cas	Mus musculus MAP kinase kinase kinase 1 (Mekk1) mRNA, complete cds	Mus musculus MAP kinase kinase kinase 1 (Mekk1) mRNA, complete cds	Human scRNA (BC200 beta) pseudogene	Human scRNA (BC200 beta) pseudogene	Human beta-cytoplasmic actin (ACTBP9) pseudogene	2q87c05.r1 Stratagene hNT neuron (#937233) Homo sapiens cDNA clone IMAGE:648968 5'	Mus musculus vinculin gene, exon 3	MRo-HT0067-201099-002-c10 HT0067 Homo sapiens cDNA	Homo sapiens diaphanous (Drosophila, homolog) 2 (DIAPH2), transcript variant 156, mRNA	Synechocystis sp. PCC6803 camplete genome, 19/27, 2392729-2538999	Gallus gallus T-box containing protein (Ch-TbxT) mRNA, complete cds	Gallus gallus T-box containing protein (Ch-TbxT) mRNA, complete cds	Homo sapiens gene for fukutin, complete cds	AV756238 BM Hamo sapiens cDNA clane BMFAHC06 5'	Streptocococus pyogenes phosphotidyglycerophosphate synthase (pgsA) and ABC transporter ATP-binding protein (stpA) genes, complete cds; and unknown genes	Streptococcus pyogenes phosphotidyglycerophosphate synthase (pgsA) and ABC transporter ATP-binding protein (strA) genes complete cds: and unknown genes	Human glycophorin B gene, exon 4	Human glycophorin B gene, exon 4	Mycoplasma pneumoniae M129 section 45 of 63 of the complete genome	Homo saplens homeobox B7 (HOXB7) gene, partial cds; and homeobox B6 (HOXB6), homeobox B5 (HOXB5), homeobox B4 (HOXB4), and homeobox B3 (HOXB3) genes, complete cds	Bacillus halodurans DNA, complete and partial cds, strain:C-125	Mus musculus nm23-M1 gene, promoter region	E.coli sepA and sepB genes	Pan troglodytes MeCP2 gene 3 UTR	Mouse HD protein mRNA, complete cds
Top Hit Database Source	Ĭ	M LN	N P	Ω⊥							H LN	EST_HUMAN 20		EST_HUMAN M		NT			H	EST_HUMAN A	S TN	io i				ΙE					M
Top Hit Acesslon No.	2.2E-01 AL163285.2	2.2E-01 AF213391.1	2.2E-01 U68174.1	2.2E-01 AF119102.1				2.2E-01 AF117340.1	2.2E-01 U01307.1	2.2E-01 U01307.1	2.2E-01 D50604.1	2.2E-01 AA211216.1	2.2E-01 L13299.1	BE141035.1	5803002 NT		2.2E-01 U67087.1		2.2E-01 AB038490.1	2.2E-01 AV756238.1	2.2E-01 AF082738.1				52	2.2E-01 AF287967.1	2.2E-01 AB024553.1	2.2E-01 AF155143.1	2.2E-01 Z49933.1	8.1	2.2E-01 L23312.1
Most Similar (Top) Hit BLAST E Value	2.2E-01	2.2E-01	2.2E-01	2.2E-01		2.2E-01	2.2E-01	2.2E-01	2.2E-01	2.2E-01	2.2E-01	2.2E-01	2.2E-01	2.2E-01	2.2E-01	2.2E-01	2.2E-01	2.2E-01	2.2E-01	2.2E-01	2.2E-01	10.20.0	2.2E-01	2.2E-01	2.2E-01	2.2E-01	2.2E-01	2.2E-01	2.2E-01	2.2E-01	2.2E-01
Expression Signal	0.62	0.69	0.6	1.07		6.62	2.74	2.74	1.07	1.07	1.08	2.2	1.57	<u>8.</u> 1	1.89	3.75	0.78	0.78	77.0	10.63	1.61	20	236	2.36	0.62	88	0.71	2.45	2.68	0.61	0.52
ORF SEQ ID NO:		30349					30502	20503				31058			32360		32640				33815		33991					L	34881		35705
Exon SEQ ID NO:	17008	17360		17471		- [	17522	17522	17615	L	18077	18082	18278	L	19053	19064	19301	19301	19998	20299	20362		L	L	L			ı	21362	1	
Probe SEQ ID NO:	3848	4211	4242	4328		4335	4379	4379	4475	4475	4947	4952	5156	5226	5863	5874	6122	6122	6845	7166	7279	20.2	7447	7442	7655	7878	7905	8210	8280	8748	9083

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	Top Hit Descriptor	Mouse HD protein mRNA, complete cds	Thermotoga maritima section 25 of 136 of the complete genome	Mus musculus ICR/Swiss glyceraldehyde 3-phosphate dehydrogenase (Gapd-S) gene, complete odc	PM3-CT0263-241289-009-b07 CT0263 Homo sapiens cDNA	Mus musculus deformed epidermal autoregulatory factor 1 (Drosophila) (Deaf1), mRNA	MR1-TN0045-110900-006-c02 TN0045 Homo saplens cDNA	za04f08.rf Scares melanocyte 2NbHM Homo sapiens cDNA clone IMAGE:291591 51	LARGE PROLINE-RICH PROTEIN BAT2 (HLA-B-ASSOCIATED TRANSCRIPT 2)	Xenopus laevis mRNA for kinesin-like protein 3 (xklp3)	Mus musculus asteoblast specific factor 2 (OSF-2), mRNA	Brachydanio rerio ependymin beta and gamma chains (Epd) gene, complete cds	CYCLIC NUCLEOTIDE GATED CHANNEL, ROD PHOTORECEPTOR, ALPHA SUBUNIT (CNG CHANNEL 3) (CNG-3) (CNG-3)	Funaria hygrometrica chloroplast-localized small heat shock protein (CPsHSP21) mRNA, complete cds;	nuclear gene for chloroplast product	601669724F1 NIH_MGC_19 Homo sapiens dDNA clone IMAGE:4100189 5	Human herpesvirus 5, complete genome	yb63d08.r1 Stratagene overy (#937217) Homo saptens cDNA clone IMAGE:75855 5	yb63d08.r1 Strategene ovary (#937217) Homo sapiens cDNA clone IMAGE:75855 5'	Pseudomonas aeruginosa quinoprotein ethand dehydrogenase (exaA) gene, partial cds, cytochrome c550	precursor (exaB), NAD+ dependent acetalderyde denydrogenase (exaC), and pyrroroguindine quindre synthesis A (nonA) news, complete cds: and pyrrologijit)	Green the DHR (Phr) can partial cds	Halisobarter poloni strain 199 section 123 of the complete genome	Helicohorter nderl etrain 100 section 123 of 132 of the complete cenome	Interception professional after addless (MOS1) report alternative express (1 and 5.5	100110 Septiers in Paul Main Louise symmetric and the communication of the communication of the communication of the communication of the communication of the communication of the communication of the communication of the communication of the communication of the communication of the communication of the communication of the communication of the communication of the communication of the communication of the communication of the communication of the communication of the communication of the communication of the communication of the communication of the communication of the communication of the communication of the communication of the communication of the communication of the communication of the communication of the communication of the communication of the communication of the communication of the communication of the communication of the communication of the communication of the communication of the communication of the communication of the communication of the communication of the communication of the communication of the communication of the communication of the communication of the communication of the communication of the communication of the communication of the communication of the communication of the communication of the communication of the communication of the communication of the communication of the communication of the communication of the communication of the communication of the communication of the communication of the communication of the communication of the communication of the communication of the communication of the communication of the communication of the communication of the communication of the communication of the communication of the communication of the communication of the communication of the communication of the communication of the communication of the communication of the communication of the communication of the communication of the communication of the communication of the communication of the communication of the communication of the communication of the communication of t	Homo sapiens KNA bridging protein MCC to gene, complete cus, alternatively spliced	Drosophila 68C glue gene cluster	Homo sapiens H-2K binding factor-2 (LOC51580), mRNA	601446957F1 NIH_MGC_65 Homo sepiens oDNA clone IMAGE:3850670 5	Homo sapiens chromosome Xq28 melanoma antigen family A2a (MAGEA2A), melanoma antigen family A12 (MAGEA12), melanoma antigen family A2b (MAGEA2B), melanoma antigen family A3 (MAGEA3), caltractin (MAGEA1T), MADYDHA debudromassedika norden (MSDH), and IT)	
	Top Hit Database Source		NT	LN	EST_HUMAN			i	SWISSPROT	LN		LNT	SWISSPROT			EST_HUMAN		EST_HUMAN	EST_HUMAN		H			L L	Z	Z	-2	LN	LΝ	EST_HUMAN	·	Z
, [	Top Hit Acession No.	2.2E-01 L23312.1	2.2E-01 AE001713.1	2.2E-01 U09964.1	2.2E-01 AW855039.1	8393247 NT	2.2E-01 BF376354.1	2.2E-01 W02988.1	P48634	2.2E-01 AJ009839.1	7657428 NT	2.2E-01 M89643.1	090380		2.2E-01 AF197941.1	2.2E-01 BF206507.1	9625671 NT	2.2E-01 T59472.1	2.2E-01 T59472.1		1 10 00 TO TO TO TO TO TO TO TO TO TO TO TO TO	AF024004.1	2.2E-01 AF07 1001.1	2.ZE-01 AEVO130Z.1	AE001352.1	2.2E-01 AF049720.1	2.2E-01 AF257772.1	2.2E-01 X01918.1	7706215 NT	2.2E-01 BE870959.1	6	2.2E-01 U82671.2
	Most Similar (Top) Hit BLAST E Value	2.2E-01	2.2E-01	2.2E-01	2.2E-01	2.2E-01	2.2E-01	2.2E-01	2.2E-01 P48634	2.2E-01	2.2E-01	2.2E-01	2.2E-01 Q90980		2.2E-01	2.2E-01	2.2E-01	2.2E-01	2.2E-01		L	2.25-01	2.25-01	2.2E-01	2.2E-U1	2.2E-01	2.2E-01	2.2E-01	2.2E-01	2.2E-01	i i	2.2E-01
	Expression Signal	0.52	4.58	0.48	2.88	1.98	1.13	1.42	15.08	97.0	1.05	4.29	0.65		3.84	1.53	1.11	99:0	9.0		Č	0.0	0.78	0.34	VC.0	0.48	1.65	60.9	3.7	1.33	,	1,96
	ORF SEQ ID NO:	35706		35740		35942				36187	36271				36654	36792						3/220			3/345				L			
	Exon SEQ ID NO:	22162		22196	L		İ	ı	ı	ı	22705	ı	1			23196	1		ı	1		1	-1				24450	L	L	1_	i i	26156
	Probe SEQ ID NO:	9083	606	9117	9224	8315	9399	9489	9507	8552	9563	9576	9820		10020	10159	10380	10540	10540		-	09001	8000	20,01	10/01	10853	11389	11707	11748	12207		12319

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Top Hit Descriptor	Vitis vinifera cultivar Pinot Noir plasma membrane aquaporin (PIP1a) mRNA, complete cds	RC1-CT0249-141199-021-g04 CT0249 Homo sapiens cDNA	hi17b02.x1 NCI_CGAP_GU1 Homo sapiens aDNA done IMAGE:2972523 3'	AV694801 GKC Homo saplens cDNA clone GKCAHB02 5'	nm31e11.s1 NCL_CGAP_Lip2 Homo saplens cDNA clone IMAGE:1061804	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 16	Chlamydia muridarum, section 45 of 85 of the complete genome	Mus musculus interferon (alpha and beta) receptor 2 (Ifnar2), mRNA	Mus musculus interferon (alpha and beta) receptor 2 (Ifnar2), mRNA	Mus musculus mas proto-oncogene and Igf2r gene for insulin-like growth factor type 2 and L41ps and Au76 pseudogenes	ok73e02.s1 NCI_CGAP_GC4 Homo sapiens cDNA clone IMAGE:1519610 3' sImilar to dic/K02765 COMPLEMENT C3 PRECURSOR (HUMAN);	602083129F1 NIH MGC 81 Homo sapiens cDNA done IMAGE:4247503 5'	Homo sapiens potassium voltage-gated channel, subfamily H (eag-related), member 4 (KCNIH4), mRNA	nq90b10.s1 NCI_CGAP_Co9 Homo sapiens cDNA clone IMAGE:1159579 3'	Beta vulgaris mitochondrion, complete genome	Thermotoga maritima section 105 of 136 of the complete genome	IMMEDIATE-EARLY PROTEIN IE180	IMMEDIATE-EARLY PROTEIN IE180	Homo sapiens mRNA for KIAA1215 protein, partial cds	Homo sapiens pshsp47 gene, complete cds	P.faiciparum mRNA for small GTPase rab11	Lempetra japonica mRNA for alpha-2-macroglobulin, complete cds	602/152001F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4283001 5'	Doto fragilis mitochondrial 16S rRNA gene, partial	Human olfactory receptor (OR17-2) gene, partial cds	VOLTAGE-GATED POTASSIUM CHANNEL PROTEIN KV3.3 (KSHIIID)	VOLTAGE-GATED POTASSIUM CHANNEL PROTEIN KV3.3 (KSHIIID)	Archaeoglobus fulgidus section 135 of 172 of the complete genome	Canis familiaris keratin (KRT9) gene, complete cds	Glycine max malate dehydrogenase (Mdh-2) gene, nuclear gene encoding mitochondrial protein, partial cds
Top Hit Database Source	LN⊤	EST_HUMAN	EST HUMAN	EST_HUMAN	EST_HUMAN	NT	TN	NT	NT	L	EST HUMAN	EST HUMAN	LZ	EST_HUMAN	F	۲N	SWISSPROT	SWISSPROT	Ę	NT	님	NT	EST_HUMAN	ΤN	TN	SWISSPROT	SWISSPROT	ΙNΤ	NT	ΤN
Top Hit Acession No.	2.2E-01 AF188843.1	2.2E-01 AW361098.1	2.2E-01 AW661922.1	2.2E-01 AV694801.1	2.1E-01 AA569289.1	2.1E-01 AL161504.2	2.1E-01 AE002314.2	6754299 NT	6754299 NT	2.1E-01 AJ249895.1	2.1E-01 AA906824.1	2.1E-01 BF695073.1	6912445 NT	2.1E-01 AA639482.1	TN 19838361	2.1E-01 AE001793.1				2.1E-01 AB010273.1	2.1E-01 X93161.1	2.1E-01 D13567.1	2.1E-01 BF672695.1	2.1E-01 AJ223392.1	2.1E-01 U04642.1	Q01956	Q01956	2.1E-01 AE000972.1	2.1E-01 AF000949.1	2.1E-01 AF068687.1
Most Similar (Top) Hit BLAST E Value	2.2E-01	2.2E-01	2.2€-01 /	2.2E-01	2.1E-01	2.1E-01	2.1E-01	2.1E-01	2.1E-01	2.1E-01	2.1E-01	2.1E-01	2.1E-01	2.1E-01	2.1E-01	2.1E-01	2.1E-01 P11675	2.1E-01 P11675	2.1E-01	2.1E-01	2.1E-01	2.1E-01	2.1E-01	2.1E-01	2.1E-01	2.1E-01 Q01956	2.1E-01 Q01956	2.1E-01	2.1E-01	2.1E-01
Expression Signal	3.24	1.86	1.47	3.08	1.88	0.72	2.43	1.45	1,45	429	2.15	3.55	2.52	6.1	5.61	78.0	1.57	1.57	1.63	1.82	0.93	0.7	6.31	1.05	1.8	77.0	77.0	1.88	1.54	1.38
ORF SEQ ID NO:		31531				27228			27447			1		L			30310			30819	30871	31228	31592		33508	34111	34112		34441	34488
Exon SEQ ID NO:	25286	18492		26148	14165	14167	14312	14385	14385	1	<u> </u>	1	16167	16698	L	17279	L		17635	<u>.</u>	17892	18261	18618	_			<u> </u>	20647	20935	20980
Probe SEQ ID NO:	12407	12518	12519	13115	863 863	966	1148	1225	1225	1540	1963	2224	2991	3533	3908	4125	4165	4165	4496	4699	4757	5138	5416	7027	7038	7564	7564	7575	7883	7930

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Most Similar (Top) Hit Top Hit Acession Database BLAST E No. Source	2.0E-01 AF260700.1 NT	0.96 2.0E-01 U22346.1 NT Human bradykinin B1 receptor (bradyb1) gene, complete cds	2.0E-01 AF111170.3 NT		2.0E-01 8922238 NT	2.0E-01 X82877.1 NT	2.0E-01 AF074990.1 NT	2.0E-01 P46607 SWISSPROT	A HOGOGOTANA NA TAO	Z.UE-UI AW Z.30003.1 E.S.I. LIGWININ	2.0E-01 P34641 SWISSPROI	20E-01 6680797 NT	2.0E-01 BE826165.1 EST_HUMAN	8922080 NT	2.0E-01 P34641 SWISSPROT		2.0E-01 11432540 NT	2.0E-01 X91856.1 NT	2.0E-01 U15300.1 NT	2.0E-01 M75967.1 NT	2.0E-01 X61033.1 NT	3.74 2.0E-01 AW360865.1   EST_HUMAN   PM1-CT0247-141089-001-g06 CT024 Homo septens culviv		0.88 2.0E-01 P64422   SWISSPROT   GAMMA-GLUTAMYLTRANSPEPTIDASE PRECURSOR	2.0E-01 AF028026.1 NT	INT	2.0E-01 BE562247.1 EST_HUMAN	2.0E-01 U82511.1 NT	0.62 2.0E-01 U71122.1 INT Arabidopsis pyruvate decarboxylase-2 (Pdc2) gene, complete ods		2.0E-01 P11420 SWISSPROT	2.0E-01 P11420 SWISSPROT	2.0E-01 AF146692.1
Similar p) Hit \ST E alue	2.0E-01 AF	20E-01 U2	2.0E-01 AF	2.0E-01 UG	2.0E-01	2.0E-01 X8	2.0E-01 AF			Z.UC-01 AY			2.0E-01 BE	2.0E-01							١.												
Expression Signal				3.87	1.46	1.9	0.79			LR:O	0.86	0.6	8.71																				
ORF SEQ ID NO:	1	27973			28185			29758	1		28963			31243	29963	31797	32355		32709		33098	33206	ļ	L	L	35003	L		36215		36579		
Exon SEQ ID NO:	14740	14882	14904	14945	15084	15552	16132	1	1	-	16959	16963	17823	18274	16959	18758		19149	19361		L	19818	<u></u>		L	<u> </u>	1	22616	Ι.	L		22986	1 1
					1941		2855	3576		3658	3798	3802	4688		5243	5561	1=	-	6185	8303	16	6659	Tio	7603	8139	8395	8021	9551	10	9756	9947	9947	10095

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	Top Hit Descriptor	Arabidopsis thallana root gravitropism control protein (PIN2) gene, complete cds	Arabidopsis thallana root gravitropism control protein (PIN2) gene, complete cds	Homo sapiens cAMP specific phosphodiesterase (PDE4C) gene, exons 2 through 12	Homo saplens cAMP specific phosphodiesterase (PDE4C) gene, exons 2 through 12	D. melanogaster DNA mobile element (hoppel)	R.norvegicus mRNA for NTR2 receptor	Salvellnus pluvius mRNA for transferrin, complete cds	Salvetinus pluvius mRNA for transferrin, complete cds	Chlorella vulgaris chioroplast, complete genome	Chlorella vulgaris chloropiast, complete genome	Pimephales prometas liver glucose-6-phosphate-1-dehydrogenase mRNA, partial cds	Homo sapiens ninein-Lm isoform (ninein) mRNA, complete cds	EST387405 MAGE resequences, MAGN Homo capians cDNA	oy80a10.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1643610 3'	Homo saplens Ku70-binding protein (KUB3) mRNA, partial cds	Rattus norvegicus Aryl hydrocarbon receptor nuclear transfecator 1 (Arnt1), mRNA	Mus musculus pale ear (ep) gene, wild type allele, 3' region, partial cds	Homo sapiens lambda/iota protein kinase C-interacting protetn mRNA, complete cds	Homo sapiens lambda/fota protein khase C-interacting protein mRNA, complete cds	RC3-BT0502-251199-011-d01 BT0502 Homo sapiens cDNA	RC3-BT0502-251199-011-d01 BT0502 Homo sapiens cDNA	Mus musculus interleukin 2 receptor, gamma chain (II2rg), mRNA	EST67784 Fetal lung II Homo sapiens cDNA 5' end	Sorghum bicolor 22 kDa kafirin chuster	Plasmodium wwax reticulocyte binding protein-2 (rbp-2) gene, complete cds	Homo saplens hypothetical protein FLJ10581 (FLJ10581), mRNA	Sigmodon hispidus p53 gene, partial cds	Gallus gallus ovalbumin (Y) gene, complete cds	Mouse gene for immunoglabulin diversity region D1	yf42f10.r1 Scares fetal liver spleen 1NFLS Homo saplens cDNA clone IMAGE:129547 5	Rattus norvegicus arylacetamide deacetylase gene, complete cds	Schizosaccharomyces pombe DNA for cytoplasmic dynein heavy chain, complete cds	CM3-CT0315-271199-045-b11 CT0315 Hamo sapiens cDNA	Deinococcus radiodurans R1 section 49 of 229 of the complete chromosome 1
	Top Hit Database Source	NT	LN.	FZ	L	NT	ΝT	NT	NT	NT	ΙN	IN	F	EST_HUMAN	EST_HUMAN	LN	۲	LN	LN	HN	EST_HUMAN	EST_HUMAN	TN	EST_HUMAN	. TN	NT	NT	LN	Nī	Ħ	EST_HUMAN	ΙN	NT	EST HUMAN	¥
16	Top Hit Acession No.	2.0E-01 AF086907.1	2.0E-01 AF086907.1		2.0E-01 AF157814.1					7524759 NT	7524759 NT	2.0E-01 AF205637.2	2.0E-01 AF302773.1				7549743 NT	1,9E-01 AF004353.1				1.9E-01 BE070801.1	7305180 NT	1.9E-01 AA358B13.1	1.9E-01 AF061282.1	1.9E-01 AF184623.1	8922533 NT		J00922.1		1.9E-01 R16467.1	1.9E-01 AF264017.1	1.9E-01 AB006784.1	1.9E-01 AW754106.1	1 9F-01 AF001912.1
	Most Similar (Top) Hit BLAST E Value	2.0E-01	2.0E-01	2.0E-01	2.0E-01	2.0E-01 X78388.1	2.0E-01 X97121.1	2.0E-01 D89088.1	2.0E-01 D89088.1	2.0E-01	2.0E-01	2.0E-01	2.0E-01	2.0E-01	2.0E-01	2.0E-01	1.9E-01	1.9E-01	1.9E-01 U32581.2	1.9E-01 U32581.2	1.9E-01	1.9E-01	1.9E-01	1.9E-01	1.9E-01	1.9E-01	1.9E-01	1.9E-01 U66066.1	1.9E-01 J00922.1	1.9E-01 D13197.1	1.9E-01	1.9E-01	1.9E-01	1.9E-01	1 9F-01
	Expression Signal	1.89	1.89	29.0	0.67	9.0	0.88	2.12	2.12	1.33	1.33	1.24	1.64	1.63	1.83	17.48	4.89	5.58	75.	1.54	8.31	6.7	1.72	5.63	2.42	4.34	3.66	3.81	7.53	4.07	4.94	1.09	3.68		
	ORF SEQ ID NO:	36878				L	37259		37792	38597				31851		] .		26604						L	27629		28711			29666	L	L			
	Exon SEQ ID NO:	23282	23282	23406	23406	23454	I_	上	L.	24895	1_			١	_		L			L		L	<u>1</u>		14555	14620	15584	1	1	16650	ı	1_	L	L	L
	Probe SEQ ID NO:	10247	10247	10371	10371	10419	10616	11079	11079	11908	11908	12666	12899	12912	12952	12977	113	362	673	673	88	681	1010	1128	1401	1466	2456	2989	3004	3482	3569	3907	4100	4193	1251

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
4346	17489		0.89	1.9E-01	.9E-01 BE834943.1	EST_HUMAN	MR1.+N0010-290700-007-d04 FN0010 Homo sapiens cDNA
4592	1	30711	0.8	1.9E-01	.9E-01 AL161493.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 5
5124	1			1.9E-01	.9E-01 AF223642.1	NT	Rattus norvegicus chemokine receptor CXCR3 mRNA, complete cds
8734	1		n 1	1 9E-04	9E-01 AW130149 1	FST HUMAN	x/29907 x1 NCI_CGAP_Ut1 Home sapiens cDNA clone IMAGE::2619444 3' simitar to gb:M73779 RETINOIC ACID RECEPTOR ALPHA-1 (HUMAN);
5761	Γ			1.9E-01	9E-01 AF127937.1	Т	Homo sapiens DNA polymerase epsilon catalytic subunit protein (POLE1) gene, exon 1a
5962		32463		1.9E-01	.9E-01 AF091216.1	LN LN	Mus musculus Wrn protein (Wrn) gene, complete cds
9009	ı			1.9E-01	.9E-01 AU133116.1		AU133116 NT2RP4 Homo sapiens cDNA clone NT2RP4001328 6
6457	1	32987		1.9E-01	.9E-01 AI762391.1		wi54h02x1 NCI_CGAP_Co16 Homo sapiens cDNA clone IMAGE:2394099 3'
6518	l		1.1	1.9E-01	9E-01 AW148452.1	EST_HUMAN	xf14c08.x1 NC _CGAP_Kid8 Homo sepiens cDNA clone IMAGE:2618030 3' similar to gb:X03559 ATP SYNTHASE BETA CHAIN, MITOCHONDRIAL PRECURSOR (HUMAN);
	i i					1400	yg09a12.s1 Sogres infent brain 1NIB Homo sapiens cDNA clone IMAGE:31663 3' sImilar to contains MER13
7112				1.9E-01	.9E-01 R43212.1	ESI HOMAN	repetitive definent;
7138	20273			1.9E-01	1.9E-01 AF034920.1	NT	Homo saplens tubby like protein 1 ( I OLET ) gene, exans 9-11
7138		33713		1.9E-01	.9E-01 AF034920.1	NT	Homo sapiens tubby like protein 1 (TULP1) gene, exons 9-11
7409	L		26.0	1.9E-01	.9E-01 U73846.1	NT	Drosophila melanogaster testis-specific RNA-binding protein (bruno) mKNA, complete cos
2	1		0.40	`	OE-04   103688 1	L <sub>Z</sub>	Staphytococcus aureus toxic shock syndrome toxin-1 (tst), enterotoxin (ent), and integrase (int) genes, complete cds
3 3		200,0		ľ	. SE 04 1180022 4	TIV	Ambidonsis (haliana serine/threonine protein phosphatase type one (TOPP8) gene, complete cds
100/	20773				9E-01 AF072724.1	LZ	Zea mays starch branching enzyme I (sbe1) gene, complete,cds
27.74				-	9F-01 At 16/1557.2	L	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 57
8885	1			-	.9E-01 AB033024.1	FZ	Homo sapiens mRNA for KIAA1198 protein, partial cds
9146	22225	35768			.9E-01 M14568.1	ΤN	Marsupial cat beta-globin gene mRNA, partial cds
9146	1			-	.9E-01 M14568.1	NT	Marsupial caf beta-globin gene mRNA, partial cds
	ı					;	ol96g10.s1 NCI_CGAP_PNS1 Homo saplens cDNA clone IMAGE:1537506 3' similar to contains Alu
10079				1	.9E-01 AA912486.1	EST_HUMAN	repetitive element;
10447	23482		0.81	1.9E-01	.9E-01 BE830353.1	EST_HUMAN	RC5-ET0082-060700-022-A02 ET0082 Homo sapiens cDNA
10447	ı				.9E-01 BE830353.1	EST_HUMAN	RC3-ET0082-060700-022-A02 ET0082 Homo saplens cDNA
10880	<u> </u>			_	.9E-01 AL161503.2	Ę	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 15
10880		37594		-	.9E-01 AL161503.2	F	Arebidopsis thallana DNA chromosome 4, contig fragment No. 15
	l_						Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively
10992	24071	37704	2.18	_	.9E-01 AF223391.1	L	peojiced
12025	i i	38711		,	.9E-01 AJ243213.1	ᅜ	Homo sapiens partial 5-HT4 receptor gene, exons 2 to 5
12047	l	38735	1.48		1.9E-01 L07344.1	N	Influenza A/Guangdong/243/72 nucleoprotein (seg 5) gene, 5' end

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	Top Hit Descriptor	Mus musculus p116Rip mRNA, complete cds	Mus musculus Cetg gene for chaperonin containing TCP-1 gamma subunit, partial cds	Homo sapiens calcium channel, voltage-dependent, beta 2 subunit (CACNB2) mRNA, and translated	products	Oryzias latipes gene for membrane guanylyl cyclase OIGC1, complete cds	wd71f02,x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2337051 3'	Dictyostelium discoideum plasmid Ddp5, complete genome	Yersinia pestis plasmid pCD1	Mus musculus guanylate nuclectide binding protein 1 (Gbp1), mRNA	Mus musculus guanylate nucleotide binding protein 1 (Gbp1), mRNA	gg22d10.x5 NCI_CGAP_Kld3 Homo sapiens cDNA clone IMAGE:1761811 3' sImilar to TR:O75936 O75936 GAMMA BUTYROBETAINE HYDROXYLASE;	Mus musculus Scyaß, Scyaß-, Scyaß genes for small inducible cytokine A6 precursor, small	inducible cytokine A9 precursor, Scya16 pseudogene, small inducible cytokine A5 precursor, complete cds	QV3-DT0018-081299-036-g04 DT0018 Homo sapiens cDNA	Jonopsidium acaule LEAFY protein (LEAFY2) gene, partial cds	x/41a03.x1 Soares_NFL_T_GBC_S1 Homo saplens cDNA clone IMAGE:2659756 3'	QV0-BN0041-070300-147-c04 BN0041 Homo sapiens cDNA	601809723R1 NIH_MGC_18 Homo sapiens cDNA clone IMAGE:4040621 3'	y/45e01.s1 Soares placenta Nb2HP Homo sapiens cDNA clone INAGE:151704.3' similar to contains Alu repetitive element	y45e01.s1 Soares placenta NbZHP Homo sapiens cDNA clone IMAGE:151704 3' similar to contains Alu	repetitive element;	Bovine NB25 mRNA for MHC class II (BoLA-DQB), complete cds	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 56	Mus musculus Scya6, Scya9, Scya16-ps, Scya5 genes for small inducible cytokine A6 precursor, small inducible cytokine A9 precursor, complete cds inducible cytokine A9 precursor, complete cds	N. tabacum mRNA pNLA-35	MR3-ST0203-151299-112-906 ST0203 Hamo sapiens cDNA	Mesocricetus auratus Na-taurocholate cotransporting polypeptide mRNA, partial cds	#57e04.x1 NCI_CGAP_Lym12 Homo sapiens cDNA clone IMAGE:2134590 3'	M.barkeri mlaC and mtaB genes
	Top Hit Databese Source	N LN	LN LN			) LN	T_HUMAN	Г	LN TN			EST_HUMAN C		Ē	EST_HUMAN C	LN TN	EST_HUMAN >	EST_HUMAN (	EST_HUMAN	NAMILE TOE	1	EST_HUMAN r	LN	NT /	L		EST_HUMAN !	LN	EST_HUMAN t	П
3	Top Hit Acession No.	1.8E-01 U73200.1	1.8E-01 AB022090.1		4502532 NT	1.8E-01 AB021490.2	1.8E-01 AI912212.1	1.8E-01 AF000580.1	1.8E-01 AL117189.1	6753947 NT	6753947 NT	1.8E-01 AI733708.1		1.8E-01 AB051897.1	1.8E-01 AW935728.1	1.8E-01 AF184589.1	1.8E-01 AW182300.1	1.8E-01 AW995178.1	1.8E-01 BF183582.1	4 BE 04 H03360 4		1.8E-01 H03369.1	1.8E-01 D37954.1	1.8E-01 AL161556.2	1 8E-01 AB051897 1	1.8E-01 X79794.1	1.8E-01 AW814270.1	1.8E-01 AF181258.1	1.8E-01 AI439881.1	1.8E-01 Y08310.1
	Most Similar (Top) Hit BLAST E Value	1.8E-01	1.8E-01		1.8E-01	1.8E-01	1.8E-01	1.8E-01	1.8E-01	1.8E-01	1.8E-01	1.8E-01		1.8E-01	1.8E-01	1.8E-01	1.8E-01	1.8E-01	1.8E-01	1 BE 04		1.8E-01	1.8E-01	1.8E-01	1.85-01	1.8E-01	1.8E-01	1.8E-01	1.8E-01	1.8E-01
	Expression Signal	1.85	1.47		1.9	0.78	1.8	2.14	6.87	1.49	1.49	1.91		2.28	3.34	2.3	1.16	1.61	0.77	0 0		78.0	0.92	5.61	996	0.65	1.79	2.55	0.89	1.2
	ORF SEQ ID NO:	26274			28625	26993	27235	27335		L				28208			29163	29375				29878		30801	34011	İ	L	L	l _	H
	SEQ ID NO:	13270	16009		13589	13946	14178	14279	14473	14686	14686	15058		15108	15873	16140	16144	18369	_	18070	1	16873	17593	17813	18025	L	L	18327	18340	18409
	Probe SEQ ID NO:	32	270		381	765	1005	1115	1317	1533	1533	1915		1965	2756	2963	2968	3194	3452	0322	4	3712	4453	4678	4805	5129	5158	5206	5218	5291

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		Γ	Τ	Τ	Γ	Γ	Τ		Γ	Γ	<u> </u>	Γ	Γ	Γ	Ŧ		7	Т	ī	Т	T	7	-		<u> </u>	Т	П		_				П
Top Hit Descriptor	DOG BTACK LYSTER BY	Average to the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the s	Mabuopsis trailana UNA chromosome 4, contig fragment No. 90	Wisconson National States metanocyte 2NbHM Homo septens cDNA clone IMAGE:264063 5	With Stringschius I'm receptor-especiated factor 6 (Traf6), mRNA	ivius musculus I m receptor-associated factor 6 (Traf6), mRNA	PORKHEAD BOX PROTEIN E3	Offulling languist mRNA for usua.	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continue to matter continue to matter continue to matt	SOLFARRED WILL MACE SOLL	Recillis heldrings and the Park	FST378404 MA/CE TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL 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complete de	Offullus lanahis mBNA for usus	ichostellim discoderim unknamm (DO2011)	Human carcinoemboonic antireo (DEA) asset 2000	xp40h10.x1 NCI_CGAP_HIN11 Homo sapiens cDNA clone IMAGE:27499R3 3'
Top Hit Database Source	FOT HIMAN	EN PA	EST HIMANI	LI CINCIPAL PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PR		1000001110	Т	Т		T HIMAN	Т		TN			Т		/ISSPROT		٦	ISSPROT	LN L	Į.				Z	E E	IN				L HUMAN
Top Hit.Acession No.	1.8E-01 BE082828 1	T	Ī	878428	F678428 NT	8F-01 090V14		-	Γ		l	L		3626232		21.1							8E-01 AF200252.1		-				8E-01 AB018561.1 N	8E-01 AB018561.1 N		Γ	BE-01 AW275728.1
Most Similar (Top) Hit BLAST E Value	1.8E-01	1.8E-01	1.8E-01	1.8E-01	1.8E-01	1.8F-01	1.8E-01	1.8E-01	1.8E-01	1.8E-01	1.8E-01 A	1.8E-01 A	1.8E-01 N	1.8E-01	100	1.0E-01 AA4837	1.0-10.1	1.8E-01 P15272	1.8E-01 MZ6019.1	1.8E-01 MZ6019.1	1.8E-U1 P08123	1.8E-01 U67548.1	1.8E-01 A	1.8E-01 X63440.1	1.8E-01 A	4 8E 04 V77256 4		1.8E-01 U38906.1	1.8E-01 AE	1.8E-01 AE	1.8E-01 AF	1.8E-01 M59257.1	1.8E-01 AV
Expression Signal	0.61	1.19	0.95	0.89	0.89	1.16	2.12	1.11	1.11	29'0	0.81	0.58	1.58	1.52	9	200	3	65.0	707	- 02	0.0	0.71	0.67	1.46	1.21	200		3	3.05	3.05	4.41	2.06	1.41
ORF SEQ ID NO:	31589	32428			32777	33189		33722	33723	33477	34148	35431	36176	36284		36392	38303	36432	36433	26613	2000	71000		37218	37441	37588		37633	33722	33723	37688	37976	38284
Exen SEQ ID NO:	18615					19800	ĺ	20281	ı	ı	- 1	- 1	- 1	22716	22741	22814	22814	22854	22854	23020	2000	3300	23372	23613	23818	23058		24000	20281	20281	24054	24338	24606
Probe SEQ ID NO:	5413	5929	6047	6256	6256	6641	9899	7146	7146	7202	7604	8810	9543	9574	9692	9774	9774	9814	9814	88	808		10337	10578	10785	10873		/1001	10974	10974	10975	11270	11551

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Top Hit Descriptor	B.taurus mRNA for potassium channel	Rattus norvegicus Thromboxane receptor (Tbxa2r), mRNA	cp2798.seq.F Human fetal heart, Lambda ZAP Express Homo saplens cDNA 5	Bovine ephemeral fever virus, complete genome	602019928F1 NCL_CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4155318 5	Yersinia pestis plasmid pCD1	DNA TERMINAL PROTEIN (BELLETT PROTEIN) (PTP PROTEIN)	yh48h10,r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:133027 5	E.dispar mRNA for hexokinase (hxk1)	Rattus norvegicus procollagen C-proteinase enhancer protein (Pcolce), mRNA	601274604F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3615768 5	P.dumerilli histone gene cluster for core histones H2A, H2B, H3 and H4	NEUROFILAMENT TRIPLET L PROTEIN (NEUROFILAMENT LIGHT POLYPEPTIDE) (NF.1.)	Lymantria dispar nucleopolymedrovinus, complete genome	Lymantria dispar nucleopolyhechownus, complete genome	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 69	Homo sapiens BNIP3H (BNIP3H) gene, complete cds; nuclear gene for mitochondrial product	Vibrio cholerae hypoxanthine phosphoribosyltransferase (hpt) gene, partial cds, hemagglutinin/protease regulatory protein (hapR) gene, complete ods, and YRAL VIBCO gene, partial cds	///princholerae hymwenthine abosecharthos/Itransferase (htt) dene partial cds. hemaggiuthin/graßase	regulatory protein (hapR) gene, complete cds, and YRAL VIBCO gene, partial cds	EST41651 Endometrial tumor Homo sapiens cDNA 5' end	Naja naja atra ctv-1 gene, exons 1-3	Naja naja atra otk-1 gene, exons 1-3	Taxus canadensis geranyigeranyi diphosphate synthase mRNA, complete cds	J2346F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA clone J2346 5	Anabaena sp. ORF4 (partial), ORF3, ORF2, ORF1, adpA gene, adpB gene, adpC gene, adpD gene, adpE	gene and adpl gene	Homo sapiens derivative 11 breakpoint fragment; partial intron 10 of the ALL-TMLL/HXX gene rused to involve. 5 of the AF-4/FEL dene	Schistocerca gregaria alpha repetitive DNA	Homo sapiens fragile 16D oxido reductase (FOR) gene, exons 8, 9, and partial cds
Top Hit Database Source	LN		T_HUMAN		EST HUMAN			T HUMAN			EST_HUMAN		SWISSPROT	NT	NT		NT	TN		Į.	EST_HUMAN	칟	LN	TN	EST_HUMAN		¥	FZ	Į.	NT
Top Hit Acession No.	!	8394421 NT	1.8E-01 AA095094.1	10086561 NT	1.8E-01 BF348623.1	1.8E-01 AL117189.1	<b>196682</b>	<b>२</b> 24494.1	r11114.1	9506952 NT	1.7E-01 BE385164.1		P35616	1.7E-01 AF081810.1	1.7E-01 AF081810.1	1.7E-01 AL161573.2	1.7E-01 AF255061.1	1.7E-01 AF000716.1		1.7E-01 AF000716.1	1.7E-01 AA336909.1	1.7E-01 AJ238736.1	1.7E-01 AJ238736.1	1.7E-01 AF081514.1	1.7E-01 N55763.1	-	1.7E-01 AJ269505.1	4 7E 04 A 1935377 4	1 7E-01 X52936.1	1.7E-01 AF217490.1
Most Similar (Top) Hit BLAST E Value	1.8E-01 X57033.1	1.8E-01	1.8E-01	1.8E-01	1.8E-01	1.8E-01	1.8E-01 Q96682	1.8E-01 R24494.1	1.8E-01 Y11114.1	1.8E-01	1.7E-01	1.7E-01 X53330.1	1.7E-01 P35616	1.7E-01	1.7E-01	1.7E-01	1.7E-01	1.7E-01		1.7E-01	1.7E-01	1.7E-01	1.7E-01	1.7E-01	1.7E-01		1.7E-01	4 7E 04	1 7E-01	1.7E-01
Expression Signal	29.	3.48	1.77	1.79	1.28	1.18	3.28	20.8	4.98	1.7	6.4	3.16	1.79	0.89	0.89	244	3.23	2.13		2.13	1.47	1.09	1.09	1.65	0.81		1.52	90 9	2 49	0.59
ORF SEQ ID NO:	37563	38751	38808		32103	27540				31548	26801		:	27305		28113		29112		29113		L		L			29710		01200	30998
Exan SEQ ID NO:	23936	25042		1		14473	İ	L			13782			14249	14249	15006	L	16100		16100	Ĺ	16237	16237	16349	L		16699	1	17816	Ш
Probe SEQ ID NO:	11750	12061	12124	12239	12306	12719	12811	12942	12988	13035	591	828	883	1083	1083	1880	2038	2922		2922	2993	3081	3061	3174	3451		3534	3,00	4049	4884

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ph57e09.x1 Soares\_fefal\_liver\_spleen\_1NFLS\_S1 Homo sapiens cDNA clone IMAGE:18488083' similar to ne13a02.s1 NCI\_CGAP\_Co3 Homo sapiens cDNA clone IMAGE:881066 3' similar to gb:M17886 60S ne13a02.s1 NCI\_CGAP\_Co3 Homo sapiens cDNA clone IMAGE:881066 3' similar to gb:M17886 60S Homo sapiens homogentisate 1.2-dioxygenase gene, complete cds
Pseudomonas putida fong-chain-fatty-acid-CoA ligase (fadD) gene, complete cds
Homo sapiens cleavage and polyadenylation specificity factor 3, 73kD subunit (GPSF3), mRNA
Homo sapiens cleavage and polyadenylation specificity factor 3, 73kD subunit (GPSF3), mRNA
RC2-BN0032-120200-011-e10 BN0032 Homo sapiens cDNA Brugia pahangi microfilarial sheath protein SHP3 (shp3) gene, complete cds ysD2g06.st Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:213658 3' te29c11x1 Soeres fetal Lung NbHL19W Homo ceptens cDNA clone INAGE:20454923' 600944087T1 NIH\_MGC\_17 Homo sapiens cDNA clone IMAGE:29602493' Mesocricetus auratus oviductin precursor (OVI) gene, complete cds ta29c11.x1 Soares\_fetal\_lung\_NbHL19W Homo sapiens cDNA clone IMAGE:2045492 3 601569022F1 NIH\_MGC\_21 Homo sapiens cDNA clone IMAGE:3843964 5' PROBABLE PROCESSING AND TRANSPORT PROTEIN ULS6 (HFLF0 PROTEIN) Rattus norvegicus mRNA for MIBP1 (c-myc Infron binding protein 1), complete cds yi66g02.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:144242 5 Escherichia coli O157:H7 genomic DNA, Sakal-VT2 prophage inserted region 601118872F1 NIH MGC 16 Homo sapiens cDNA clone IMAGE:3357184 5' 601116872F1 NIH MGC\_16 Homo sapiens cDNA clone IMAGE:3357184 5' Bacillus halodurans genomic DNA, section 2/14 601557256F1 NIH\_MGC\_58 Homo sapiens cDNA done IMAGE:3827197 5 Homo saplens neuroligin 3 isoform gene, complete cds, alternatively spliced Homo sapiens neuroligin 3 iscrorm gene, complete cds, alternatively spliced EST389564 MAGE resequences, MAGO Homo sapiens cDNA EST389564 MAGE resequences, MAGO Homo sapiens cDNA Top Hit Descriptor Zea mays starch branching enzyme IIb (ae) gene, complete cds COLLAGEN ALPHA 3(IV) CHAIN PRECURSOR ACIDIC RIBOSOMAL PROTEIN P1 (HUMAN); ACIDIC RIBOSOMAL PROTEIN P1 (HUMAN); contains OFR.b1 OFR repetitive element Rat (SHR strain) SX1 gene Homo saplens HFE gene HUMAN EST\_HUMAN EST\_HUMAN EST\_HUMAN EST\_HUMAN EST HUMAN HUMAN EST\_HUMAN EST\_HUMAN HUMAN HUMAN EST\_HUMAN EST HUMAN EST\_HUMAN Top Hit Database Source SWISSPROT EST EST EST NT EST F Top Hit Acession No. 7706426 1.7E-01 292910.1 1.7E-01 AP000422.1 1.7E-01 BE734179.1 .7E-01 AW992873.1 AW977455.1 1.7E-01 BE253142.1 1.7E-01 BE253142.1 1.7E-01 AA470686.1 1.7E-01 AF026552.3 1.7E-01 AF217413.1 1.7E-01 AF217413.1 1.7E-01 AP001508.1 BF030010.1 A1247635.1 1.7E-01 AI370976.1 1.7E-01 H72118.1 D37951.1 1.7E-01 001955 1.7E-01 1.7E-01 1.7E-01 1.7E-01 1.7E-01 1.7E-01 1.75-01 Vost Similar (Top) Hit BLAST E 9. 0.94 88 12.64 0.59 8.51 0.72 Expression Signa ORF SEQ ID NO: 33052 33053 31503 34752 35083 31066 31359 31737 31738 32198 32988 35084 35667 3551 22124 25850 21974 18090 18353 18391 19682 18511 21653 18721 19626 SEQ ID 6686 6686 9045 6986 6517 6517 6992 7369 9045 9369 9789 Probe SEQ ID 5272 5312 5524 5710 6459 8045 8150 8472 8895 5524 7019 7666 8472 5231 4961

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Top Hit Descriptor	Human class IV alcohol dehydrogenase (ADH7) gene, exon 3	Human immunodeficlency virus type 1 (B7.05) env gene (partial)	Human immunodeficiency virus type 1 (B7.05) env gene (partial)	Drosophila melanogaster mRNA for serine protease inhibitor (serpin-6), (sp6 gene)	Homo sapiens chromosome 21 segment HS21C084	Homo sapiens solute carrier family 7 (cationic amino acid transporter, y+ system), member 2 (SLC7A2), mRNA	nq60e07.s1 NCI_CGAP_Co9 Homo sapiens cDNA clone IMAGE:1148292.3' similar to gb:L25081 TRANSFORMING PROTEIN RHOC (HUMAN);	601286547F1 N.H_MGC_44 Homo sapiens cDNA clone IMAGE:3613258 6'	of43e03.s1 NCI_CGAP_CNS1 Homo sapiens cDNA clone IMAGE:1426924 3'	Mus musculus adenomatosis polyposis coli binding protein Eb1 (Eb1), mRNA	Mus musculus adenomatosle polyposis coli binding protein Eb1 (Eb1), mRNA	al45f09.s1 Soares_NFL_T_GBC_S1 Homo sepiens cDNA clone IMAGE:1460297 3'	AMP NUCLEOSIDASE	IGG RECEPTOR FCRN LARGE SUBUNIT PS1 PRECURSOR (FCRN) (NEONATAL FC RECEPTOR) (IGG FC FRAGMENT RECEPTOR TRANSPORTER, ALPHA CHAIN)	IGG RECEPTOR FORN LARGE SUBUNIT PB1.PRECURSOR (FORN) (NEONATAL FC RECEPTOR)	Homo sapiens calcium channel, voltage-dependent, alpha 11 subunit (CACNA11), mRNA	Homo saplens chromosome 21 segment HS21C078	to the common of the common control of the company of the company of the common of the common of the common of the common of the common of the common of the common of the common of the common of the common of the common of the common of the common of the common of the common of the common of the common of the common of the common of the common of the common of the common of the common of the common of the common of the common of the common of the common of the common of the common of the common of the common of the common of the common of the common of the common of the common of the common of the common of the common of the common of the common of the common of the common of the common of the common of the common of the common of the common of the common of the common of the common of the common of the common of the common of the common of the common of the common of the common of the common of the common of the common of the common of the common of the common of the common of the common of the common of the common of the common of the common of the common of the common of the common of the common of the common of the common of the common of the common of the common of the common of the common of the common of the common of the common of the common of the common of the common of the common of the common of the common of the common of the common of the common of the common of the common of the common of the common of the common of the common of the common of the common of the common of the common of the common of the common of the common of the common of the common of the common of the common of the common of the common of the common of the common of the common of the common of the common of the common of the common of the common of the common of the common of the common of the common of the common of the common of the common of the common of the common of the common of the common of the common of the common of the common of the common of the common of the common of the common of the common of the common of the	Human beta globin region on chromosome 11	Homo sapiens mevalonale kinase gene, exon 6 and 7	yh75f12.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:135599 5	Homo sapiens homeobox protein OTX2 gene, complete cds	Rickettsia prowazekii strain Madrid E, complete genome, segment 3/4	AXONIN-1 PRECURSOR (AXONAL GLYCOPROTEIN TAG-1)	Crassostrea gigas RNA polymerase II largest subunit mRNA, partial cds	H.sapiens mRNA for novel T-cell activation protein	Homo sapiens mRNA for KIAA1308 protein, partial cds	Homo sapiens cytochrome P450 3A4 (CYP3A4) gene, promoter region	Horno sapiens cytochrome P450 3A4 (CYP3A4) gene, promoter region
Top Hit Database Source	TN	NT		ΙN	NT	IN	EST_HUMAN	EST_HUMAN	EST_HUMAN	NT	N	EST_HUMAN	SWISSPROT	SWISSPROT	TOGGGGING	NT	NT	EST HUMAN	NT	NT	EST_HUMAN	NT.	ΙN	SWISSPROT	NT ·	NT	LN	NT	TN
Top Hit Acession No.	U16288.1	Z34508.1	.7E-01 Z34508.1	.7E-01 AJ251749.1	.7E-01 AL163284.2	11427203 NT	.7E-01 AA627972.1	.7E-01 BE390835.1	.7E-01 AA814617.1	7106300 NT	7106300 NT	.7E-01 AA883375.1	7E-01 P15272	7E-01 P55899	0000	11418157 NT	7E-01 AL163278.2	7E-01 AI824404.1	.7E-01 U01317.1	.6E-01 AF217532.1	6E-01 R31497.1	.6E-01 AF298117.1	.6E-01 AJ235272.1	.6E-01 P22063	.6E-01 U10334.1	.6E-01 X94232.1	.6E-01 AB037729.1	.6E-01 AF185589.1	6E-01 AF185589.1
Most Similar (Top) Hit BLAST E Value	1.7E-01	1.7E-01	1.7E-01	1.7E-01	1.7E-01	1.7E-01	1.7E-01	1.7E-01	1.7E-01	1.7E-01	1.7E-01	1.7E-01	1.7E-01	1.7E-01	4 75 04 1055000	1.7E-01	1.7E-01	1.7E-01	1.7E-01	1.6E-01	1.6E-01	1.6E-01	1.6E-01	1.6E-01	1.6E-01	1.6E-01	1.6E-01	1.6E-01	1.6E-01
Expression Signal	2.08	0.47	0.47	0.93	2.77	1.58	1.66	9.54	2.12	6.81	6.81	1.71	1.5	1.67		2	1.45	1.18	7.24	1.7	1.16	4.25	127	2.14	1.43	8.1	2.73	14.1	14.1
ORF SEQ ID NO:	36543	36621				37247	(	37636	37756	38090	38091	38427	ĺ	38727					31972			27783	Ì.,	28221		28712		29149	
Exon SEQ ID NO:	22956	1	l	ı	23473	ļ	1		<u> </u>	24434	L	L	24996	25023		L	1_	1	L	L		14703	15053	15120		16063		Ы	
Probe SEQ ID NO:	8916	9992	3665	10013	10438	10605	10607	10919	11045	11373	11373	11657	12011	12042	200	12142	12275	12567	12907	128	697	1551	1910	1977	2041	2457	2562	2957	2957

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Top Hit Descriptor	Populus trichocarpa cv. Trichobel ABI3 gene	Populus trichocarpa cv. Trichobel ABI3 gene	Archaeoglobus fulgidus section 145 of 172 of the complete genome	Vibrio cholerae chromosome II, section 70 of 93 of the complete chromosome	Crithidla fasciculata tryparedoxin I (brnl) gene, complete cds	Hamo sapiens apelin gene, complete cds	EST380677 MAGE resequences, MAGJ Homo saplens cDNA	Mus musculus chaperonin subunit 3 (gamma) (Cct3), mRNA	2/84/109.s1 Stratagene colon (#837204) Homo sapiens cDNA done IMAGE:511361 3' similar to TR:E221955 E221955 as 355 BP SEGMENT OF CHROMOSOME XIV.;	Lycopersicon esculentum Rsal fragment 2, satellite region	Lycopersicon esculentum Rsal fragment 2, satellite region	Gallus gallus smooth muscle/non-muscle myosin light chain kinase gene, exon 29	Plasmodium falciparum (strain Dd2) variant-specific surface protein (var-1) gene, complete cds	xm43f01.x1 NCI_CGAP_GC6 Homo sepiens cDNA clone IMAGE:2686969 3' similar to TR:075984 075984 HYPOTHETICAI 127 6 KD PROTEIN	xm43f01.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone iMAGE;2686969 3' similar to TR:075984 075984 HYPOTHETICAL 127 6 KD PROTEIN	Raftis noveatisis CCAAT/enhancer binding prefets ensiles (return) gene complete ede	RC3-BN0034-310800-113-h01 BN0034 Homo sapiens cDNA	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 84	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 84	Hamo sapiens mRNA for KJAA1566 protein, partial cds	602139855F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4301004 5'	UI-H-BI2-agi-b-06-0-UI.s1 NCI_CGAP_Sub4 Homo sapiens cDNA clone IMAGE:27244183'	S.cerevisiae chromosome X reading frame ORF YJR132w	2822248.5prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2822248 5'	Mus musculus Ca<2+>dependent activator protein for secretion (Cadps), mRNA	AU136525 PLACE1 Homo sapiens cDNA clone PLACE1004468 5'	Gorilla gorilla androgen receptor gene, partial exon	TCBAP1E0607 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project≔TCBA Homo sapiens cDNA clone TCBAP0607	Bacteroides vulgatus beta-lactamase (टॉग्र्स) gene, complete cds and mobilization protein (mobA) gene,	complete cds
Top Hit Dafabase Source	NT	LΝ	LN	L		LN	EST_HUMAN	TN	EST_HUMAN	LZ	TN	LN	FZ	HST HIMAN	Т	Т	HUMAN	Г	LN	LN	EST_HUMAN	EST_HUMAN		EST_HUMAN		EST_HUMAN		EST HUMAN		L
Top Hit Acession No.	1.6E-01 AJ003165.1	1.6E-01 AJ003165.1	1.6E-01 AE000962.1	1.6E-01 AE004413.1	1.6E-01 AF084456.1	1.6E-01 AF179680.:	1.6E-01 AW968601.1	6753319 NT	1.6E-01 AA088343.1	1.6E-01 AJ006356.1	1.6E-01 AJ006356.1	1.6E-01 AF045283.1	_40608.1	1 6F-01 AW 197496 1	1 6F-01 AW197498 1	Γ		1.6E-01 AL161588.2	1.6E-01 AL161588.2	1.6E-01 AB046786.1	1.6E-01 BF683630.1	1.6E-01 AW291215.1	1:6E-01 Z49632.1	1.6E-01 AW246359.1	6753237 NT	5.1		1.6E-01.BE244087.1		1.6E-01 U38243.1
Most Similar (Top) Hit BLAST E Value	1.6€-01	1.6E-01	1.6E-01	1.6E-01	1.6E-01	1.6E-01	1.6E-01	1.6E-01	1.6E-01	1.6€-01	1.6E-01	1.6E-01	1.6E-01 L40609.1	165-01	1.65-01	16191	1.65.01	1.6E-01	1.6E-01	1.6E-01	1.6E-01	1.6E-01	1.6E-01	1.6E-01	1.6E-01	1.6E-01	1.6E-01 L49349.1	1.6E-01		1.65.01
Expression Signal	1.23	1.23	0.82	2.8	1.21	10.91	2.49	4.39	1.39	1.8	1.8	0.93	0.81	9.6	00	8	20	2.06	2.06	62.0	99'0	4.15	0.71	1.63	0.84	1.03	1.62	0.53		0.77
ORF SEQ ID NO:	29889	29890	30030			30569			31162	31183	31184		31719	31909	31040	32128	32674	33098	33097	33688		31485		34516			34657			34916
Exan SEO ID NO:	16884	16884	17031	17261	17296	17588	17715	17723	18188	18211	18211	18458	18702	18833	Į.	18845	19328	19720	19720	20262	20213	18530		21005		21035	21136	21297		21392
Probe SEQ ID NO:	3723	3723	3872	4107	4144	4448	4578	4586	0909	2083	5083	5345	5503	5635	5630	1651	6152	6558	6558	66933	6985	2103	7431	7955	7982	7986	8023	8215		8310

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Table 4
Single Exon Probes Expressed in Placenta

								_	_														_				_	_	_	<del>-</del> -	-	<del></del>	_,	_
	Top Hit Descriptor	Bacillus subtilis complete genome (section 16 of 21): from 2997771 to 3213410	y60h08.r1 Scares infant brain 1NIB Homo saplens cDNA clone IMAGE:26873 5	Homo saplens guanylate cyclase activating protein (GCAP) gene exons 1-4, complete cds	S.cerewisiae chromosome X reading frame ORF YJR001w	Hcmo sapiens jun dimerization protein gene, partial cds; cfos gene, complete cds; and unknown gene	RC3-ST0200-041199-011-h01 ST0200 Homo sapiens cDNA	S.cerevisiae chromosome X reading frame ORF YJR001w	PM2-HT0353-270100-004-111 HT0353 Homo sapiens cDNA	Homo sapiens nuclear autoantigen (GS2NA), mRNA	IL3-CT0220-111199-028-G01 CT0220 Homo sapiens cDNA	CHROMODOMAIN-HELICASE-DNA-BINDING PROTEIN 2 (CHD-2)	CHROMODOMAIN-HELICASE-DNA-BINDING PROTEIN 2 (CHD-2)	601145793F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3161183 5'	Plasmodium falciparum calcium-dependent protein kinase-3 (cdpk3) gene, complete cds	Mus musculus adaptor-related protein complex AP-1, beta 1 subunit (Ap1b1), mRNA	AV719585 GLC Homo sapiens cDNA clone GLCEMF07 5	Rat convertase PC5 mRNA, 5' end	RC1-LT0074-120200-014-h01_1 LT0074 Homo sapiens aDNA	Cucumis sativus KS mRNA for ent-kaurene synthase, complete cds	Horno sapiens mRNA for FLJ00104 protein, partial cds	Fuch sia hybrid cultivar Qiu 94208 ribosomal protein S10 gene, partial cds; nuclear gene for mitochondrial	product	Rattus norvegicus chondroitin sulfate proteoglycan 5 (neuroglycan C) (Cspg5), mRNA	601125459F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3345038 5'	602/52004F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4293145 5	IL3.HT0619-040700-197-E05.HT0619.Homo sapiens cDNA	IL3-HT0619-040700-197-E05 HT0619 Homo saplens cDNA	AV711696 DCA Homo capiens cDNA clone DCAADH08 5'	Homo sapiens chromosome 21 segment HS210084	Cyprinus carpio mRNA for EGGS22 myosin heavy chain, 3'UTR	Homo sapiens partial SLC22A2 gene for organic cation transporter (OCT2), exon 1	Rettus norvegicus insulin-responsive glucose transporter (GLUT4) gene, 5' end	xr39d11.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2896085 31
	Top Hit Database Source	NT	EST_HUMAN	NT	NT	TN	EST_HUMAN	NT	EST_HUMAN	NŢ	EST_HUMAN	SWISSPROT	SWISSPROT	EST_HUMAN	NT	NT	EST_HUMAN	NT	EST_HUMAN	TN	TN		N	INT	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	NT	NT	NT	μ	EST_HUMAN
	Top Hit Acession No.	1.6E-01 Z99119.1	1.6E-01 R13673.1	L36861.1	249501.1	1.6E-01 AF111167.2	1.6E-01 BF375171.1	1.6E-01 Z49501.1	1.6E-01 BE155664.1	11128016 NT	1.6E-01 AW850853.1	014647	014647	1.6E-01 BE259649.1	1.6E-01 AF106064.1	6671552 NT	1.6E-01 AV719585.1	1.6E-01 L14933.1	1.6E-01 AW839711.1	1.6E-01 AB045310.1	1.6E-01 AK024496.1		1.6E-01 AF287344.1	9506522 NT	1.6E-01 BE267894.1	1.6E-01 BF672698.1	1.5E-01 BE710087.1	1.5E-01 BE710087.1	1.5E-01 AV711696.1	1.5E-01 AL163284.2	1.5E-01 AJ009735.1	1.5E-01 AJ251885.1	1.5E-01 L36125.1	1.5E-01 AW 195516.1
0 7 - 7	Most Similar (Top) Hit BLAST E Value	1.6E-01	1.6E-01	1.6E-01 L36861.1	1.6E-01 Z49501.1	1.6E-01	1.6E-01	1.6E-01	1.6E-01	1.6E-01	1.6E-01	1.6E-01   O14647	1.6E-01 014647	1.6E-01	1.6E-01	1.6E-01	1.6E-01	1.8E-01	1.6E-01	1.6E-01	1.6E-01		1.6E-01	1.6E-01	1.6E-01	1.6E-01	1.5E-01	1.5E-01	1.5E-01	1.5E-01	1.5E-01	1.5E-01	1.5E-01	1.5E-01
	Expression Signal	1.08	0.77	0.74	1.85	0.78	11.17	1.99	1.16	0.5	2.34	1.34	1.34	1.62	3.6	7.53	3.89	2	1.38	11.64	2.71		5.04	1.69	4.1.4	8.	1.7	1.7	2.5	1.38	1.44	2.7	1.85	2.37
	ORF SEQ ID NO:	ſ '	35646		35792			36475		37482	37609	37951					නෙනෙ							31964				26509			L			27463
	Exon SEQ ID NO:	1	22105			22387		L	22931	L	23977	24313	24313	24318	24438	24694	25207	25402	25423		25615				25694	25782	_			_	14281			14402
I.			9026				_	_	9891	10826	10893	11244	14	11249	11377	11697	12277	12597	12630	12733	12933		13029	13054	13060	13189	258	258	10	805	m	1121	1137	1243

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Top Hit Descriptor	Human gene for dihydrolipoamide succinyltransferase, complete cds (exon 1-15)	Human gene for dihydrolipoamide succinyltransferase, complete cds (exon 1-15)	Mus musculus MAP kinase kinase kinase 1 (Mekkt) mRNA, complete cds	UI-H-BI3-akb-b-09-0-UI,s1 NCI_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2733841 3'	xw56a02.x2 NC_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2831978 3' similar to gb:X55072_ma1 THYROID HORMONE RECEPTOR ALPHA-1 (HUMAN);	Bos taurus factor V variant 2 (factor V) mRNA, complete cds	NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 4	oc68d05.s1 NCI_CGAP_GC4 Homo sapiens cDNA clone IMAGE:1571337 3' similar to gb:M11433 RETINOL-BINDING PROTEIN I, CELLULAR (HUMAN);	L.stagnalis mRNA for G protein-coupled receptor	Listagnalis mRNA for Giprotein-coupled receptor	Mus musculus ICR/Swiss glyceraldehyde 3-phosphate dehydrogenase (Gapd-S) gene, complete cds	Homo sapiens pyruvate dehydrogenase kinase, isoenzyme 1 (PDK1), nuclear gene encoding mitochondrial	protein, mKNA	X*NA, Inemoanaerobacterum, xyra, 4162 base-bars	hj10f06x1 Soares_NFL_T_GBC_S1 Homo septens cDNA clone IMAGE:29814113	Populus trichocarpa cv. Trichobel ABI3 gene	Populus trichocarpa cv. Trichobel ABI3 gene	RC2-HT0149-191099-012-c09 HT0149 Homo sapiens dDNA	Buspus mitochondrion DNA for ORF158	Homo sapiens chromosome 21 segment HS21C084	802087192F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4086223 5'	602083269F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4247537 5'	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 60	THROMBOSPONDIN 1 PRECURSOR	Carman crocodilus MHC class II beta chain (hclibeta) gene, complete cds	SEX HORMONE-BINDING GLOBULIN PRECURSOR (SHBG) (SEX STEROID-BINDING PROTEIN) (SRP) (TESTIS-SPECIFIC ANDROGEN-BINDING PROTEIN) (ABP)	1.3-CT0219-160200-064-F10 CT0219 Homo sapiens cDNA	Mus musculus transforming growth factor alpha (TGFa) mRNA, complete cds	Mus musculus transforming growth factor alpha (TGFa) mRNA, complete cds	Homo sapiens sodium channel, voltage-gated, type VI, alpha polypeptide (SCN5A) mRNA
Top Hit Database Source	F	Į.	LN LN	EST_HUMAN	EST HUMAN	-Z	SWISSPROT	EST_HUMAN	LN	L F	IN			٦	T HUMAN		NT	EST_HUMAN	NT			EST_HUMAN	, TN	SWISSPROT	Į.	TOBIOSONIS	EST HUMAN	LN	Ę	N
Top Hit Acessian No.	.6E-01 D26535.1	.5E-01 D26535.1		.6E-01 AW 444451.1		.5E-01 M81441.1		.5E-01 AA935049.1	.5E-01 Z23104.1		.5E-01 U09964.1		7108358		1		1.5E-01 AJ003165.1	1.5E-01 AW36659.1	1.5E-01 Z12628,1			1.5E-01 BF695381.1			1.5E-01 AF256652.1	D15108	1 5F-01 AW850754 1	1.5E-01 (45016 1	1.5E-01 U65016.1	4506810 NT
Most Similar (Top) Hit BLAST E Value	1.6E-01	1.5E-01	1,5E-01	1.6E-01	1.5E-01 /	1.5E-01	1.5E-01 O78687	1.5E-01	1.5E-01	1.5E-01	1.5E-01		1.5E-01	1.5E-01 M97882.	1.5E-01/	1.5E-01	1.5E-01	1.5E-01	1.5E-01	1.5E-01	1.5E-01	1.5E-01	1.55-01	1.5E-01 P07998		1 KE 01 D15108	155-01	15.10	1.5E-01	1.55.01
Expression	3.22	3.22	1.38	96.0	60	0.91	0.62	5.78	67.0	0.73	2.35		0.83	0.77	2.45	89.0	0.68	1.16	79.0	9.85	1.54	2,33	1.5	1.91	1.33	90	48	88.8	6,66	0.82
ORF SEQ ID NO:	L	27527					29308	29620	29641								30150	30308	30348			29002	31207	31441	L		32131		1	Ц
Exon SEQ ID NO:	14460	14460	14664	15100	l	l	16294	16601	}	F	17011		17028	17040	17128	17144	17144	17312	17359	l.	L _	15891	18242	18573		l	4	L	┸	Ш
Probe SEQ ID NO:	1304	1304	1511	1957	2980	3100	3118	3433	3454	3454	3861		3867	3881	3970	3987	3987	4161	4210	4299	4847	4874	5114	5370	5399	6773	5655	2000	2692	6029

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Top Hit Descriptor	Mus musculus DNA methytransferase 2 (Dnmt2), mRNA	Mus musculus DNA methyltransferase 2 (Dnmt2), mRNA	Mus musculus genomic fragment, 279 Kb, chromosome 7	601564322F1 NIH_MGC_20 Homo saplens dDNA done IMAGE:3833981 5'	Homo sapiens RAD54 (S.cerevisiae)-like (RAD54L) mRNA	Influenza B virus (B/Nanchang/480/94) NB protein gene, complete cds; and neuraminidase gene, partial cds	Archaeoglobus fulgidus section 68 of 172 of the complete genome	Homo saplens chromosome 5 open reading frame 3 (C5ORF3), mRNA	GLUTAMATE-CYSTEINE LIGASE REGULATORY SUBUNIT (GAMMA-GLUTAMYLCYSTEINE SYNTHETASE) (GAMMA-ECS) (GCS LIGHT CHAIN)	AMELOGENIN	nw30d10.s1 NCI_CGAP_GCB0 Homo sapiens cDNA olone IMAGE:1241971 3'	HYPOTHETICAL 51.7 KD PROTEIN IN THRC-TALB INTERGENIC REGION (ORF8)	EST382376 MAGE resequences, MAGK Homo saplens cDNA	ob73f02.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1337019 3' similar to contains element	LTR2 repetitive element;	Homo sapiens HARP (HARP) gene, exon 17 and complete cds	wr52c08x1 NCI_CGAP_Ut1 Homo sepiens cDNA clone IMAGE:2491310 31	Bos taurus Niemann-Pick type C1 disease protein (NPC1) mRNA, complete cds	Bos taurus Niemann-Pick type C1 disease protein (NPC1) mRNA, complete cds	UI-HF-BN0-akk-d-05-0-UI.r1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3077409 5	ULHF-BN0-akk-d-05-0-U.r1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3077409 5	Saccharamyces cerevisiae weak multicopy suppressor of bs1-1 (SOL3) gene, complete cds	MEROZOITE RECEPTOR PK66 PRECURSOR (66 KD PROTECTIVE MINOR SURFACE ANTIGEN)	oo88g12.s1 NOI_CGAP_KId5 Homo sapiens cDNA clone IMAGE:1573030 3' similar to gb:M26062 INTERLEUKIN-2 RECEPTOR BETA CHAIN PRECURSOR (HUMAN);	601510523F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3912004 5'	C16800 Clontech human aorta polyA+ mRNA (#5572) Homo sepiens cDNA clone GEN-529H09 5'	Pangaslanodon gigas growth hormone (GH) mRNA, complete cds	Homo sapiens mRNA for ASK1, complete cds	WNT-10A PROTEIN PRECURSOR	Homo sapiens adaptor-related protein complex 1, beta 1 subunit (ADTB1), mRNA
Top Hit Database Source	TN	Z	.LN	8.1 EST_HUMAN	ΙN	FZ	IN	١	SWISSPROT	SWISSPROT	EST_HUMAN	SWISSPROT	EST_HUMAN		EST_HUMAN	١	EST_HUMAN	LN	LN	EST_HUMAN	EST_HUMAN	LΝ	SWISSPROT	EST HUMAN	EST HUMAN	EST HUMAN	ΝŢ	ΙN	SWISSPROT	Ā
Top Hit Acession No.	6753659 NT	6753659 NI	1.5E-01 AJZ76505.1	1.5E-01 BE727658.1	4506396	1.5E-01 AF134907.1	1.5E-01 AE001039.1	11417236 NT	P48508	Q28462	1.5E-01 AA714760.1		1.5E-01 AW970295.1		1.5E-01 AA811545.1	1.5E-01 AF210842.1	1.5E-01 AI973157.1	1.5E-01 AF299073.1	1.5E-01 AF299073.1	1.5E-01 AW 500611.1	1.5E-01 AW500611.1	1.5E-01 U46560.1	P21303	17.1			1.5E-01   L27835.1	1.5E-01 D84476.1	P43446	4501972 NT
Most Similar (Top) Hit BLAST E Vælue	1.5E-01	1.5E-01	1.5E-01	1.5E-01	1.5E-01		1.5E-01	1.5E-01	1.5E-01 P48508	1.5E-01 Q28462	1.5E-01	1.5E-01 P30143	1.5E-01			1.5E-01	1.5E-01	1.5E-01	1.5E-01	1.5E-01	1.5E-01	1.5E-01	1.5E-01 P21303	1.55-01	1.5E-01	1.5E-01	1.5E-01	1.5E-01	1.5E-01 P43446	1.5E-01
Expression Signal	1.71	1.71	2.19	3.40	1.98	1.74	3.58	4.73	1.51	2.35	0.86	2.24	9		0.8	4.73	1.63	0.88	98.0	1.68	1.68	0.79	66.0	- 1	1.06	14.14	1.87	217	0.79	3.12
ORF SEQ ID NO:	32647		L	32852		33002	33179	33207								<u> </u>	34099	34314	34315	34322	34323			L			35245			35660
Exon SEQ ID NO:	19307	L	Ĺ			19641	25828	19820		<u> </u>		l_				20444			L	L	L		L	<u> </u>		上			ı	22117
Probe SEQ ID NO:	6128	6128	6168	6324	9376	6474	6631	6661	6672	6719	6823	6852	7118		7158	7365	7550	7764	7764	7775	7775	7919	8248	8414	8507	8594	8628	8793	8814	9038

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Top Hit Descriptor	za59e06.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:296866 3' similar to PIR:S44443 S44443 RAD23 protain homolog2 - human;	GV0000404 Human PsoriasIs Differential Display Homo sapiens cDNA	AV754819 TP Homo sapiens cDNA clane TPAAHB12 5'	AU130007 NT2RP3 Homo saplens cDNA done NT2RP3000080 5	Acipenser transmontano vitellogenin mRNA, partial cds	Human type II 3-beta hydroxysteroid dehydrogenase/ 5-delta - 4-delta isomerase gene, complete cds	Aplysia californica carboxypeptildase D mRNA, complete cds	Aplysia californica carboxypeptidase D mRNA, complete cds	P.leniusculus mRNA for integrin bela subunit	Mesocricetus auratus mRNA for collagen type XVII, complete cds	wk53h12.r1 NC_CGAP_Pr22 Homo sapiens cDNA clone IMAGE:2419176 3' similar to gb:M27608 BETA GALACTOSIDASE-RELATED PROTEIN PRECURSOR (HUMAN);	wk33h12.x1 NCI_CGAP_Pr22 Homo sapiens cDNA clone IMAGE:2419175 3' similar to gb:M27508 BETA GALACTOSIDASE-RELATED PROTEIN PRECURSOR (HUMAN);	Danio rerio transcription factor Pax9b (Pax9) mRNA, complete cds.	Claviceps purpurea ps1 gene	Claviceps purpurea ps1 gene	CM2-BT0688-210300-122-f11 BT0688 Homo sapiens cDNA	CM2-BT0688-210300-122-f11 BT0688 Homo sapiens cDNA	Homo sapiens chromosome 21 segment HS210080	Homo sapiens chromosome 21 segment HS21C080	IL5-CN0024-030300-025-D04 CN0024 Homo sapiens cDNA	qe/Ze01.x1 Soares_fetal_lung_NbHL19W Homo saplens cDNA clone IMAGE:1744536 3' sImilar to qb:M17887 60S ACIDIC RIBOSOMAL PROTEIN P2 (HUMAN);	602/28753F1 NIH_MGC_56 Homo saplens cDNA clone IMAGE:4285549 6	Rattus norvegicus chemokine CX3C mRNA, complete cds	Mus musculus mRNA for death Inducer-obliterator-1 (Dio-1)	yp87e04.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:194430 5'	Bacillus halodurans genomic DNA, section 8/14	Lymphocystis disease virus 1, complete genome	AV741272 CB Hamo sapiens cDNA clone CBDAGD04 5'	Campylobacter jejuni NCTC11168 complete genome; segment 1/6
Top Hit Database Source		EST_HUMAN		EST_HUMAN /	П	IN IN	/ IN	/ LN	JN LN		EST_HUMAN (	EST HUMAN	Π	LN		EST_HUMAN	EST_HUMAN	Γ		EST_HUMAN	EST HUMAN	HUMAN	Г		T HUMAN	Г		EST_HUMAN	
Top Hit Acession No.	6E-01 N74226.1	.5E-01 BF585465.1	.5E-01 AV754819.1	.5E-01 AU130007.1	5E-01 U00455.1	5E-01 M77144.1	.5E-01 AF007570.1	5E-01 AF007570.1	.5E-01 X98852.1	5E-01 AB027759.1	5E-01 AI814046.1	5E-01 A 814046,1	.5E-01 U40932.1	5E-01 AJ011964.1	.5E-01 AJ011964.1	.5E-01 BE088492.1	.5E-01 BE088492.1	6E-01 AL163280.2	.6E-01 AL163280.2	5E-01 AW841915.1	5E-01 Al193704.1	Ľ		.5E-01 AJ238332.1	.5E-01 R83077.1	5E-01 AP001514.1	9695413 NT	.5E-01 AV741272.1	.5E-01 AL139074.2
Most Similar (Top) Hit BLAST E Value	1.6E-01	1.5E-01	1.5E-01	1.5E-01	1.5E-01	1.5E-01	1.5E-01	1.5E-01	1.5E-01	1.5E-01	1.5E-01	1.5E-01	1.5E-01	1.5E-01	1.5E-01	1.5E-01	1.5E-01	1.6E-01	1.6E-01	1.5E-01	1.5E-01	1.5E-01	1.5E-01	1.5E-01	1.5E-01	1.5E-01	1.5E-01	1.5E-01	1.5E-01
Expression Signal	2.56	1.34	2.52	0.64	6.7	0.71	7.82	7.82	2.59	0.51	2.38	2.36	122	1.69	1.69	1.67	1.67	4.46	4.48	1.38	28.	38.98	1.62	123	5.64	1.52	1.41	2.59	7.68
ORF SEQ ID NO:	35932	36033		-	34609	36656	36761	36762			37161	37162	37242	37413	37414	37649	37850			38042							32002		31857
Exan SEQ ID NO:	22381	l	l	22660	1	23060	23163		23442		l	23551	١.	L	l '	1		ı			L	L		1_	L	1	ı		25896
Probe SEQ ID NO:	9305	9394	9401	3605	9652	10022	10125	10125	10407	10495	10516	10516	10598	10761	10761	10935	10935	11063	11063	11331	11925	12232	12629	12633	12696	12749	12778	12807	12932

Page 109 of 550 Table 4 Single Exon Probes Expressed in Placenta

_		_	_	_	_	_	_	_	_	_	_	_		_				_			_	_		-		_	,		_		_	
	Top Hit Descriptor	Sus scrofa mRNA for sodium iodide symporter	Melanoplus sanguinipes entomopoxvirus, complete genome	Homo sapiens T cell receptor beta locus, TORBV8S5P to TORBV21S2A2 region	Xenopus laevis mRNA for DNA (cytosine-5-)-methyltransferase, complete cds	yd54c01.s1 Soares fetal liver spleen 1NFLS Homo saplens cDNA clone IMAGE:112032.3'	Mus musculus growth differentiation factor 5 (Gdf5), mRNA	Thermotoga maritima section 22 of 136 of the complete genome	UI-H-Bi1-acf-a-09-0-UI s1 NCI_CGAP_Sub3 Homo saplens cDNA clone IMAGE:27140093'	Iny72d07.s1 NCI_CGAP_GCB1 Homo saplens cDNA clone IMAGE:1283821 3'	GLYCEROL-3-PHOSPHATE ACYLTRANSFERASE PRECURSOR (GPAT)	wm74d01.x1 NCI_CGAP_Ut2 Hamo saplens cDNA clone IMAGE:2441665 3'	tx56c02.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2273570 3'	bs6c02.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2273570 3'	Thermotoga maritima section 22 of 136 of the complete genome	460b01.s1 Soares fetal liver spleen (NRLS_S1 Homo sapiens cDNA clone IMAGE:453673 3' similar to	gb:X01067_ma1 IN LERLEUKIN-2 RECEP LOR ALPHA CHAIN PRECURSOR (FlowAN);contains Aluranatina element:	I CHOULIVE CICILICI II,	Homo sapiens phosphodiesterase 4A, cAMP-specifio (dunce (Drosophila)-homolog phosphodiesterase E2) (PDE4A), mRNA	Lycopersicon esculentum genomic RAPD band 26	ye15c11.s1 Strategene lung (#937210) Homo sapiens cDNA clone IMAGE:117812.3'	Candida tropicalis DNA for mitochondrial NADP-linked isocitrate dehydrogenase, complete cds	Candida tropicalis DNA for mitochondrial NADP-linked isocitrate dehydrogenase, complete cds	hr67c02.x1 NCI_CGAP_Kld11 Homo sapiens cDNA clone IMAGE:31335383'	AU117147 HEMBA1 Homo sepiens cDNA clone HEMBA1000769 5	AU117147 HEMBA1 Homo sapiens cDNA clone HEMBA1000769 5'	xb71d12.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:25817513'	601193523F1 NIH_MGC_7 Homo saplens cDNA clone IMAGE:3537581 5'	QV1-UM0036-080300-103-d09 UM0036 Homo sapiens cDNA	DKFZp761A0910_r1 761 (syrronym: hamy2) Homo sapiens cDNA clone DKFZp761A0910 5'	UI-H-BI0-aat-c-09-0-UI.s1 NCI_CGAP_Sub1 Homo sapiens cDNA clone IMACE::2710289 3'	wi04f12.x1 NCI_CGAP_CLL1 Home sapiens cDNA clone IMAGE;2389295 3' similar to SW:ICE4_HUMAN P49882 CASPASE-4 PRECURSOR;
	Top Hit Database Source	IN.	LNI	LN.	ΤN	EST_HUMAN	INT	N T	EST_HUMAN	EST_HUMAN	SWISSPROT	EST_HUMAN	EST HUMAN	EST_HUMAN	TN		HOT LINAAN	ESI DOMAIN	둗	본	EST_HUMAN	F	TN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN
	Top Hit Acession No.	1.5E-01 AJ276242,1	9631294 NT	1.4E-01 AF009663.1	1.4E-01 D78638.1	1.4E-01 T91864.1	TN 0866799	1.4E-01 AE001710.1	1.4E-01 AW135741.1	1.4E-01 AA720615.1	P30706	1.4E-01 AI933496.1	1.4E-01 AI699094.1	1.4E-01 AI699094.1	1.4E-01 AE001710.1		4 45 04 0 4 7 2 2 2 4	AA/ /020/ . I	5453861 NT	1.4E-01 AJ005180.1	1.4E-01 T90677.1	1.4E-01 AB004556.1	1.4E-01 AB004556.1	1.4E-01 BE326891.1	1.4E-01 AU117147.1	1.4E-01 AU117147.1	1.4E-01 AW082796.1	1.4E-01 BE266536.1	1.4E-01 BF378533.1	1.4E-01 AL118568.1	1.4E-01 AW015373.1	1.4E-01 AI762827.1
	Most Similar (Top) Hit BLAST E Value	1.6E-01	1.5E-01	1.4E-01	1.4E-01	1.4E-01	1.4E-01	1.4E-01	1.4E-01	1.4E-01	1.4E-01 P30706	1.4E-01	1.4E-01	1.4E-01	1.4E-01		70	1.4E-UI	1.4E-01	1.4E-01	1.4E-01	1.4E-01	1.4E-01	1.4E-01	1.4E-01	1.4E-01	1.4E-01	1.4E-01	1.4E-01	1.4E-01	1.4E-01	1.4E-01
	Expression Signal	6.61	2.26	1.23	3.24	2.99	1.46	1.84	1.27	14.84	1.02	3.34	9.45	9.45	4.28			7.5	0.79	0.62	6.21	4.33	4.33	3.17	4.45	4.45	3.7	1.51	2.48	0.71	1.78	0.73
	ORF SEQ ID NO:	31932						28032			28793								30920	31406	31598	31621	L			33162			33286			
	Exan SEQ ID NO:	25769	26138	13526	14108		14936	14939	15097	l	15669	i i	ı		17495		17000	800/	17933	18436	18622	18644	18644	19595	19771	19771	19859	19873	19895	20359	20617	1
	Probe SEQ ID NO:	13183	13227	310	933	1288	1787	1790	1954	2042	2544	2853	4289	4289	4352		7607	4031	4798	5322	5421	442	5444	6427	6611	6611	6701	6715	6239	7276	7546	7618

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Table 4
Single Exon Probes Expressed in Placenta

			_,	_				_	_		_		_	_	_	_	_		_		-	_	_	_	т	_	-т		_	_	_
. Top Hit Descriptor	ye90f11,r2 Stratagene placenta (#937225) Homo sapiens cDNA clone IMAGE:68973 5' simitar to contains Alu repotitive element	Oryctolagus cuniculus fructose 1,6, bisphosphate aldolase (AldB) gene, complete cds	q190b12.x1 Scares_NihHMPu_S1 Homo sapiens cDNA done IMAGE:1879583 3'	601894760F1 NIH_MGC_19 Homo capiens cDNA clone IMAGE:4124199 5	AV659047 GLC Homo sapiens cDNA clone GLCFSH06 3'	th92b12.x1 Soares_NSF_FB_9W_OT_PA_P_S1 Homo sapiens cDNA done IMAGE:2126111 3' similar to TR:002710 002710 GAG POLYPROTEIN. ;	EST178192 Colon carcinoma (HCC) cell line Homo sapiens cDNA 5 end	df38b03.y1 Morton Fetal Cochlea Homo sapiens cDNA clone IMAGE:2487485 5'	y10h05.rl Soares placenta Nb2HP Homo saplens cDNA clone IMAGE:138873.5'	y10h05.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:138873 5'	601895485F1 NIH_MGC_19 Homo sepiens cDNA clone IMAGE:4124824 5'	2d94a04.r1 Soares_feta  heart_NbHH19W Homo saplens cDNA clone IMAGE:357102 5' smiler to contains	מפוונתו עבע ופלפתיה מפוופוני	M.vannielij genes rpoH, rpoB and rpoA	M.vannielii genes rpoH, rpoB and rpoA	Homo sapiens PHEX gene	Homo sapiens PHEX gene	Drosophila melanogaster signal transducting adaptor protein (STAM), serine threorine kinase lal (IAL), and zine finger protein (DNZ1) genes, complete cds	C,perfringens ORF for putative membrane transport protein	Macromitrium levatum small ribosomal protein 4 (rps4) gene, chloropiast gene encoding chloropiast protein,	Partial cus	d/29/08.y1 Morton Feta Coonlea Homo sapiens CLINA clone INACE: 2400094 3	d/29h08.y/ Morton Fetal Cochlea Homo sapiens cDNA clone IMAGE:2485094.5	MR3-ST0218-211299-013-a08 ST0218 Hamo sapiens cDNA	MR3-ST0218-211299-013-a08 ST0218 Homo sapiens cDNA	yd47d03.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:111365 5'	Bacillus subtilis complete genome (section 14 of 21): from 2590451 to 2812870	oagga03.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1320364 3'	ly70c05.r1 Scares breast 2NbHBst Homo sapiens cDNA clone IMAGE:154088 5	xd73e10 x1 Sogres_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2603274 3	ye47g10.r1 Scares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:120930 5
Top Hit Database Source	EST_HUMAN	LN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST HUMAN	EST_HUMAN	1444 III - 1401	ES! HOMAN	Ę	NT	NT	NT	Į	N		Į.	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	NT	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST HUMAN
Top Hit Acession No.	1.4E-01 T53770.1	1.4E-01 U85845.1	1.4E-01 Al305192.1	1.4E-01 BF310258.1	1.4E-01 AV659047.1			1.4E-01 AW023636.1	1.4E-01 R62746.1	1.4E-01 R62746.1	E-01 BF310959.1	, , , , , ,	1.4E-01 W93411.1	E-01 X73283.1	E-01 X73293.1	E-01 Y10196.1	E-01 Y10198.1	AF121361.1	1.4E-01 X66092.1		E-01 AF023813.1	E-01 AW021908.1	E-01 AW021908.1	E-01 BF375285.1	E-01 BF375285.1	E-01 T84293.1	4E-01 Z99117.1	1.4E-01 AA811480.1	4E-01 R53400.1	4E-01 AW104982.1	4E-01 T96102.1
Most Similar (Top) Hit BLAST E Value	1.4E-01	1.4E-01	1.4E-01	1.4E-01	1.4E-01	1.4E-01	1.4E-01	1.4E-01	1.4E-01	1.4E-01	1.4E-01	•		1.4	1.4	1.4	1.4				4.	1.4E-01	1.4E-01	1,4	1.4	1.4			÷	1.1	1.
Expression Signal	0.63	96'0		0.54	1.32	9.0	40.4	0.76	1.07	1.07	8.52			0.54	0.54						0.89	0.81	0.81	0.76		0.51	0.7	1.32	2.67		1.58
ORF SEQ ID NO:	34167	34345	1			!	35738		35951		l				36181		36195					36931	36932				37481		37783	3 37985	
SEQ ID NO:	20691	i		1	1	22063	22193	1	1	İ	22463				22612	L	22623	L	١.	ľ	i	23328	l	l_	Ŀ		23858		24156	24348	24416
Probe SEQ ID NO:	7621	7799	7932	8162	8670	8984	9114	9194	9322	9322	9388		9475	9547	9547	9558	9558	9849	10009		10192	10293	10293	10463	10463	10680	10825	10948	11081	11282	11354

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Top Hit Descriptor	ye47g10.r1 Soares fetal liver spleen 1NFLS Homo septiens cDNA clone IMAGE:120930 5	INTEGRIN ALPHA-5 PRECURSOR (FIBRONECTIN RECEPTOR ALPHA SUBUNIT) (INTEGRIN ALPHA- F) (VLA-5) (CD49E)	C. perfringens ORF for putative membrane transport protein	UI-H-Bi0-aat-c-09-0-UI,s1 NCI_CGAP_Sub1 Homo saplens cDNA clone IMAGE:2710289 3'	Borrelia burgdorferi glyceraldehyde-3-phosphate dehydrogenase (GAPDH), phosphoglycerate Kinase (PGK), triosephosphate isomerase (TPI) genes, complete cds	M.musculus p16K gene for 16 kDa protein	Mus musculus neuromedin U precursor (Nmu) gene, partial cds; tPhLP (Tphlp) gene, partial cds; CLOCK (Clock) gene, complete cds; PFT27 (Pft27) gene, complete cds; and H5AR (H3ar) gene, complete cds	P.salina plastid gene secY	Rattus norvegicus desmin (Dcc), mRNA	601658490R1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3885671 3	601315638F1 NIH_MGC_8 Homo seplens cDNA clone IMAGE:3634329 6'	Fugu rubripes putative neurotransmitter receptors, YDR140w homolog, and glycinamide ribonucleotide	transformylase (GART) genes, complete cds	Synechocystis sp. PCC6803 complete genome, 23/21, 2858/67-3002965	TYROSINE-PROTEIN KINASE I RANSFORMING PROTEIN ABL	V.planifolia mRNA for methyltrensferase	Mus muscutus mRNA for prolidase, complete cds	MR0-H10208-221299-204-c08 H	Homo sapiens G protein-coupled receptor 50 (GPR50) mKNA	Homo sapiens G protein-coupled receptor 50 (GPR50) mKNA	Homo sapiens gene for NBS1, complete cds	Human calicivirus HU/NLV/Girlington/93/UK RNA for capsid protein (ORF2), strain HU/NLV/Girlington/93/UK	Human calicivirus HU/NLV/Girlington/93/UK RNA for capsid protein (ORF2), strain HU/NLV/Girlington/93/UK	P.dumerilii histone gane cluster for core histones H2A, H2B, H3 and H4	Rattus norvegicus A-kinase anchor protein mRNA, complete cds	Botrytis cinerea strain T4 cDNA library under conditions of nitrogen deprivation	Botrytis cinerea strain T4 cDNA library under conditions of nitrogen deprivation	AV712467 DCA Homo saplens cDNA clone UCAAFFUS S
Top Hit Database Source	EST_HUMAN	SWISSPROT	Π	EST HUMAN	F F	Ľ	L L	L		EST_HUMAN (	EST_HUMAN (			٦	ISSPROT	NT		r HUMAN			۲N	۲N	노	ΙN	NT	NT		EST_HUMAN
Top Hit Acession No.	4E-01 T96102.1		-	73.1	.4E-01 U28760.1		.4E-01 AF146793.2	.4E-01 X74773.1	11968117 NT	1.4E-01 BE964835.2	.4E-01 BE513802.1		1.4E-01 AF083221.1	1.4E-01 D64004.1	P10447	1.4E-01 X69192.1	1.4E-01 D82983.1	1.4E-01 AW377998.1	4758467 NT	4758467 NT	1.3E-01 AB013139.1	1.3E-01 AJ277606.1	1.3E-01 AJ277606.1	1.3E-01 X53330.1	1.3E-01 AF139518.1	1.3E-01 AL117078.1	1.3E-01 AL115265.1	1.3E-01 AV712467.1
Most Similar (Top) Hit BLAST E Value	1.4E-01	1 4E-01 P08648	1.4E-01	1.4E-01	1.4E-01	1.4E-01	1.4E-01	1.4E-01	1.4E-01	1.4E-01	1.4E-01		1.4E-01	1.4E-01	1.4E-01 P10447	1.4E-01	1.4E-01	1.4E-01	1.3E-01	1.3E-01	1.3E-01	1.3E-01	1.3E-01	1.3E-01	1.3E-01	1.3E-01	1.3E-01	1.3E-01
Expression Signal	1.58	236	185	1.57	2.07	1.51	10.18	88.4	3.28	1.71	2.83		7.52	4.02	3.2	1.45	3.36	1.68	227	2.27	1.88	2.43	2.43	1.55	1.26	2.14	2.04	1.67
ORF SEQ ID NO:	38072				37570		38724													26577		26866	26867					1 27462
Exan SEQ ID NO:	24418	1	ı	1		1		25382		İ			25482	25493	26193	1	i		L_	L	13735	13839	13839	L	L	上	↓_	14401
Probe SEQ ID NO:	11354	442EB	11872	11613	11757	11816	12038	12560	12574	12605	12627		12724	12742	12834	12928	13084	13178	332	332	542	953	653	298	917	1052	1151	1242

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	_		_			_	-					_	_	_	_			_	_	_	_	_	_	_	_			_	_	7
Top Hit Descriptor	Homo saplens adapter protein CMS mRNA, complete cds	Mus musculus procollegen, type XI, alpha 1 (Col11a1), mRNA	Botrytis cinerea strain T4 cDNA library under conditions of nitrogen deprivation	Rhodopseudomonas addophila pueB5, pucA5, pucA6, pucA6, pucA7, pucA7, pucA8, pucA8 and pucC genes and OR+161	RC4_ST0173-191099-032-d12 ST0173 Home septens cDNA	Archaeoglobus fulgidus section 91 of 172 of the complete genome	Carassius auratus keratin type I mRNA, complete cds	Homo sapiens transcription factor IGHM enhancer 3, JM11 protein, JM4 protein, JM5 protein, T54 protein,	JM10 protein, A4 differentiation-dependent protein, triple LIM domain protein 6, and synaptophysin genes, complate cyte, and L-tune calculum channel a>	Bovine branched chain alpha-keto acid dihydrolipoyi transacylase mRNA, complete cds	Pyrococcus harkoshii OT3 genomio DNA, 1-287000 nt. position (1/7)	Pyrocaccus horikoshii OT3 genamic DNA, 1-287000 nt. positian (1/7)	Homo sapiens DD4 gene for dihydrodiol dehydrogenase 4 [AKR 1C4], exon 2	Rattus norvegicus Fibrinogen, gamma polypeptide (Fgg), mRNA	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 77	Human calicivirus HUNLV/Girlington/93/UK RNA for capsid protein (ORF2), strain HUNLV/Girlington/93/UK	Human calicwrus HUMLV/Girlington/93/UK RNA for capsid protein (ORF2), strain HUMLV/Girlington/93/UK	Bacteriophage SPBc2 complete genome	QV3-DT0018-081299-036-a03 DT0018 Homo sepiens cDNA	Schistosoma mansoni fructose bisphosphate aldolase mRNA, complete cds	xv23f10.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2813995 3'	Homo sapiens chromosome 21 segment HS21C080	Bovine branched chain alpha-keto acid dihydrollpoyl transacylase mRNA, complete cds	601126096F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:2990063 5'	602154308F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4295544 5'	Pyrococcus harikoshii OT3 genomic DNA, 994001-1166000 nt. position (5/7)	ha07b06.x1 NCI_CGAP_Kid12 Homo saplens cDNA clone IMAGE:2872979 3' similar to contains L1.b1 L1	LT I Eperuve Berneitt, OIAL INANGEL AND AND EINANGS Home saniens cDNA	AVOIDINGS TOWN TO THE TOWN TO THE TOWN TO THE TOWN TOWN TO THE TOWN TOWN TOWN TOWN TOWN TOWN TOWN TOWN	Emericella nidulans UNA-dependent KNA polymerase if KPB 140 (KPDZ) gene, parual cus
Top Hit Database Source	NT	٦	NT	IN	POT HIMAN	TN TN	NT		H	LN	NT	TN	NT	TN	NT	INT	NT	١N	EST_HUMAN	TN	EST_HUMAN	IN	NT	EST_HUMAN	EST_HUMAN	NT		EST HUMAN	ESI HOMAN	-N
Top Hit Acession No.	3E-01 AF146277.1	TN 2680957 NT	3E-01 AL117078.1	3E-01 AJ243578.1	Ţ	Ī			0E 04 A E408770 4		-			6978840 NT	.3E-01 AL161581.2	.3E-01 AJ277606.1	.3E-01 AJ277606.1	.3E-01 AF020713.1	.3E-01 AW364341.1		.3E-01 AW273741.1	.3E-01 AL163280.2	.3E-01 M21572.1	.3E-01 BE272339.1	.3E-01 BF679654.1	3E-01 AP000005.1		3E-01 AW 466988.1	.3E-01 AW604417.1	.3E-01 AF107793.1
Most Similar (Top) Hit BLAST E Value	1.3E-01	1.3E-01	1.3E-01	1.35-01	1 25 04	1.3E-01	1.3E-01		10.0	13F-01	1.3F-01	1.3E-01	1.3E-01	1.3E-01	1.3E-01	1.3E-01	1.3E-01	1.3E-01	1.3E-01	1.3E-01	1.3E-01	1.3E-01	1.3E-01	1.3E-01	1.3E-01	1.3E-01		1.35-01	1.35-01	1.3E-01
Expression Signal	26.0	1.02	2.73	1.09	1 20	3.31	2.78		č	1.11	0 85	0.85	1.65	990	1.08	0.88	0.88	0.82	3.74	1.82	21.62	1.19	0.61			0.78			1.83	0.92
ORF SEQ ID NO:			28259				28880		90000		97995					26866	26867			30415			30717	30776	_	31401		$\perp$	31690	
SEQ ID NO:	14628	_	L	-	ı		}_	1		16704	1	1		L		13839	13839	L	L	L		L	17738	17792	17883	18431	<u></u>	- 1	- 1	18812
Probe SEQ ID NO:	1475	1905	2014	2230	Yack	2455	2653		9	3530	3816	3816	3822	3005	4096	4162	4162	4257	4274	4281	4302	4434	4601	4656	4748	5314		5440	2478	5618

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Top Hit Descriptor	Hepatitis C virus 68_CL10 genome polyprotein gene, partial cds	601874591F1 NIH_MGC_54 Homo septens cDNA clone IMAGE:4101119 5'	602039337F2 NCI_CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4177233 5'	602039337F2 NCI_CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4177233 5'	Schizosaccharomyces pombe gene for Alp41, complete cds	C.jacchus intron 4 of visual pigment gene (red allele)	2673 Human retina cDNA randomly primed sublibrary Homo sapiens cDNA	601465957F1 NIH_MGC_67 Homo sapiens cDNA done IMAGE:3869079 5'	601465957F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3869079 5'	602044345F1 NCI_CGAP_Brn67 Homo saptens cDNA clone IMAGE:4181866 5'	yr33d02.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:207075 5'	601126096F1 NIH_MGC_9 Homo sepiens cDNA clone IMAGE:2990063 5'	Homo sapieno PRO0611 protein (PRO0611), mRNA	602187015T1 NIH_MGC_49 Homo sapiens cDNA clone IMAGE:4299074 3'	Homo sapiens TED protein (TED), mRNA	S.cerevisiae chromosome IV reading frame ORF YDL054c	Homo sapiens core histone macroH2A2.2 (MACROH2A2), mRNA	602187015T1 NIH_MGC_49 Homo sapiens cDNA clone IMAGE:4299074 3'	y39g11.r1 Soares fetal liver spleen 1NFLS Homo sepiens cDNA clone IMAGE:129284 5' similar to SP:RL2B RAT P29316 60S RIBOSOMAL PROTEIN;	y/39g11.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:129284 5' similar to	SP:RL2B_RAT P29316 60S RIBOSOMAL PROTEIN;	Plutella xylostella granulovirus, complete genome	Plutella xylostella granulovirus, complete genome	Oryctolagus cuniculus H+,K+-ATPase alpha 2c subunit mRNA, complete cds	J7837F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA clone J7837 5' similar to B-CELL	RECEPTOR ASSOCIATED FROTEIN (BAP) 29	Rattus norvegicus peptidyl argitrine deiminase, type IV (Pdi4), mRNA	MR2-CT0222-201099-001-e01 CT0222 Homo sapiens cDNA	Homo sapiens chromosome 21 segment HS21C046	AU121237 HEMBB1 Homo sapiens cDNA clone HEMBB1002387 5	2820637.3prtme NIH_MGC_7 Horno saplens cDNA clone IMAGE:2820637 3'	MR4-BT0358-130700-010-h08 BT0358 Homo sapiens cDNA	MR4-TN0112-120900-102-e08 TN0112 Homo sapiens cDNA
Top Hit Database Source	IN	EST_HUMAN	EST_HUMAN	EST_HUMAN	LN	NT	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	LN	EST_HUMAN	IN	LN	N	EST_HUMAN	EST HUMAN		EST_HUMAN	LN	. 1N	ΙN		EST HUMAN	NT	EST_HUMAN	LN	EST_HUMAN	EST HUMAN	EST HUMAN	EST_HUMAN
Top Hit Acession No.	1.3E-01 AF056880.1	1.3E-01 BF210920.1	1.3E-01 BF527281.1	1.3E-01 BF527281.1	1.3E-01 AB031326.1			1.3E-01 BE782926.1	1.3E-01 BE782926.1	1.3E-01 BF529560.1	148664.1	1.3E-01 BE272339.1	11423294 NT	1.3E-01 BF690522.1	11421556 NT	774102.1	8923919 NT	1.3E-01 BF690522.1	311172.1		311172.1	11068003 NT	11068003 NT	1.3E-01 AF023129.1		V86348.1	8393940	1.3E-01 AW861599.1	1.3E-01 AL163246.2	1.3E-01 AU121237.1	1.3E-01 AW247836.1	1.3E-01 BF330999.1	1.3E-01 BF092708.1
Most Similar (Top) Hit BLAST E Value	1.3E-01	1.3E-01	1.3E-01	1.3E-01	1.35-01	1.3E-01 X88891.1	1.3E-01)\	1.3E-01	1.3E-01	1.3E-01	1.3E-01 H48664.1	1.3E-01	1.3E-01	1.3E-01	1.3E-01	1.3E-01 Z74102.1	1.3E-01	1.3E-01	1.3E-01 R11172.1		1.3E-01 R11172.1	1.3E-01	1.3E-01	1.3E-01		1.3E-01 N86348.1	1.3E-01	1.3E-01	1.3E-01	1.3E-01	1.3E-01	1.3E-01	1.3E-01
Expression Signal	0.67	0.72	0.58	0.58	18.92	2.26	0.74	0.7	0.7	0.74	1.97	62.0	1.68	1.32	99.0	4.24	4.96	1.26	25.0		0.67	69.0	69.0	4.19		0.73	1.07	96.0	1.08	0.65	0.45	2.31	1.34
ORF SEQ ID NO:		32338	32621	32622	33163	33246		33628	33629		-		34762	34797	35080			35342	35770		35771	09098		36204				08698	37244	_	37454		
Exan SEQ ID NO:	18895	19032	19287	L	19772	19856	20242			20289	20490	21228	21242		21650	21621	21861	21805	22227		22227	22494		22634				23370	25864	23776	L		24515
Probe SEQ ID NO:	5702	5842	6107	6107	6612	8699	6927	6974	6974	7155	7412	8146	8160	8192	8469	8540	8580	8725	9149		9149	9420	9420	9672		9973	10257	10335	10603	10743	10797	10868	11455

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Top Hit Descriptor	Mus musculus cofilin 2, muscle (Citz), mRNA	602087045F1 NIH_MGC_83 Home sapiens cDNA clone IMAGE:4251346 5'	602087045F1 NIH_MGC_83 Homo saplens cDNA clone IMAGE:4251346 5'	601158052F1 NIH_MGC_21 Hamo sapiens cDNA clone IMAGE:3504804 5'	Thermococcus liforalis trehalose/maltose transporter operon including trehalose/maltose binding protein	(matc) and inner memorane proteins wait (mair) and matc (maic) genes, complete cos	6014/3368F1 NIH MIGC 68 Home sapiens cunA cione IMAGE:36/6208 3	602/139/60F1 NIH MGC 46 Homo septens cone IMACE: 4300863 5	601462741F1 NIH_MGC_67 Home sapiens cDNA clone IMAGE:3866003 5	Gallus gallus scyc1 gene for lymphotactin, exors 1-3	Ephydatia fluvlatilis mRNA for sALK-6, complete cds	wu24409.x1 Soares_Diockgraefe_colon_NHCD Homo sapiens cDNA clone IMAGE:2520977 3' similar to TR-050287 OR0287 KIAAARSO PROTEIN	THEORY OF A INC. COATS Broads Live a consistent at Table A clean MAA CE 20008500 St similar to abil 105750 most	TOSON, AT INC. LOSAT DITAS HOMO SEPTENS CONTA CIONE INTACE. AUROSOSOS SIGNIEN DE COSTON TINEN ANNEXIN V (HUMAN);	Dictyostellum discoldeum ORF DG1016 gene, partial cds	Hamo sapiens colon cancer antigen NY-CO-45 mRNA, partial cds	AU149146 NT2RM4 Homo saplens cDNA clone NT2RM4001691 3'	AU 149146 NT2RM4 Hamo saplens cDNA clone NT2RM4001691 3'	AV735249 cdA Homo sapiens dDNA clone cdAAJB11 5'	Thermoplasma acidophllum complete genome; segment 4/5	al48e09.s1 Soares_NFL_T_GBC_S1 Homo saplens cDNA clone IMAGE:1460584 3' similar to TR:Q16671 Q16671 ANT-MULLERIAN HORMONE TYPE II RECEPTOR PRECURSOR. ;	NUCLEAR FACTOR OF ACTIVATED T-CELLS, CYTOPLASMIC 4 (T CELL TRANSCRIPTION FACTOR	NFAT3) (NF-ATC4) (NF-AT3)	qt69f09.x1 NCI_CGAP_Esa2 Hamo sapiens cDNA done IMAGE:19605533'	H.sapiens DNA for endogenous retroviral like element	UI-H-BI3-aki-e-10-0-UI.s1 NOL_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:27345543'	601821567F1 NIH_MGC_62 Homo sapiens cDNA clone IMAGE:4046224 5'	HSAAAEBZT TEST1, Human adult Testis tissue Homo sapiens cDNA	QV3-BN0046-220300-129-f10 BN0046 Homo sapiens cDNA	Human E1A enhancer binding protein (E1A-F) mRNA, partial cds	as80c09.x1 Barstead colon HPLRB7 Homo sapiens cDNA clone IMAGE:2335024 3' similar to gb:L05095 60S RIBOSOMAL PROTEIN L30 (HUMAN);
Top Hit Database Source		EST_HUMAN	EST_HUMAN		,	Т	7	٦	EST_HUMAN	NT	IN	NAME TO T	LO LO LO LO LO LO LO LO LO LO LO LO LO L	EST_HUMAN	Ŋ	Į,	EST_HUMAN	EST_HUMAN	EST_HUMAN	NT	EST HUMAN		SWISSPROT	EST_HUMAN	NT	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	NT	EST_HUMAN
Top Hit Acession No.	8671745 NT	3E-01 BF677328.1		.3E-01 BE279449.1		3E-01/AF012836.1	.3E-01 BE619364.1	.3E-01 BF683555.1	3E-01 BE618346.1	3E-01 AJ242790.1	3E-01 AB026829.1	2E 04 AM/001114 1		2E-01 AI421744.1	2E-01 U66912.1	ZE-01 AF039442.1	.2E-01 AU149146.1	.2E-01 AU149146.1	.2E-01 AV735249.1	.2E-01 AL445066.1	ZE-01 AA897474.1		2E-01 Q14934	.2E-01 A1285402.1	.2E-01 X89211.1	.2E-01 AW 449368.1	.2E-01 BF248490.1	2E-01 Z21405.1	2E-01 AW 996556.1	ZE-01 U18018.1	2E-01 AI720470.1
Most Similar (Top) Hit BLAST E Value	1.3E-01	1.3E-01	1.3E-01	1.3E-01		1.3E-01	1.3E-01	1.3E-01	1.3E-01	1.3E-01	1.3E-01	1 25.04	2 - 12:	1.2E-01	1.2E-01	1.25-01	1.2E-01	1.2E-01	1.2E-01	1.2E-01	1.25-01		1.2E-01	1.2E-01	1.2E-01	1.2E-01	1.2E-01	1.2E-01	1.2E-01	1.2至-01	1.2E-01
Expression Signal	3.2	2.42	2.42	7.96	,	1.41	1.72	1.52	2.13	6.39	1.31	1 07	2	13.87	1.42	3.82	2:32	2.32	3.35	0.94	0.94		1.1	2.88	25.75	1.66	1.66	0.99	1.84	1.18	1.9
ORF SEQ ID NO:		38354	38355	38581			38708	38739	32080				†	26668			27636							27919			28514		28893		29162
Exon SEQ ID NO:	24585	24667	ı	24883	<u> </u>	L				25368	25627	77880	Т	13631	L	13753	14562	14562	14568	14672	14689	ŀ		14834	14957	15113	15386	15578	15779	16083	16143
Probe SEQ ID NO:	11529	11616	11616	11895		12000	12023	12052	12399	12543	1,2964	9000	C287	36	437	561	1408	1408	1414	1419	1536		1660	1682	1808	1970	2253	2450	2656	2905	2967

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Top Hit Descriptor	Human creatine khase-B mRNA, complete cds	Wheat mRNA for a group 3 late embryogenesis abundant protein (LEA)	QV1-BT0259-261099-021-405 BT0259 Homo sapiens cDNA	Methanococcus jannaschii section 142 of 160 of the complete genome	Bacillus subtilis complete genome (section 15 of 21); from 2795131 to 3013540	Wheat mRNA for a group 3 late embryogenests abundant protein (LEA)	Wheat mRNA for a group 3 late embryogenesis abundant protein (LEA)	Bacillus subtilis complete genome (section 15 of 21): from 2795131 to 3013540	601810786R1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4053688 3'	P.clarkii mRNA; repeat region (ID 2MRT7)	P.clarkii mRNA; repeat region (ID 2MRT7)	Chicken neural cell-adhesion molecule (N-CAM) gene, exon 19	W. suaveolens mitochondrial orf1	m63c04.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1282950 3'	Homo sapiens calclum channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively	paolids	zc08d02.r1 Soares_parathyroid_tumor_NbHPA Homo sapiens cDNA clone IMAGE:321699 5'	Hano saplens gene encoding plakophilin (exons 1-13)	M.domestica Borkh. Granny Smith adh mRNA for alcohol dehydrogenase	601493518F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3895613 5	MATING-TYPE P-SPECIFIC POLYPEPTIDE PI	ILO-CT0031-221099-113-e04 CT0031 Homo saplens cDNA	Mouse galactosyltransferase mRNA, complete cds	rx85c01.s1 NCI_CGAP_GCB1 Homo sapions cDNA clone (MAGE:12690243)	602023112F1 NCI_CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4158386 5'	yp80f04.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:193769 5'	yp80f04.r1 Soares fetal liver spieen 1NFLS Homo sapiens cDNA clone IMAGE:193759 5'	Homo saplens partial ILF3 gene for interleukin enhancer binding factor 3 (alternative transcripts drbp76,	drbp76 gamma, drbp76 alpha and ILF3)	PM3-BN0137-203300-002-f09 BN0137 Homo sapiens cDNA	wc99g03.x1 NCI_CGAP_Co3 Homo sepiens cDNA clone (MAGE:2328804 3' similer to SW:GST2_HUMAN   0.98735 MICROSOMAL GLUTATHIONE S-TRANSFERASE II:	NADH-UBIQUINONE OXIDOREDUCTASE B22 SUBUNIT (COMPLEX I-B22) (CI-B22)	et71b10.x1 Barstead cdon HPLRB7 Homo sapiens cDNA cione IMAGE:2377435 3'
Top Hit Database Source	N	١	EST_HUMAN		LV.		LΝ	LN.	HUMAN		INT	INT	Į.	EST_HUMAN		닐	EST_HUMAN		N	EST_HUMAN	Г	EST_HUMAN		EST_HUMAN	EST_HUMAN	EST_HUMAN	Г	Г	F	EST_HUMAN	EST HUMAN	Т	П
Top Hit Acession No.	1.2E-01 M16364.1	1.2E-01 X56882.1	1.2E-01 AW370668.1	1.2E-01 U67600.1	1.2E-01 Z99118,1	1.2E-01 X56882.1	1.2E-01 X56882.1	1.2E-01 Z99118.1	1.2E-01 BF128551.1	1.2E-01 Z54255.1	1.2E-01 Z54255.1	1.2E-01 M15861.1	1.2E-01 X73416.1	1.2E-01 AA744369.1		1.2E-01 AF223391.1	1.2E-01 W33035.1	1.2E-01 Z98266.1	248234.1	1.2E-01 BE620945.1	P10842	1.2E-01 AW845275.1	1.2E-01 M26925.1	1.2E-01 AA747535.1	1.2E-01 BF347985.1	1.2E-01 H47799.1	1.2E-01 H47799.1		1.2E-01 AJ271741.1	1.2E-01 BE007072.1	1 2F-01 Al913753 1	002369	1.2E-01 AI832681.1
Most Similar (Top) Hit BLAST E Value	1.2E-01	1.2E-01	1.2E-01	1.25-01	1.2E-01	1.2E-01	1.2E-01	1.2E-01	1.25-01	1.2E-01	1.2E-01	1.25-01	1.2E-01	1.2E-01		1.2E-01	1.25-01	1.2E-01	1.2E-01	1.2E-01	1.2E-01 P10842	1.2E-01	1.2E-01	1.2E-01	1.2E-01	1.2E-01	1.2E-01		1.2E-01	1.2E-01	1 2F-01	1.2E-01 Q02369	1.2E-01
Expression Signal	3.44	16.0	2.52	0.74	99.0	1.12	1.12	1.22	0.95	2.1	2.1	65.0	1.04	0.89		0.93	2.5	1.65	1.14	1.9	0.81	2.26	1.52	0.58	1.18	0.64	0.64		0.62	1.13	2 45	0.64	99'0
ORF SEQ ID NO:		29265					29790			30426	30427	30552		31433		31591	31601		31885					33101	33338	33731	33732		34320		34751		35119
Exon SEQ ID NO:				l	1		16774		17024		17441	17571	18072	18567		18617	18626	18683	18816	L	L.	_		L	19940	20288			20829	21158	21231	1_	Ш
Probe SEQ ID NO:	3001	3068	3302	3330	3568	3610	3610	3694	3865	4298	4298	4431	4942	5364		5415	5425	5484	5622	6329	6377	6428	6493	6561	6785	7154	7154		7772	8076	8149	8197	8504

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Probe SEQ ID NO:	Exan SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST·E Value	Top Hit Acessian No.	Top Hit Detabase Source	Top Hit Descriptor
8590	21671		10.76	-	2E-01 AW083652.1	EST_HUMAN	xz48407.x1 NCI_CGAP_Eso2 Homo sepiens cDNA clone IMAGE:2587597 3' similar to gb:M13452 LAMIN A (HUMAN);
8611	21691		3.76	7	.2E-01 AF053772.1	FN	Staphylococcus aureus plasmid pSK23 putative recombinase Sin (sin) gene, partial cds; and transcriptional regulator QacR (qacR) and multidrug efflux protein QacB (qacB) genes, complete cds
8649	21729	35266		-	J03956.1	TN	N.crassa vacuolar ATPase 57-Kd subunit (vma-2) gene, complete cds
8649	21729		1.09	_	.2E-01 J03956.1	TN	N.orassa vacuolar ATPase 57-Kd subunit (vma-2) gene, complete cds
8800			1.02	1	1.1	TN	Homo saplens Xq pseudoautosomal region; segment 2/2
8887	1		1.44	1	2E-01 U32714.1	NT	Haemophilus influenzae Rd section 29 of 163 of the complete genome
8920	21889		77.0	1.2E-01		NT	M.musculus DNA fragment of Apolipoprotein B gene
17776	22767	36338	1.3	-	.2E-01 X77961.1		S.cerevisiae HXT5 gene
10209	23245		6.0	+	2E-01 AV710857.1	EST_HUMAN	AV710857 Cu Homo sapiens cDNA clone CuAAKE08 5'
11125	24197		2.55	1	.2E-01 D26184.1	NT	Yeast MPT5 gene for suppressor protein, complete cds
11320	24383		3.03	-	2E-01 BE962324.2	EST_HUMAN	601655578R1 NIH_MGC_65 Homo sepiens oDNA clone IMAGE:3846283 3'
11414	ı		1.73	-	2E-01 BF314481.1	EST_HUMAN	601900763F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4130103 5'
11533	ı	38264	2.78	1	.2E-01 AF190493.1		Homo sapiens dynein intermediate chain DNAI1 (DNAI1) gene, exon 17
11593	24646		1.72	1	.2E-01 R40249.1	EST_HUMAN	yf80c02.s1 Sogres infant brain 1NIB Homo sapiens cDNA clone IMAGE:28880 37
11798	24788		2.47	_	.2E-01 M65109.1	TN	Rabbit glycogen-associated protein phosphatase regulatory subunit (RG1) mRNA, complete cds
12161	25128		2.09	-	2E-01 AV658033.1	EST_HUMAN	AV658033 GLC Homo sepiens cDNA clane GLCFIB123'
12522	25355		4.37		2E-01 AJ271736.1	LN	Homo sapiens Xq pseudoautosomal region; segment 2/2
12814		31544	2	-	2E-01 Q04912	SWISSPROT	MACROPHAGE-STIMULATING PROTEIN RECEPTOR PRECURSOR (MSP RECEPTOR) (P185-RON) (CDW136) (CD136 ANTIGEN)
	1						Drosophila melanogaster strain Oregon R potential RNA-binding protein gene, complete cds; and syntaxin
12732	25486		1.65	_	.2E-01 AF188892.1	NT	gene, partial cds
12734	1_		18.32		.2E-01 AF039442.1	TN	Homo sapiens colon cancer antigen NY-CO-45 mRNA, partial cds
12863			4.1	1.2E-01	.2E-01 X53981.1	LN	R.norvegicus NF68 gene for 68kDa neurofilament
12968	L	31981	4.89	٦	2E-01 AI299903.1	EST_HUMAN	qn20g05.x1 NCL CGAP_Lu5 Hano sepiens cDNA cione IMACE:1898840 3/
12992	L		3.46		.2E-01 L10187.1	Z	Xenopus laevis integrin alpha 3 subunit mRNA, partial cds
12997	L		6.44		.2E-01 096433	SWISSPROT	CYCLINT
13031	25679	31960	1.47		2E-01 AE004428.1	TN	Vibrio cholerae chromosome II, section 85 of 93 of the complete chromosome
13221	25795		1.23	1	2E-01 AF090141.1	NT	Chryseobacterium meningosepticum GOB-1 carbapenemase gene, complete ods
578	l	26792		1	.1E-01 AI561003.1	EST_HUMAN	th18d08.x1 NCI_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2167983 3
830	13815	26838	1.33		1.1E-01 AA568006.1	EST_HUMAN	nm08g11.s1 NCI_CGAP_Co10 Homo sapiens cDNA clone IMAGE:1059620 3' similar to gb:X06985_ma1 HEME OXYGENASE 1 (HUMAN);

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Top Hit Descriptor	602129847F1 NIH_MGC_56 Homo sapiens cDNA dane IMAGE:4286771 5'	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 60	EST384142 MAGE resequences, MAGL Homo sapiens cDNA	Synechocystis sp. PCC6803 complete gename, 23/27, 2868767-3002965	AU140363 PLACE2 Homo saplens cDNA clone PLACE2000403 5'	Homo sapiens mRNA for putative serine/threonine protein kinase, partial	Mus musculus pre T-cell antigen receptor alpha (Ptcra), mRNA	Rattus norvegicus Procollagen II abha 1 (Col2a1), mRNA	RC0-ST0379-210100-032-g04 ST0379 Hamo sapiens cDNA	interleukin-12 p35 subunit [mice, Genomic, 700 nt, segment 4 of 5]	HSC1RF022 normalized infant brain cDNA Homo sapiens cDNA clone c-1rf02 3	Mus musculus calcium channel, vollage-dependent, Ttype, apha 1G subunit (Cacna1g), mRNA	601308679F1 NIH_MGC_44 Home saplens cDNA clone IMAGE:3627066 5'	C reinhardtii nuclear gene on linkage group XIX	yq62g08.s1 Scares fetal liver splean 1NFLS Homo saplens cDNA clone IMAGE:200414 3' similar to contains	Alu repetitive element;	Aimmersus gene for transposase	ANNEXIN XI (CALCYCLIN-ASSOCIATED ANNEXIN 50) (CAP-50)	G gailus gene encoding non-histone chromosomal protein HMG-14b, exons 4 and 5	MR3-ST0290-290100-025-g07 ST0290 Homo sapiens cDNA	MR3-ST0290-280100-025-g07 ST0290 Homo sapiens cDNA	Mus musculus major histocompatibility locus class III region:butyrophilin-like protein gene, partial odo;	Notch4, PBX2, RAGE, lysophatidic acid acyl transferase-alpha, patmitoyl-protein thicesterase 2 (PP12),	CREB-RP, and tenascin X (TNX) genes, complex	Drosophila melanogaster klarsicht protein (klar) mRNA, complete cds	L5-UM0070-020500-068-a08 UM0070 Hamo sapiens cDNA	Tapa-1=integral membrane protein TAPA-1 [mice, B cell lymphoma line 38C13, Genomic, 1973 nt, segment 1	of 7]	A immersus gene for transposace	Mus musculus major histocompatibility locus class III region:butyrophilin-like protein gene, partial cds,	Notch4, PBX2, RAGE, lysophatidic acid acy/ transferase-alpha, parmitoy-protein undesterase 2 (PP12),	CREB-RP, and tenascin X (TNX) genes, comple>	nx78e03.srt NCL_CGAP_Ew1 Home sapiens cDNA clone IMAGE:1268140 similar to contains Alu repetitive	element;contains element MEK35 repetitive element;
Top Hit Database Source	EST HUMAN	IN	EST_HUMAN	NT	EST_HUMAN	LN	NT	ΝΤ	EST_HUMAN	L	EST_HUMAN	IN	EST_HUMAN	IN		EST_HUMAN	LN	SWISSPROT	1N.	EST_HUMAN	EST_HUMAN			NT	Ä	EST_HUMAN		TN	TN			NT		EST HUMAN
Top Hit Acession No.	.1E-01 BF697308.1	.1E-01 AL161560.2	.1E-01 AW972158.1	.1E-01 D64004.1	.1E-01 AU140363.1	.1E-01 AJ006701.1	6755215 NT	6978676 NT	1.1E-01 AW821909.1	1.1E-01 S82418.1	1.1E-01 F03265.1	8753231 NT	1.1E-01 BE393186.1	1.1E-01 X62135.1			1		1.1E-01 X52708.1	1.1E-01 AW819412.1	1.1E-01 AW819412.1			1.1E-01 AF030001.1	1.1E-01 AF157066.1	1.1E-01 AW802056.1		1.1E-01 S44957.1	1.1E-01 Y07695.1			1.1E-01 AF030001.1		1.1E-01 AA747216.1
Most Similar (Top) Hit BLAST E Value	1.1E-01	1.1E-01	1.1E-01	1.1E-01	1.1E-01	1.1E-01	1.1E-01	1.1E-01	1.1E-01	1.1E-01	1.1E-01	1.1E-01	1.1E-01	1.1E-01		1.1E-01	1.1E-01	1.1E-01 P97384	1.1E-01	1.1E-01	1.1E-01			1.1E-01	Į			1.1E-01	1.1E-01			1.1E-01		_
Expression Signal	1.61	1.65	3.67	1.88	2.75	1.73	2.02	1.08	1.27	0.89	0.81	1.56	2.09	1.47		0.71	0.7	96.0	1.28	1.2	1.2			0.83	11.45	0.76		0.92	1.23			0.75		2.59
ORF SEQ ID NO:	27302	Ì	27405							29107		L	29685			29763			29965							30528	L	30877	31059					
Exen SEQ ID NO:	14245	14274	16031	14435	14701	Į,	15519	15999	15756	16095	16274	16591	16675	16705		16745	16836	16952	16961	17374	_			17380		17544		17897	18083	L		17380		18979
Probe SEQ ID NO:	1079	1109	1186	1278	1549	2255	2388	2603	2633	2917	3098	3422	3508	3540		3580	3673	3791	3800	4228	4226			4233	4367	4401		4762	4953			5134		5787

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Top Hit Descriptor	8 Homo sapiens diacy/glycerol kinase 3 (DAGK3) gene, exon 6	Botrytis cinerea strain T4 cDNA library under conditions of nitrogen deprivation	602039176F1 NCI_CGAP_Brn64 Homo sapiens cDNA clone IMAGE:4186818 51	602039176F1 NCI_CGAP_Brn64 Homo sapiens cDNA clone IMAGE:4186818 5'	S. pombe ste8 gene encoding protein kinase	Providencia rettgeri penicillin G amidase gene	Homo sepiens LGMD2B gene	PM3-FT0024-130600-004-f12 FT0024 Homo sepiens cDNA	RC3-CT0254-280899-011-a01 CT0254 Homo sapiens cDNA	Homo sapiens chromosome 21 segment HS21C082	AF035746 Human sallvary gland cell line HSG Homo sapiens cDNA clone RL43	qg76d06.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1841099 3'	ACETYL-COENZYME A SYNTHETASE (ACETATE-COA LIGASE) (ACYL-ACTIVATING ENZYME)	Homo sapiens syntaxin 4 binding protein UNC-18c (UNC-18c) mRNA, complete cds	Homo saplens phosphatidyfinositol glycan, class B (PIGB), mRNA	Ureaplasma urealyticum section 56 of 59 of the complete genome	Ureaplasma urealyticum section 56 of 59 of the complete genome	601816524F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4050853.5'	Pyrococcus horikoshii OT3 genomic DNA, 1166001-1485000 nt. position (6/7)	602140976F1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4302019 5'	602140976F1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4302019 5'	TRAB PROTEIN	B.subtilis gene encoding hypothetical polyketide synthase	ah31b06.s1 Soares_parathyroid_tumor_NbHPA Homo saplens cDNA clone 1240403 3' similar to gb:J03483 CHROMOGRANIN A PRECURSOR (HUMAN);	Methanococcus Jannaschii section 34 of 150 of the complete genome	nh04g10.s1 NCI_CGAP_Thy1 Homo sepiens cDNA done IMAGE:943362	nh04g10.s1 NCI_CGAP_Thy1 Homo sapiens cDNA clone IMAGE:943362	H.sapiens IL15 gene	PM1-ST0270-080200-001-109 ST0270 Homo sapiens cDNA	DKFZp547P194_r1 547 (syncnym: hfbr1) Homo sapiens cDNA clone DKFZp547P194 5'	Pediococcus addilactici H plasmid pSMB74 pediodin AcH production (pap) gene cluster papA, papB, papC and pepD genes, complete cds
Top Hit Database Source		NT	EST_HUMAN	T HUMAN	LN	LN			EST_HUMAN	TN	EST_HUMAN			NT			LΝ	EST_HUMAN	LN.	EST_HUMAN	EST_HUMAN	SWISSPROT	NT	EST HUMAN	LN.	EST HUMAN	EST HUMAN	F	EST_HUMAN	EST_HUMAN	TN
Top Hit Acession No.	.1E-01 AF020927.1	.1E-01 AL110985.1	.1E-01 BF339519.1	.1E-01 BF339519.1	.1E-01 X68851.1	.1E-01 M86533.1	.1E-01 AJ007973.1	.1E-01 BE769152.1	.1E-01 AW853699.1	.1E-01 AL163282.2	1.1E-01 AF035746.1	1.1E-01 AI216307.1	069635	1.1E-01 AF032922.1	11432372 NT	1.1E-01 AE002155.1	1.1E-01 AE002155.1	BF382758.1	1.1E-01 AP000006.1	1.1E-01 BF684628.1	1.1E-01 BF684628.1	P41067	1.1E-01 Z14098.1	1.1E-01 AA788784.1	1.1E-01 U67492.1	1.1E-01 AA493574.1	1.1E-01 AA493574.1	1.1E-01 X91233.1	1.1E-01 AW817918.1	1.1E-01 AL134349.1	1.1E-01 U02482.1
Most Similar (Top) Hit BLAST E Value	1.1E-01	1.1E-01	1.1E-01	1.1E-01	1.1E-01	1.1E-01	1.1E-01	1.1E-01	1.1E-01	1.1E-01	1.1E-01	1.1E-01	1.1E-01 O69635	1.1E-01	1.1E-01	1.1E-01	1.1E-01	1.1E-01	1.1E-01	1.1E-01	1.1E-01	1.1E-01 P41067	1.1E-01	1.1E-01	1.1E-01	1.1E-01	1.1E-01	1.1E-01	1.1E-01	1.1E-01	1.1E-01
Expression Signal	1.32	78.0	0.95	0.98	1.79	5.15	1.68	1.37	7.73	0.61	1.52	0.84	3.68	2.73	2.74	0.74	0.74	1.01	86.0	7.51	7.51	2.16	0.64	306	1.58	1.55	1.55	1.26	0.94	2.31	
ORF SEQ ID NO:				32426					32716		L	33150			33684	33468			34007		34256	34391		34433		L		L		35165	
Exon SEQ ID NO:	19047	19082	19113	19113	19144	19177	19326	19347	19367	19716	L	19762		_	<u> </u>	ļ.	20058	ı	l	L	20771	20888	20926		1	21484	1	L	L		
Probe SEQ ID NO:	5857	5894	5927	5927	5958	5992	6150	6171	6191	6554	6562	6602	6742	6843	6934	7193	7193	7337	7456	7706	7708	7833	7872	7873	8155	8403	8403	8449	8489	8546	9018

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Probe SEO ID NO:	Exan SEQ (D NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acesslon No.	Top Hit Database Source	Top Hit Descriptor
9113	22192	35737	1.04	1.1E-01	.1E-01 AI807474.1	EST_HUMAN	wf48c01.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2358816 3' similar to contains Alu repetitive element;
9210	22288	35830	0.5	1.1E-01	.1E-01 AF050081.1	۲	Homo sapiens C16orf3 large protein mRNA, complete cds
9243	22320	35863	2.25		.1E-01 AA192153.1	EST_HUMAN	zp93b12.r1 Stratagene muscle 937209 Homo sapiens cDNA clone IMAGE:627743 5
9243	22320	35864				EST_HUMAN	zp93b12.rt Stratagene muscle 937209 Homo sepiens cDNA clone IMAGE:627743 51
9335	22411	35964			1.1E-01 Y12727.1	N	P.furlosus partial doh5 gene and argF gene
9366	22441	38001	2.78	1.1E-01	.1E-01 T72675.1	EST_HUMAN	yd19h03.s1 Soaros fetal liver spieen 1NFLS Homo saplens cDNA clone IMAGE:1087253' similar to gb:M81181 SODIUM/POTASSIUM-TRANSPORTING ATPASE BETA-2 (HUMAN);
9392	22467		0.63	1.1E-01	1.1E-01 BE893260.1	EST_HUMAN	601436972F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3922048 5
3622	22677		0.99		1.1E-01 BE142305.1	EST_HUMAN	CM3+T0142-271099-026-g11 HT0142 Homo sapiens cDNA
9696	22745		2.33	Ĺ	1.1E-01 BF085149.1	EST_HUMAN	MR2-GN0027-040900-005-a08 GN0027 Homo sapiens cDNA
10114	23152		0.77		1.1E-01 AL161543.2	NT	Arabidopsis thallana DNA chrcmosome 4, contig fragment No. 43
10410	23445		1.23	ľ.	1.1E-01 R80590.1	EST_HUMAN	y96a09.s1 Soarcs placenta Nb2HP Homo sapiens cDNA clone IMAGE:1470643'
10544	23579	37188			.1E-01 U60529.1	LN	Ceratitis capitata yoyo retrotransposon gag-like, pol-like and env-like genes, complete ods
10914	23997	37631	1.38	-	.1E-01 AF245277.1	NT	Dictyostelium discoldeum kinesin Unc104/KIF1a homolog (Unc104) mRNA, complete cds
11044	16274	l		ľ	.1E-01 F03265.1	EST_HUMAN	HSC1RF022 normalized Infant brain cDNA Homo saplens cDNA clone c-1rf02 3
11162	24233	}	2.47	Ĺ	1.1E-01 AF169032.1	LN	Carassius auretus activin beta A precursor, mRNA, completa cots
77,000	9000	L	2 11	115.01	1 1E-01 P23708 1	EST HIMAN	yh35f12.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:131759 5' similar to contains Alu repetitive element:contains TAR1 repetitive element ;
11482	24547	38212		1	1E-01 Z11910.1	LN TN	Z.mobilis tgt and lig genes encoding tRNA guanine transglycosylase and DNA ligase
11483	24542				.1E-01 Z11910.1	LN LN	Z.mobilis tot and lig genes encoding tRNA guanine transglycosylase and DNA ligase
11510	24568				1.1E-01 BE802974.1	EST_HUMAN	601676924F1 NIH_MGC_21 Homo saplens cDNA clone IMAGE:3959088 5
11588	24639	ļ_	3.21	1.1E-01	.1E-01 P17437	SWISSPROT	SKIN SECRETORY PROTEIN XP2 PRECURSOR (APEG PROTEIN)
11971	24956		1.33		.1E-01 AL161511.2	LN	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 23
12378	25269		3.78		.1E-01 BE767023.1	EST_HUMAN	RC2-NT0112-120600-014-03 NT0112 Homo sapiens cDNA
12649	25910		3.18		.1E-01 BE974556.1	EST_HUMAN	601680551R2 NIH_MGC_83 Homo sapiens oDNA clone IMAGE:3950604 3'
13136	25738	31947	1.98		.1E-01 BF239753.1	EST_HUMAN	601906350F1 NIH_MGC_54 Homo sepiens cDNA done IMAGE:4134085 5'
1228	14388	L			.0E-01 O62855	SWISSPROT	DEOXYRIBONUCLEASE II PRECURSOR (DNASE II) (ACID DNASE) (LYSOSOMAL DNASE II)
							ws08d01.x1 NCI_CGAP_Kid11 Home sepiens cDNA clone IMAGE:2496577 3' sImilar to contains MER7.03
1301	14457	27523	2.18	_	.0E-01 Al985499.1	EST HUMAN	MER7 repetitive element;
1423	14577	27650	2.3	<b>L</b>	1.0E-01 AL151504.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 16
2558	15683		1.01		.0E-01 AW451366.1	EST HUMAN	UFH-Bi3-aic-d-07-0-UI:s1 NCI_CGAP_Sub5 Homo sapiens cDNA cione IMAGE::Z/35420 3
3813	16973				.0E-01 BF239818.1	EST HUMAN	601906489F1 NIH MGC 54 Home sapiens clina cidne IMAGE: 4134071 5
4064	17220	30228	2.6		1.0E-01 BF365703.1	EST_HUMAN	QV2-NT0048-160800-316-605 N I 0048 Hamo sapiens aLINA

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Top Hit Descriptor	Chlamydophila pneumoniae AR39, section 91 of 94 of the complete genome	an32c04.y5 Gessler Wilms tumor Homo sepiens cDNA clone IMAGE:1700358 5'	Drosophila melanogaster tyrosine kinase p45 isoform (fer) mRNA, complete cds	EST384414 MAGE resequences, MAGB Homo sapiens cDNA	601286969F1 NIH_MGC_44 Homo saplens cDNA clane IMAGE:3613552 5'	本62h04,s1 Soares_fetal_livar_spleen_1NFLS_S1 Homo sapiens cDNA clone iMAGE:416695 3'	X campestris genes for sensor and regulator protein	Homo sapiens mRNA for FLJ00065 protein, partial cds	Homo sapiens growth factor receptor-bound protein 7 (GRB7) gene, complete cds	2/4/1910.s1 Soares ovary tumor NbHOT Homo sapiens cDNA clone IMAGE:756258 3' similar to contains L1.t3 L1 repetitive element ;	zu67c12.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:743062 3'	yh34h06.r1 Soares placenta Nb2HP Homo sapiens cDNA done IMAGE:131675 5' similar to contains Alu	repetitive element;	M.musculus whn gene	ak32g01.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1407696 3' similar to gb:M34182 CAMP- DEPENDENT PROTEIN KINASE, GAMMA-CATALYTIC SUBUNIT (HUMAN);	Homo sapiens TESTIN 2 and TESTIN 3 genes, complete cds, alternatively spliced	Homo sapiens TESTIN 2 and TESTIN 3 genes, complete cds, alternatively spliced	x09b01.x1 NO_C6AP_U4 Hono sapiens cDNA clone IMAGE:2675689 3' similar to gb:X17206 40\$ RIBOSOMAL PROTEIN S4 (HUMAN);contains TAR1.t3 TAR1 repetitive element ;	Rattus norvegicus synaptic SAPAP-interacting protein Synamon mRNA, complete cds	yg33h04.s1 Soares Infant brain 1NIB Homo sapiens cDNA clone IMAGE:34549 3'	Human pro-alpha-1 (V) collagen mRNA, complete cds	Helkcobacter pylori, strain J89 section 62 of 132 of the complete genome	zc66c10.s1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:327282 3'	601905661F1 NIH_MGC_54 Homo saplens cDNA clone IMAGE:4133487 5'	Homo saplens mRNA for KIAA1579 profein, partial cds	Homo sapiens mRNA for KIAA1579 protein, partial cds	EST369615 MAGE resequences, MAGE Homo sepiens aDNA	ytzzag6,s1 Stratagene fetal spleen (#837205) Homo sapiens cDNA clone IMAGE:72562 3' similar to cortains Alu repetitive element	601584604F1 NIH_MGC_7 Homo saplens cDNA clone IMAGE:3939096 5'	AU159127 THYRO1 Homo sapiens cDNA clone THYRO10008953
Top Hit Database Source	NT	r_HUMAN	NT		EST_HUMAN	EST_HUMAN			NT	EST HUMAN	Т		EST_HUMAN		EST HUMAN	Г	<u>L</u>	EST HUMAN	Г	EST_HUMAN			EST_HUMAN	EST_HUMAN	۲	뇐	EST_HUMAN	FST HIMAN	П	EST_HUMAN
Top Hit Acession No.	AE002265.2	1.0E-01 AI792349.1	.0E-01 U50450.1	1.0E-01 AW952344.1	1.0E-01 BE389100.1	.0E-01 W88490:1	.0E-01 X54015.1	.0E-01 AK024472.1	.0E-01 AF274875.1	.0E-01 AA481879.1	1.0E-01 AA406039.1		1.0E-01 R23821.1	1.0E-01 Y12488.1	1.0E-01/AA861091.1	1.0E-01 AF260225.1	1.0E-01 AF260225.1	1.0E-01 AW189797.1	1.0E-01 AF102855.2	1.0E-01 R44993.1	1.0E-01 M76729.1	1.0E-01 AE001501.1	1.0E-01 W01955.1	1.0E-01 BF240154.1	1.0E-01 AB046799.1	1.0E-01 AB046799.1	1.0E-01 AW957425.1	1 0F-01 T51952 1	1.0E-01 BE792750.1	1.0E-01 AU159127.1
Most Similar (Top) Hit BLAST E Velue	1.0E-01	1.0E-01	1.0E-01	1.0E-01	1.05-01	1.0E-01	1.0E-01	1.0E-01	1.0E-01	1.0E-01	1.0E-01		1.0E-01	1.0E-01	1.0E-01	1.0E-01	1.0E-01	1.0E-01	1.0E-01	1.0E-01	1.0E-01	1.0E-01	1.0E-01	1.0E-01	1.0E-01	1.0E-01	1.0E-01	1 0E-04		
Expression Signal	1.44	0.76	2.17	2.17	0.61	9.49	29'0	1.08	13.08	60	0.72		1.87	2.39	69.0	2.17	2.17	0.96	1.12	0.87	6.1	3.15	0.55	1.88	8.92		1.06	<u>.</u>		
ORF SEQ ID NO:	30651		30955	31143	31346	Ĺ			32670	32993					34721				36026				36331			36775		36005		
Exon SEQ ID NO:	17665	17812	17967			L	18731	19186	19325	19632			20297	20965	ł	1	1		1	ı	Ĺ	1	22761	ł	$l_{-}$	L		上		23978
Probe SEQ ID NO:	4527	4677	4834	5039	5261	5436	5534	6001	6148	6465	6479		7164	7914	8118	8141	8141	8689	9387	9696	9707	9750	9764	10026	10139	10139	10347	400E4	10537	10894

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Probe SEQ ID NO:	Exen SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
1617	14769		1.01	9.7E-02	4503710 NT		Homo sapiens fibroblast growth factor receptor 3 (achondroplasia, thanatophoric dwarfism) (FGFR3) mRNA
2335	1	28601	2.58	ြိ	.7E-02 BE168660.1	1	QV1-HT0516-070300-095-a04 HT0516 Homo sapiens cDNA
4091	ļ	_	4.05	6	.7E-02 Q99795	SWISSPROT	CELL SURFACE A33 ANTIGEN PRECURSOR (GLYCOPROTEIN A33)
5461	18661	31639	0.59	9.7E-02	.7E-02 AF099189.1	LN	Caulobacter crescentus thymydilate kinase (tmk) and DNA polymerase III delta prime subunit (dnaC) genes, complete cds
3	70007			0.75-03	7E-02 AE000180 1	ΤN	Caulobacter crescentus thymydllate kinase (tmk) and DNA polymerase III delta prime subunit (dnaC) genes, complete cds
2 2	10316			9.7E-02	9 7F-02 AW954476 1	EST HUMAN	EST366546 MAGE resequences, MAGC Homo sapiens cDNA
3/5	20507					L	Bacillus subtilis complete genome (section 16 of 21); from 2997771 to 3213410
8171	21253					EST HUMAN	yw41c03.s1 Weizmann Offactory Epithellum Homo sapiens cDNA clone IMAGE:254788 3'
8171	21253				9.7E-02 N22798.1	EST HUMAN	yw41c03.s1 Weizmann Olfactory Epithelium Homo saplens cDNA clone IMAGE:254788 3'
	1				7	MANIET TOO	wx78b08.x1 NCI_CGAP_Ov38 Homo sapiens cDNA clone IMAGE:2649747 3' similar to gb:X52851_ma1 peptiny1_ppoiny1_cis_rpans1sowFpasF A (H1MAN);
0606	_1	355/3			Alegged.	בים בים	Mars involved in the Name of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Con
11472					9.7E-02 U58337.1	- N	Mus musculus igaini (Lgul) mante, par da cus 72444 -4 Samma NEUMB. St Light seriens child chip IMAGE-16784853'
2073					9.6E-02 AI080721.1	EST_HUMAN	OZ4/011.XI SOBIES, WITHINITY OF THE SOUND COURT COURTS OF THE SOUND COURTS OF THE SOUND COURTS OF THE SOUND COURTS OF THE SOUND COURTS OF THE SOUND COURTS OF THE SOUND COURTS OF THE SOUND COURTS OF THE SOUND COURTS OF THE SOUND COURTS OF THE SOUND COURTS OF THE SOUND COURTS OF THE SOUND COURTS OF THE SOUND COURTS OF THE SOUND COURTS OF THE SOUND COURTS OF THE SOUND COURTS OF THE SOUND COURTS OF THE SOUND COURTS OF THE SOUND COURTS OF THE SOUND COURTS OF THE SOUND COURTS OF THE SOUND COURTS OF THE SOUND COURTS OF THE SOUND COURTS OF THE SOUND COURTS OF THE SOUND COURTS OF THE SOUND COURTS OF THE SOUND COURTS OF THE SOUND COURTS OF THE SOUND COURTS OF THE SOUND COURTS OF THE SOUND COURTS OF THE SOUND COURTS OF THE SOUND COURTS OF THE SOUND COURTS OF THE SOUND COURTS OF THE SOUND COURTS OF THE SOUND COURTS OF THE SOUND COURTS OF THE SOUND COURTS OF THE SOUND COURTS OF THE SOUND COURTS OF THE SOUND COURTS OF THE SOUND COURTS OF THE SOUND COURTS OF THE SOUND COURTS OF THE SOUND COURTS OF THE SOUND COURTS OF THE SOUND COURTS OF THE SOUND COURTS OF THE SOUND COURTS OF THE SOUND COURTS OF THE SOUND COURTS OF THE SOUND COURTS OF THE SOUND COURTS OF THE SOUND COURTS OF THE SOUND COURTS OF THE SOUND COURTS OF THE SOUND COURTS OF THE SOUND COURTS OF THE SOUND COURTS OF THE SOUND COURTS OF THE SOUND COURTS OF THE SOUND COURTS OF THE SOUND COURTS OF THE SOUND COURTS OF THE SOUND COURTS OF THE SOUND COURTS OF THE SOUND COURTS OF THE SOUND COURTS OF THE SOUND COURTS OF THE SOUND COURTS OF THE SOUND COURTS OF THE SOUND COURTS OF THE SOUND COURTS OF THE SOUND COURTS OF THE SOUND COURTS OF THE SOUND COURTS OF THE SOUND COURTS OF THE SOUND COURTS OF THE SOUND COURTS OF THE SOUND COURTS OF THE SOUND COURTS OF THE SOUND COURTS OF THE SOUND COURTS OF THE SOUND COURTS OF THE SOUND COURTS OF THE SOUND COURTS OF THE SOUND COURTS OF THE SOUND COURTS OF THE SOUND COURTS OF THE SOUND COURTS OF THE SOUND COURTS OF THE SOUND COURTS OF THE SOUND COURTS OF THE SOUND COURTS OF THE SOUND COURTS OF THE SOUND COURTS OF THE SOUND COURTS OF THE SOUN
2073	15213			**	9.6E-02 AI080721.1	EST HUMAN	0247011.X1 Sogres NIHMMPU_S1 Homo sapiens CLINA Cone INVACE. 1070460 5
4464	17604		. 6.67		9.6E-02 Z32686.2	Į.	Proteus mirabilis fimbrial operon, strain HI4320
5117	18244	31209		ì	9.6E-02 AW966230.1	EST_HUMAN	EST378303 MAGE resequences, MAGI Homo sapiens cDNA
6231	19408				BE91003	EST_HUMAN	601498088F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3900165 6
2108	1		0.79		E 6678753 NT		Mus musculus lymphocyte antigen 78 (Ly78), mRNA
8571	l		0.65		9.6E-02 AU137084.1	EST HUMAN	AU137084 PLACE1 Homo saplans cDNA clone PLACE1005740 5
9744	ı	36386	1.49		9.6E-02 AV687898.1	EST_HUMAN	AV687898 GKC Homo sepiens cDNA clone GKCAAH02 5
10076	23114		1.34		9.6E-02 BE894895.1	EST_HUMAN	601434080F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3919363 5
10245	ı	36876	1.04		9.6E-02 AJ243211.1	N	Homo sapiens DMBT1 candidate tumour suppressor gene, exons 1 to 55
10245	23280	36877			9.6E-02 AJ243211.1	L	Homo sapiens DMBT1 candidate tumour suppressor gene, exons 1 to 55
10325	l	36970	0.62		9.6E-02 BF677270.1	EST_HUMAN	602086769F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4250969 5
10354		36998	1.56		9.6E-02 AB013985.1	M	Antirhinum majus transposon Tam3 pseudogene for transposase (in S-5 copy)
10354			1.56		9.6E-02 AB013985.1	NT	Antirhinum majus transposon Tam3 pseudogene for transposase (in S-5 copy)
10465	L		3.43		9.6E-02 P08174	SWISSPROT	COMPLEMENT DECAY-ACCELERATING FACTOR PRECURSOR (CDbb)
10981	<u> </u>	37694			9.6E-02 Z79702.1	NT	Mycobacterium tuberculosis H37Rv complete genome; segiment 102/162
12019	l	3 38704	1 2.8		9.6E-02 AA625755.1	EST_HUMAN	zug1g01.s1 Soares_testis_NHT Homo sapiens cDNA cione IMAGE: 745392.3
13015	5 25668	8	1.7		9.6E-02 H14599.1	EST_HUMAN	ym19h03.61 Soares infant brein 1NIB Homo sapiens cLINA cione imAGE. 40035 3

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Most Similar   Top Hit Acession   Top Hit Signal   No.   Source   Signal   Value   Source   Source   Source   Source   Source   Source   Source   Source   Source   Source   Source   Source   Source   Source   Source   Source   Source   Source   Source   Source   Source   Source   Source   Source   Source   Source   Source   Source   Source   Source   Source   Source   Source   Source   Source   Source   Source   Source   Source   Source   Source   Source   Source   Source   Source   Source   Source   Source   Source   Source   Source   Source   Source   Source   Source   Source   Source   Source   Source   Source   Source   Source   Source   Source   Source   Source   Source   Source   Source   Source   Source   Source   Source   Source   Source   Source   Source   Source   Source   Source   Source   Source   Source   Source   Source   Source   Source   Source   Source   Source   Source   Source   Source   Source   Source   Source   Source   Source   Source   Source   Source   Source   Source   Source   Source   Source   Source   Source   Source   Source   Source   Source   Source   Source   Source   Source   Source   Source   Source   Source   Source   Source   Source   Source   Source   Source   Source   Source   Source   Source   Source   Source   Source   Source   Source   Source   Source   Source   Source   Source   Source   Source   Source   Source   Source   Source   Source   Source   Source   Source   Source   Source   Source   Source   Source   Source   Source   Source   Source   Source   Source   Source   Source   Source   Source   Source   Source   Source   Source   Source   Source   Source   Source   Source   Source   Source   Source   Source   Source   Source   Source   Source   Source   Source   Source   Source   Source   Source   Source   Source   Source   Source   Source   Source   Source   Source   Source   Source   Source   Source   Source   Source   Source   Source   Source   Source   Source   Source   Source   Source   Source   Source   Source   Source   Source   Source   Source   Source	1.41 9.6E-02 AJ295624.1 NT	2.16 9.5E-02 AW992395.1 EST_HUMAN	0.88 9.5E-02 P51854 SWISSPROT TRANSKETOLASE 2 (TK 2) (TRANSKETOLASE RELATED PROTEIN)	4.64 9.5E-02 AB003473.1 NT Trimeresurus flavoviridis DNA for phospholipase A2 inhibitor, complete cds	7.77 9.5E-02 AL161538.2 NT	0.81 9.5E-02 P51854 SWISSPROT	2.85 9.5E-02 BF035861.1 EST_HUMAN	2.85 9.5E-02 BF035861.1   EST_HUMAN	4.09 9.5E-02 BF035861.1 EST_HUMAN	4.09 9.5E-02 BF035861.1 EST_HUMAN	57416 NT	9.5E-02 AF272732:1 NT	3.95 9.4E-02 BF671063.1	4.64 9.4E-02 Z33059.1 NT	0.95 9.4E-02 AF097363.1 INT Triticum aestivum heat shock protein 101 (Hsp101a) mRNA, complete cds	0.68 9.4E-02 L78833.1	2.5 9.4E-02 Z46883.1 NT Acinetobacter sp. cysD, cobQ, codM, lysS, rubA, rubB, estB, oxyR, ppk, mtgA, ORF2 and ORF3 genes	1.9 9.4E-02 L78833.1 NT	N	4.84 9.4E-02 U27699.1 NT	3280 NT	2525 NT	2.17 9.3E-02 BF575511.1   EST_HUMAN	3.17 9.3E-02 BE391943.1   EST_HUMAN	3.17 9.3E-02 BE391943.1 EST_HUMAN	1.82 9.3E-02 AV732224.1 [EST_HUMAN   AV732224 HTF Homo sapiens cDNA clone HTFAUA06 5	Į.	95.0	0.5 9.3E-02/AL113179.1 INT	2.3 9.3E-02 BE962631.2 EST_HUMAN	3.6 9.3E-02 Q15034 SWISSPROT	
Most Similar (Top) Hit BLAST E Value	9.6E-02	L									L								L	-	L			L			L	L				Į
Expression Signal	1.41	2.16	0.88	4.64	77.7	0.81	2.85	2.85	4.09	4.09	1.82	2.81	3.95	4.64	0.95	0.68	2.5	1.9	7.72	4.84	2.37	8.03	217	3.17	3.17	1.82	0.67	0.56	0.5	2.3	3.6	
ORF SEQ ID NO:	31949	30355	32280	34006	34292	32280	34666	34667	37634	37635			28130	30147	32978	34318		34318		31936			29521	30400	30401	-		35052		36537	37035	
Exon SEQ ID NO:	25743	17366	18974	20532	20802		١.	21146	24001		Ĭ.	1	15024		L	L	21878	20827	26011	上	L	16270	16502	17413	L	17990	1897:	21523		L	l	
Probe SEQ ID NO:	13143	4217	5782	7455	7741	7875	8064	8064	10918	10918	12104	13097	1880	3985	6447	7769	8799	11174	12214	13198	3054	3094	3329	4268	4268	4857	67.79	8442	9324	981	10394	

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Top Hit Descriptor	UI-H-BI1-afx-h-05-0-UI s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2723553 3'	Photobacterium damselae subsp. damselae partial gyrB gene for DNA gyrase B subunit	hd28h12.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:29108873'	Mus musculus major histocompatibility locus class II region; Fas-binding protein Daxx (DAXX) gene, partial cds; Bing1 (BING1), tapasin (tapasin), RalGDS-like factor (RLF), KE2 (KE2), BING4 (BING4), beta1, 3-	galactosy transferase (betaf, 3-galactosy tr>	Molluscum contagiosum virus subtype 1, complete genome	Mollusoum contagiosum virus subtype 1, complete genome	Molluscum contagiosum virus subtype 1, complete genome	yg98f07.r1 Soares infant brain 1NIB Homo saplens cDNA clone IMAGE:41618 5	MAJOR EPIDIDYMIS-SPECIFIC PROTEIN E4 (EPIDIDYMAL PROTEIN BE-20)	nf79e01.s1 NCI_CGAP_Cc3 Homo sapiens cDNA clone IMAGE:926136 31	Mus musculus pre T-cell antigen receptor alpha (Ptcre), mRNA	Human herpesvirus 1 strain KOS-63, latency-associated transcript, promoter region	600944365F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:2960176 5'	G.gallus Mia-CK gene	yа99с09.r1 Stratagene placenta (#837225) Homo sapiens cDNA clone IMAGE:69808 5' similar to similar to gь:Х56009 GUANINE NUCLEOTIDE-BINDING PROTEIN G(S), ALPHA SUBUNIT (HUMAN)	H.vulgare xylose isomerase gene	Podospora anserina mitochondrion, complete genome	O. cuniculus k12 keratin gene	PM2-BT0349-161299-001-f02 BT0349 Homo sapiens cDNA	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 54	Homo sapiens MSH55 gene, partial cds; and CLIC1, DDAH, G6b, G6c, G5b, G6d, G6e, G6f, BAT5, Ĝ5b, CSK2B, BAT4, G4, Apo M, BAT3, BAT2, AIF-1, 1C7, LST-1, LTB, TNF, and LTA genes, complete cds	Homo sapiens chromosome 9 duplication of the T cell receptor beta locus and trypsinogen gene familles	au74a05.y1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2781968 5'	Aeropyrum pernix genomic DNA, section 4/7	Mus musculus thymopoietin zeta mRNA, complete cds	Homo saplens gamma adducin gene, exon 9	FB19F10 Fetal brain, Stratagene Homo sapiens cDNA clone FB19F10 3'end	Tg616=Cyl actin [Tripneustes gratilla=sea urchins, embrycs, Genomic, 5275 nt]
Top Hit Database Source	EST_HUMAN	IN	EST_HUMAN		NT	INT	NT	LN		SPROT	EST_HUMAN		NT	EST_HUMAN	Г	EST_HUMAN	IN		ΝŢ	EST_HUMAN	LN	. +	LN	EST_HUMAN			NT	EST_HUMAN	N
Top Hit Acession No.	W 206117.1	·	9.3E-02 AW468850.1					J60315.1	354156.1	9.2E-02 Q28631		6755215 NT		3E299722.1	96402.1	149920.1	(95256.1	11466872 NT	<b>&lt;77665.1</b>	.1E-02 AW372569.1	1E-02 AL161554.2	9.1E-02 AF129756.1	9.1E-02 AF029308.1	4W160658.1	4P000061.1	9.1E-02 U39073.1	Y14379.1	F02984.1	574059.1
Most Similar (Top) Hit BLAST E Value	9.3E-02	9.3E-02	9.3E-02		9.3E-02	9.2E-02	9.2E-02	9.2E-02	9.2E-02 F	9.2E-02	9.2E-02	9.2E-02	9.2E-02	9.2E-02	9.2E-02)	9.2E-02 T49920.1	9.2E-02	9.2E-02	9.1E-02 X77665.1	9.1E-02/	9.1E-02	9.1E-02/	9.1E-02	9.1E-02/	9.1E-02	9.1E-02	9.1E-02 Y14379.1	9.1E-02 T02984.1	9.1E-02 S74059.1
Expression Signal	3.96	2.08	22.03		2.87	4.72	4.72	4.72	3.08	3.7	1.01	1.14	1.05	0.88	3.44	1.82	2.18	1.2	2.23	76.0	1.78	1.23	0.61	12.21	0.95	1.02	96.0	1.46	1.02
ORF SEQ ID NO:	-				!	26486	26487	26488		29437	29564		-		30875	34802	34974		26237		30723	32345		34094					37316
Exen SEQ ID NO:	l l	ı	25964	l	26010	13460	13460	13460	15434	<u> </u>	16551	16839	17496	17565	17895	21280		<u></u>	13236	16921	17744	19038	26218	L	20907	ı	22203		23708
Probe SEQ ID NO:	10526	12485	12905		13139	238	238	238	2302	3247	3379	3676	4353	4425	4760	8198	8370	13120	436	3760	4607	5848	7459	7546	7852	7887	9124	10642	10674

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
10703	23736	37341	0.8	9.1E-02	9.1E-02 Y11187.1	N	A.thaliana RH1, TC1, G14587-5, G14587-6, and PRL1 genes
11441	L		2.13	9.1E-02	AF037625.1	IN	Rena catesbeiana dihydropyridine receptor mRNA, complete cds
12151	ᆚ_			9.1E-02	9633494 NT		Bactertophage Mu, complete genome
12393	1		1.42	9.1E-02	AA179901.1	HUMAN	平38h12.s.1 Stratagene muscle 937209 Homo sepiers cDNA clone IMAGE:611783 3' similar to SW:TRT3_HUMAN P45378 TROPONIN T, FAST SKELETAL MUSCLE, ISOFORM BETA;
12473	١.		1.32	9.1E-02		Г	Rattus norvegicus cell cycle protein p55CDC gene, complete cds
12996	L		13.49	l.	9.1E-02 AJ291390.1	N	Homo saplens partial MUC3B gene for MUC3B mucin, exons 1-11
13230			1.27		9.1E-02 AF226688.1	NT	Bombyx mort fibroin heavy chain Fib-H (fib-H) gene, complete cds
	<u> </u>						FOLATE RECEPTOR ALPHA PRECURSOR (FR-ALPHA) (FOLATE RECEPTOR 1) (FOLATE RECEPTOR, ADULT) (ADULT FOLATE-BINDING PROTEIN) (FBP) (OVARIAN TUMOR-ASSOCATED
763	13944	26990	5.89	9.0E-02 P15328	P15328	SWISSPROT	ANTIGEN MOV18) (KB CELLS FBP)
7887	<u> </u>	00826	7 33	0.F.02	9 0F-02 BF230482 1	EST HUMAN	hv39g10.x1 NCI_CGAP_Lu24 Homo sapiens cDNA dono IMAGE:3176842 3' stmilar to contains Alu repetitive element;
3 6	┸				9 0F-02 AW801364.1	EST HUMAN	IL5-UM0067-240300-050-h06 UM0067 Homo septens cDNA
2864	_				9.0E-02 AF138522.1	L	HIV-1 p8c095-06 from USA envelope glycoprotein (env) gerie, partial cds
2864	1_				9.0E-02 AF138522.1	LN	HIV-1 p8c095-08 from USA envelope glycopratein (env) gene, partial ods
3417	L.	29603	1.11	9.0E-02	9.0E-02 AF279135.1	NT	Dictyostefium discoldeum spore coat structural protein SP65 (cotE) gene, complete cds
4414	L				9.0E-02 S68757.1	TN	corticosteroid-binding globulin [Saimiri sciureus≂squirrel monkeys, liver, mRNA, 1474 nt]
4414	L				9.0E-02 S68757.1	LN	corticosteroid-binding globulin [Salmiri schreus≂squirrel monkeys, liver, mRNA, 1474 nt]
4790	L	1	2.03		9.0E-02 X65740.2	IN	Plasmodium falciparum P-type ATPase 3 gene
27	l				9.0E-02 W56037.1	EST HUMAN	ze68a12.r1 Soares_fetal_lung_NbHL19W Homo sapiens cDNA clone IMAGE:297694 5' similær to PIR:S62171 S52171 small G protein - human ;
3	1_	L		<u> </u>			7h63d03.x1 NCI_CGAP_Co16 Homo septens cDNA clone IMAGE:3320845 3' similar to contains Alu
6860	20012		0.93		9.0E-02 BF062651.1	EST_HUMAN	repetitive element;
							Escherichia coli strain E2348/69 pathogenicity island, rOrf1 (rof1), rOrf2 (rof2), Esch (esch), Esch (esch), Esch (esch), Esch (esch), Esch (esch), Esch (esch), Esch (esch), Esch (esch), Esch (esch), Esch (esch), Esch (esch), Esch (esch), Esch (esch), Esch (esch), Esch (esch), Esch (esch), Esch (esch), Esch (esch), Esch (esch), Esch (esch), Esch (esch), Esch (esch), Esch (esch), Esch (esch), Esch (esch), Esch (esch), Esch (esch), Esch (esch), Esch (esch), Esch (esch), Esch (esch), Esch (esch), Esch (esch), Esch (esch), Esch (esch), Esch (esch), Esch (esch), Esch (esch), Esch (esch), Esch (esch), Esch (esch), Esch (esch), Esch (esch), Esch (esch), Esch (esch), Esch (esch), Esch (esch), Esch (esch), Esch (esch), Esch (esch), Esch (esch), Esch (esch), Esch (esch), Esch (esch), Esch (esch), Esch (esch), Esch (esch), Esch (esch), Esch (esch), Esch (esch), Esch (esch), Esch (esch), Esch (esch), Esch (esch), Esch (esch), Esch (esch), Esch (esch), Esch (esch), Esch (esch), Esch (esch), Esch (esch), Esch (esch), Esch (esch), Esch (esch), Esch (esch), Esch (esch), Esch (esch), Esch (esch), Esch (esch), Esch (esch), Esch (esch), Esch (esch), Esch (esch), Esch (esch), Esch (esch), Esch (esch), Esch (esch), Esch (esch), Esch (esch), Esch (esch), Esch (esch), Esch (esch), Esch (esch), Esch (esch), Esch (esch), Esch (esch), Esch (esch), Esch (esch), Esch (esch), Esch (esch), Esch (esch), Esch (esch), Esch (esch), Esch (esch), Esch (esch), Esch (esch), Esch (esch), Esch (esch), Esch (esch), Esch (esch), Esch (esch), Esch (esch), Esch (esch), Esch (esch), Esch (esch), Esch (esch), Esch (esch), Esch (esch), Esch (esch), Esch (esch), Esch (esch), Esch (esch), Esch (esch), Esch (esch), Esch (esch), Esch (esch), Esch (esch), Esch (esch), Esch (esch), Esch (esch), Esch (esch), Esch (esch), Esch (esch), Esch (esch), Esch (esch), Esch (esch), Esch (esch), Esch (esch), Esch (esch), Esch (esch), Esch (esch), Esch (esch), Esch (esch), Esch (esch), Esch (esch), Esch (esch), Esch (esch), Esch (esch), Esch (esch), Esch (esch), Esch (esch),
12819	25546		1.82		9.0E-02 AF022236.1	TN	(escN), SepQ (sepQ), TIr (ttr), OrfU (orfU), >
1469	1	27706	1.25		8.9E-02 BF701593.1	EST_HUMAN	602129030F2 NIH_MGC_56 Hamo sapiens cDNA clane IMAGE:42859515
1469		L		L	8.9E-02 BF701593.1	EST_HUMAN	602129030F2 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4285951 5
2460	L	7 28714	1.64		8.9E-02 BE153572.1	EST_HUMAN	PMo-HT0339-251199-003-d01 HT0339 Homo sepiens oDNA
4316	_		1.69		8.9E-02 AF286055.1	NT	Atrichum angustatum AtranFio2 protein (AtranFio2) gene, partial cds
5972	١	32474		L	8.9E-02 AW452122.1	EST HUMAN	UI-H-Bi3-alo-f-08-0-UI,s1 NCI_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:3068284 3
5972	ł	ł			8.9E-02 AW 452122.1	EST_HUMAN	UI-H-Bi3-alo-f-08-0-UI.s1 NCI_CGAP_Sub5 Homo sapiens cDNA clone IMAGE: 3068294 3
5987	ı		60	8.9E-02	11433478 NT	LNT	Homo sapiens similar to endoglycan (H. sapiens) (LOC63107), mRNA

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Top Hit Descriptor	FOLD BIFUNCTIONAL PROTEIN [INCLUDES: METHYLENETETRAHYDROFOLATE DEHYDROGENASE ; METHENYLTETRAHYDROFOLATE OYCLOHYDROLASE ]	H. sapiens flow-sorted chromosome 6 Hindill fragment, SC5pAZ0F8	NITRIC-OXIDE SYNTHASE, BRAIN (NOS, TYPE I) (NEURONAL NOS) (N-NOS) (NNOS) (NOOS) (CONSTITUTIVE NOS) (NC-NOS) (BNOS)	602129111F2 NIH_MGC_56 Homo saplens cDNA clone IMAGE:4285827 5	602/29111F2 NIH MGC 56 Homo sapiens dDNA clone IMAGE:425567 5	EST180187 Liver, hepatocellular cardinoma Homo sapiens culvia 3 end	qu55c05.x1 NCI_CGAP_Lymb Homo saplens curva clone invade recocco 5 similiar to contain over the NER10 repetitive element;	qu55c05.x1 NCI_CGAP_Lym6 Homo saplens cDNA clone IMAGE:1968680 3' similar to contains MEK10.b1 MER10 repetitive element :	EST44434 Fetal brain I Homo sapiens cDNA 5' end	MYCISIN'S ISOFORM	MI COUNT TOO ON WAR HOME Seniens CDNA clone IMAGE 4286180 6	0021280021 1 111 MIC O CONTINUE CONTINUE CONTINUE CONTINUE CONTINUE CONTINUE CONTINUE CONTINUE CONTINUE CONTINUE CONTINUE CONTINUE CONTINUE CONTINUE CONTINUE CONTINUE CONTINUE CONTINUE CONTINUE CONTINUE CONTINUE CONTINUE CONTINUE CONTINUE CONTINUE CONTINUE CONTINUE CONTINUE CONTINUE CONTINUE CONTINUE CONTINUE CONTINUE CONTINUE CONTINUE CONTINUE CONTINUE CONTINUE CONTINUE CONTINUE CONTINUE CONTINUE CONTINUE CONTINUE CONTINUE CONTINUE CONTINUE CONTINUE CONTINUE CONTINUE CONTINUE CONTINUE CONTINUE CONTINUE CONTINUE CONTINUE CONTINUE CONTINUE CONTINUE CONTINUE CONTINUE CONTINUE CONTINUE CONTINUE CONTINUE CONTINUE CONTINUE CONTINUE CONTINUE CONTINUE CONTINUE CONTINUE CONTINUE CONTINUE CONTINUE CONTINUE CONTINUE CONTINUE CONTINUE CONTINUE CONTINUE CONTINUE CONTINUE CONTINUE CONTINUE CONTINUE CONTINUE CONTINUE CONTINUE CONTINUE CONTINUE CONTINUE CONTINUE CONTINUE CONTINUE CONTINUE CONTINUE CONTINUE CONTINUE CONTINUE CONTINUE CONTINUE CONTINUE CONTINUE CONTINUE CONTINUE CONTINUE CONTINUE CONTINUE CONTINUE CONTINUE CONTINUE CONTINUE CONTINUE CONTINUE CONTINUE CONTINUE CONTINUE CONTINUE CONTINUE CONTINUE CONTINUE CONTINUE CONTINUE CONTINUE CONTINUE CONTINUE CONTINUE CONTINUE CONTINUE CONTINUE CONTINUE CONTINUE CONTINUE CONTINUE CONTINUE CONTINUE CONTINUE CONTINUE CONTINUE CONTINUE CONTINUE CONTINUE CONTINUE CONTINUE CONTINUE CONTINUE CONTINUE CONTINUE CONTINUE CONTINUE CONTINUE CONTINUE CONTINUE CONTINUE CONTINUE CONTINUE CONTINUE CONTINUE CONTINUE CONTINUE CONTINUE CONTINUE CONTINUE CONTINUE CONTINUE CONTINUE CONTINUE CONTINUE CONTINUE CONTINUE CONTINUE CONTINUE CONTINUE CONTINUE CONTINUE CONTINUE CONTINUE CONTINUE CONTINUE CONTINUE CONTINUE CONTINUE CONTINUE CONTINUE CONTINUE CONTINUE CONTINUE CONTINUE CONTINUE CONTINUE CONTINUE CONTINUE CONTINUE CONTINUE CONTINUE CONTINUE CONTINUE CONTINUE CONTINUE CONTINUE CONTINUE CONTINUE CONTINUE CONTINUE CONTINUE CONTINUE CONTINUE CONTINUE CONTINUE CONTINUE CONTINUE CONTINUE CONTINUE CONTINUE CONTINUE CONTINUE CONTINUE CONTINUE CONTINUE CONTINUE CONTINUE CONTINUE CONTINUE CONTINU	Mus muscallus nippocampus abuntani gara gara anno anno anno anno anno anno anno a	Human 4-hydroxypnenylpyruvare-droxygerisse gerie; curitaren de	Ceratitis capitata marner transposon transposase gene, complete dus	Helicobacter pylori, strain J99 section / 5 of 132 of the complete genome	PROBABLE DNA LIGASE (POLYDEOXYRIBONOCLEOTIDE STINITASE (ATT.)	EST11696 Uterus Homo saplens cDNA 5' end	TRANSCRIPTION INITIATION FACTOR THID 135 KDA SUBUNIT (TATIFFES) (TATIFFES) (TATIFFES)	Homo sapiens paired box gene 6 (aniridia, keratitis) (PAX6), isoform b, mRNA	Sheep mRNA for angiotensinogen, complete cds	zn99a05.s1 Stratagene colon (#937204) Homo saplens cDNA clone IMAGE:566288 3	601191770F1 NIH_MGC_7 Homo saplens cDNA clone IMAGE:3535648 5'	601191770F1 NIH MGC 7 Homo sapiens cDNA clone IMAGE:3535648 S	DKFZb434D1313 r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434D1313 5	S consisten chromosome XIV reading frame ORF YNL286w		Homo sepiens zinc finger proteín 92 (ZFP92), expressed-Xq28STS proteín (XQ28ORF), and biglycan (BCN) genes, complete cds; and plasma membrane calcium ATPase isoform 3 (PMCA3) gene, partial cds
Top Hit Database Source	SWISSPROT	L	SWISSPROT			EST_HUMAN	EST HUMAN	EST HIMAN	EST HUMAN	TOGGGGIA	ONIGORACIO	EST HUMAN	TN	Ę	LZ.	N	SWISSPROT	EST HUMAN	TORGODIANS	LZ	Z	EST HUMAN	EST HUMAN	FST HUMAN	EST HIMAN	TIV	•	TN
Top Hit Acession No.		9E-02 Z79021.1		8.9E-02 BF701665.1	8.9E-02 BF701665.1		9E-02 AI285627.1	00 00 000000000000000000000000000000000	ł	١	1	3F696918.1	6680220 NT	J29895.1		8.9E-02 AE001514.1	227474	8E-02 AA299128.1	980000	4580423 NT	8 8E-02 D17520.1	AA151872.1	BE264455.1	RE COUREDRAGES 1	SE 02 A 040420 4	774504 4	OE-02 27 100 1.1	.7E-02 U82695.2
Most Similar (Top) Hit BLAST E	8.9E-02 P47259	8.9E-02 Z	8.9E-02	8.9E-02	8.9E-02	8.9E-02	8.9E-02/		8 9F-02 /	200	8.9E-02			8.9E-02		L		80	896000	L	L	L		L	ٵۨ	٥	1	- σ
Expression Signal	9.	1.77	1.19	0.76	0.76		0.84		50.0		1.8	3.82	2.75	2	1.16	1.54	96.0	1.07	i i	77.0	220						1.18	4.17
ORF SEQ ID NO:	33886		34839				36439		38440	1								30177				25907				382/3		29953
Exon SEQ ID NO:	20423	1_			ı	ı	22859	1	- 1	١				25393	L		L	$l_{-}$	1	1671 CA	1.	L	ᆚ	1	1	1	3 25314	16946
Probe SEQ ID NO:	7343	7731	8240	8323	8323	8797	0810		9819	4588	12213	12366	12637	12584	12827	12880	1404	4012		4145	4410	2 2	44300		1380	11541	12443	3785

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Top Hit Descriptor	Homo sapiens zinc finger protein 92 (ZFP92), expressed-Xq28STS protein (XQ28ORF), and biglycan (BGN) genes, complete cds; and plasma membrane calcium ATPase isoform 3 (PMCA3) gene, partial cds	Mus musculus JNK interacting protein-3a (Jlp3) mRNA, complete cds	Methanobacterium thermoautotrophicum from bases 1176181 to 1189406 (section 101 of 148) of the complete genome	2s55g08.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:701438 3'	zs55g08.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:701438 3'	Mus musculus partial Kong1 gene for potassium channel protein, exons 10-14	Mus musculus partial Konq1 gene for potassium channel protein, exons 10-14	Oncorhynchus myklss TAT-binding protein 1 mRNA, partial cds	zt20e03.s1 Soares ovary tumor NbHOT Homo sapiens culva cione IMAGE:713092.3	Pseudomonas aeruginosa PA01, section 348 of 529 of the complete genome	Pseudomonas aeruginosa PA01, section 348 of 529 of the complete genome	Oryctolagus cuniculus cytochrome P-450 (CYP4A4) gene, 6' end	Gluconobacter oxydans tRNA-lle and tRNA-Ala genes	Human DNA for immunoglobulin alpha heavy chain from a case of alpha heavy chain clisease	Mus musculus nidogen 2 (Nid2), mRNA	G gallus mRNA for vigilin	Homo saplens Xq pseudoautosomal region; segment 2/2	B01304016F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3638643 5	Trichomonas vaginalis beta-tubulin (btub1) gene, complete cds	Dictyostelium discoideum adenytyl cyclase (acrA) gene, complete cds	Mus musculus long incubation prion protein (Prnpb) and prion-like protein (Pmd) genes, complete cds	Oryctolagus cuniculus galectin-3 gene, untranslated exon and 5' flanking region	Homo sapiens mRNA for KIAA0591 protein, partial cds	Homo sapiens LCN1b gene	Mouse germline IgM chain gene, D region; D-q52, mu switch region (part a)	Mouse germline IgM chain gene, D region; D-q52, mu switch region (part a)	INSULIN RECEPTOR-RELATED PROTEIN PRECURSOR (IRR) (IR-RELATED RECEPTOR)	Homo sapiens Snf2-related CBP activator protein (SRCAP) mRNA	Homo sapiens Snf2-related C3P activator protein (SRCAP) mRNA	Homo sapiens hypothetical protein FLJ11008 (FLJ11008), mRNA
Top Hit Database Source	L <sub>N</sub>	LN	LN	EST HUMAN	EST_HUMAN	L	NT		EST HUMAN	L	TN	NT	LΝ	IN	LΝ	ΤN		EST_HUMAN	LΝ	Z.	岁	뉟	FZ	ᅜ	NT	NT	SWISSPROT	NT	TN	F
Top Hit Acession No.	8.7E-02 U82695.2	8.7E-02 AF178636.1	8.7E-02 AE000895.1	8.7E-02 AA288875.1	8.7E-02 AA286875.1	8.7E-02 AJ271885.2	8.7E-02 AJ271885.2	8.7E-02 AF281342.1	8.7E-02 AA284532.1	8.7E-02 AE004787.1	8.7E-02 AE004787.1	8.7E-02 L04758.1	8.7E-02 AJ007763.1	8.7E-02 X17116.1	6679057 NT	8.7E-02 X65292.1	8.6E-02 AJ271736.1		8.6E-02 L05468.1	8.6E-02 AF153362.1	8.6E-02 U29187.1	8.6E-02 U68179.1	8.6E-02 AB011163.1	8.6E-02 Y10826.1	8.6E-02 J00440.1	8.6E-02 J00440.1		5730066 NT		11427428 NT
Most Similar (Top) Hit BLAST E Value	8.7E-02	8.7E-02	8.7E-02	8.7E-02	8.7E-02	8.7E-02	8.7E-02	8.7E-02	8.7E-02	8.7E-02	8.7E-02	8.7E-02	8.7E-02	8.7E-02	8.7E-02	8.7E-02	8.6E-02	8.6E-02	8.6E-02	8.6E-02	8.6E-02	8.6E-02	8.6E-02	8.6E-02	8.6E-02	8.6E-02	8.6E-02 P14616	8.6E-02	8.6E-02	8.6E-02
Expression Signal	4.17	4.1	1.07	5.49	5.49	න.0	න:0	29.0	0.56	0.66	99.0	2.01	1.48	2.2	2.85	. 2.05	7.73	2.2	2.35	3.69	0.6	0.66	1.02	4.74	1.29	1.29	0.89	1.09	1.09	0.58
ORF SEQ ID NO:	29954			31605	31606		33643			35329	35330		38326				27506		29448			30725		32743		33036	34306	34716	34717	
SEQ ID	16946	17962	18332	18629	18629	20212	20212	20053	21129	21793	21793	24033	24644	25306	25432	25680	14437	15449	16431	16895	17039	17748	18443	ı		19670	20814	21197	21197	ı
Probe SEQ ID NO:	3785	4829	5241	5429	5429	6984	6984	7188	8046	8713	8713	10951	11591	12431	12648	13033	1281	2317	3257	3734	3880	4609	5330	6218	6504	6504	7755	8115	8115	8261

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Probe SEQ ID NO:	Exan SEQ ID NO:	ORF SEQ ID NO:	Expression Signel	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
8324	21408		0.76	8.6E-02	8.6E-02 U60168.1	NT	Dictyostellum discoldeum proteasome subunit C2 homolog PrtC (prtC) gene, complete cds
9938	ı	36568	1.24	8.6E-02	8.6E-02 AF111170.3	NT	Homo sapiens 14q32 Jagged2 gene, complete cds; and unknown gene
9975	1		1.4	8.6E-02	8.6E-02 AW662153.1	EST_HUMAN	hi20c08.x1 NCI_CGAP_GU1 Homo sapiens cDNA done IMAGE:29728463'
10356	L	37001	1.07	8.6E-02	8.6E-02 AF026504.1	LN	Reftus norvegicus SPA-1 like protein p1294 mRNA, complete cds
11188	24257	37892	1.82	8.6E-02	8.6E-02 AF206551.1	NT	Lacerta media cytochrome c oxidase subunit 1 gene, partial cds; mitochondrial gene for mitochondrial product
11188	ľ	37893	1.82	8.6E-02	8.6E-02 AF206551.1	NT	Lacerta media cytochrome c oxidase subunit 1 gene, partial cds; mitochondrial gene for mitochondrial product
11527		38259	3.02	8.6E-02		EST_HUMAN	601893437F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4139216 5'
11527	24583	38260		8.6E-02		EST_HUMAN	601893437F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4139216 5
11724	L	37534	79.7	8.6E-02	8.6E-02 AE001073.1	NT	Archaeoglobus fulgidus section 34 of 172 of the complete genome
	İ				0 00 00 00 00 00	±14	Becilus stearothermophilus BsrFl methylase (FIM) and BsrFl restriction endonuclease (FIK) genes, complete
11875	24863	38059	2.25		8.5E-02 AF283050.1	Z	Helicobacter pylori 26695 section 130 of 134 of the complete genome
5202	L.			8 5F-02	8 5F-02 N76915 1	EST HUMAN	yw46h08.r1 Soares fetal liver spieen 1NFLS Homo sapiens cDNA clone IMAGE:245823 5'
70.70	.1						og83b07.s1 NCI_CGAP_Kid6 Homo saplens cDNA clone IMAGE:1592917 3' similar to gb:K01144 HLA
5786	18978	32283			8.5E-02 AA985491.1	EST_HUMAN	CLASS II HISTOCOMPATIBILITY ANTIGEN, GAMMA CHAIN PRECURSOR (HUMAN);
5826	19016		1.39		8.5E-02 P08089	SWISSPROT	M PROTEIN, SEROTYPE 6 PRECURSOR
6135	19314	32653	6.61	8.5E-02	AF23388	LΝ	Mus musculus phospholipase C-like protein mRNA, partial cds
8805	21884		1.98	8.5E-02	6754779 NT	LN	Mus musculus myosin XV (Myo15), mRNA
10041	L				8.5E-02 BE833054.1	EST_HUMAN	RC4-0T0037-200700-014-e05 OT0037 Homo saplens cDNA
10041	L	L			8.5E-02 BE833054.1	EST HUMAN	RC4-OT0037-200700-014-e05 OT0037 Homo sapiens cDNA
10572	L				8.5E-02 X76731.1	LN	V.ammodytes gehe for animodytoxin C
10702	_	L			11418108 NT	LΖ	Homo sapiens chromosome 22 open reading frame 5 (C2ZURF5), mKNA
11424	24485		8.03		8.5E-02 AF155510.1	NT	Homo sapiens heparanase precursor, mKNA, complete cos
11446		38173	3.82		8,5E-02 AB001562.1	M	Streptococcus mutans gene for glucose-1-phosphate undylytransterase, complete cos
12873	Į.		2.76		8.5E-02 AJ005586.1	, ,	Antirrhinum majus mRNA for MYB-related transcription factor
13070	ł		2.44		8.5E-02 AA362934.1	EST_HUMAN	EST72736 Ovary II Homo sepiens cDNA 5' end
2732	16070	28961	4.05		8.4E-02 W69330.1	EST_HUMAN	zd44e11.r1 Soares fetal heart NbHH19W Homo sapiens cDNA done imAGE: 345032.0
5427	18627	31603	9.84		8.4E-02 BE267153.1	EST_HUMAN	601190436F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3534393 5
6828	1	33388			8.4E-02 AK024458.1	뉟	Homo capiens mRNA for FLJ00050 protein, partial cds
8218	l				8.4E-02 BE095074.1	EST HUMAN	CMS-BT0790-260400-162-d05 BT0790 Homo sapiens cDivA
9043		35664	1.15		8.4E-02 AF218890.1	Ā	Homo sapiens attractin precursor (A I KN) gene, exon z

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					0		
Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Velue	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
10571	23606	37211	1.84	8.4E-02	4E-02 Al735184.1	EST_HUMAN	as88g10.x1 Barstead colon HPLRB7 Homo sapiens cDNA clone IMAGE:2335842.3' stmilar to TR:O88312 O88312 GOB-4.;
10631	23865	L	0.48	8.4E-02	4E-02 AV730682.1	EST_HUMAN	AV730682 HTF Homo sapiens cDNA clone HTFBMG04 5'
12351	26264	32114	1.67	8.4E-02	8.4E-02 R79408.1	EST_HUMAN	y83h12.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:145895 5'
3682			7.77	8.3E-02		SWISSPROT	HYPOTHETICAL LIPOPROTEIN MG309 HOMOLOG PRECURSOR
3709			0.75			EST HUMAN	th82g06.x1 Scares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:2125210 3'
3709	ı	29874	0.75			EST_HUMAN	th82g06.x1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:2125210 3'
4417	17558		0.68	L	M54964.1	NT	C.thummi A2b region open reading frame, complete cds
6386	19558	32917	0.74	8.3E-02		EST_HUMAN	wo79f11.x1 NCI_CGAP_Kid11 Homo saplens cDNA clone IMAGE:2461581 3'
6496	19662					NT	Homo sapiens protocadherin 43 gene, exon 1
8169	l	L	3.08			N TN	Rattus norvegicus dystrophin-related protein 2 A-form splice variant (Drp2) mRNA, complete cds
							og88g08.s1 NCI_CGAP_Kid5 Hamo sapiens cDNA clone IMAGE:14554223' similar to contains L1.t1 L1 L1
8202			1.06		AA865285.1	EST_HUMAN	repetitive element ;
8495			1.31		8.3E-02 AA987873.1	EST_HUMAN	oq81f10.s1 NCI_CGAP_Kid6 Homo sapiens cDNA clone IMAGE:15927793'
			\ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \		7 000000	1444	ia05h10.x1 Human Pancreatic Islets Homo saplens cDNA 3' similar to TR:Q16332 Q15332 GAMMA
9738		36377	1.09		AW 583503.1	ESI_HOMAN	SUBUNIT OF SUDUM PUTASSION ATTASS LINE:
9751	22689		2.02		AL161595.2	¥	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 91
10549	23584		0.72		AF020409.1	٦	Dictyostellum discoldeum DocA (docA) mRNA, complete cds
12448	26128		1.81	8.3E-02	BE958458.1	EST_HUMAN	601644770F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:3929693 5'
1410	14564		9.13	_	Y08170.2	Z	Gallus gallus mRNA for for OBCAM protein gamma isoform
1525	14678	27759	2.03	L		TN	Canis familiaris glutamata transporter (EAAT4) mRNA, complete cds
3141	16317		1.97	8.2E-02	ļ. !	NT	Homo sapiens chromosome 21 segment HS21C006
3904	17063		1.35			TN	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 10
4114	<u>l</u>	L	66.0		AL163206.2	IN	Homo sapiens chromosome 21 segment HS21C006
4399	17542		6.58		P48960	SWISSPROT	LEUCOCYTE ANTIGEN CD97 PRECURSOR
4399	l_	L	6.58		P48960	SWISSPROT	LEUCOCYTE ANTIGEN CD97 PRECURSOR
4399	L	L	6.58			SWISSPROT	LEUCOCYTE ANTIGEN CD97 PRECURSOR
5192	L	31282		L	l	ΤΝ	Mus musculus zinc transporter (ZnT-3) gene, complete ods
5450	18650	31629	1.48		BE897030.1	EST_HUMAN	601439676F1 NIH_MGC_72 Homo sapiens cDNA done IMAGE:3924523 5'
7165	L		3.16		AF309555.1	NT	Bos taurus connective tissue growth factor precursor (CTGF) gene, complete cds
7910	L		85.0		AV743341.1	EST_HUMAN	AV743341 CB Homo saplens cDNA clone CBLANF07 5'
8905			09:0	L	U29397.1	NT	Rattus norvegicus plasma membrane Ca2+ ATPase isoform 3 (PMCA3) gene, 5' flanking region
8971	١		3.24		AW875126.1	EST HUMAN	RC2-PT0004-031299-011-d05 PT0004 Homo sapiens cDNA
9799	22839	36416	4.88	Ш	8.2E-02 X04197.1	ΤN	Beet necrotic yallow vain virus RNA-2

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	Top Hit Database Source	EST_HUMAN   601115055F1 NIH_MGC_16 Homo sepiens cDNA clone IMAGE:3355596 67	NT Chiamydophila pneumoniae AR39, section 73 of 94 of the complete genome	EST_HUMAN   QV4-CT0361-021299-049-b01 CT0361 Homo sapiens cDNA		N1 afternatively spliced	Pseudomonas putida malonate decarboxylase gene cluster (mdcA, mdcB, mdcD, mdcE, mdcB, mdcB, mdcB, mdcB, mdcB, mdcB, mdcB, mdcB, mdcB, mdcB, mdcB, mdcB, mdcB, mdcB, mdcB, mdcB, mdcB, mdcB, mdcB, mdcB, mdcB, mdcB, mdcB, mdcB, mdcB, mdcB, mdcB, mdcB, mdcB, mdcB, mdcB, mdcB, mdcB, mdcB, mdcB, mdcB, mdcB, mdcB, mdcB, mdcB, mdcB, mdcB, mdcB, mdcB, mdcB, mdcB, mdcB, mdcB, mdcB, mdcB, mdcB, mdcB, mdcB, mdcB, mdcB, mdcB, mdcB, mdcB, mdcB, mdcB, mdcB, mdcB, mdcB, mdcB, mdcB, mdcB, mdcB, mdcB, mdcB, mdcB, mdcB, mdcB, mdcB, mdcB, mdcB, mdcB, mdcB, mdcB, mdcB, mdcB, mdcB, mdcB, mdcB, mdcB, mdcB, mdcB, mdcB, mdcB, mdcB, mdcB, mdcB, mdcB, mdcB, mdcB, mdcB, mdcB, mdcB, mdcB, mdcB, mdcB, mdcB, mdcB, mdcB, mdcB, mdcB, mdcB, mdcB, mdcB, mdcB, mdcB, mdcB, mdcB, mdcB, mdcB, mdcB, mdcB, mdcB, mdcB, mdcB, mdcB, mdcB, mdcB, mdcB, mdcB, mdcB, mdcB, mdcB, mdcB, mdcB, mdcB, mdcB, mdcB, mdcB, mdcB, mdcB, mdcB, mdcB, mdcB, mdcB, mdcB, mdcB, mdcB, mdcB, mdcB, mdcB, mdcB, mdcB, mdcB, mdcB, mdcB, mdcB, mdcB, mdcB, mdcB, mdcB, mdcB, mdcB, mdcB, mdcB, mdcB, mdcB, mdcB, mdcB, mdcB, mdcB, mdcB, mdcB, mdcB, mdcB, mdcB, mdcB, mdcB, mdcB, mdcB, mdcB, mdcB, mdcB, mdcB, mdcB, mdcB, mdcB, mdcB, mdcB, mdcB, mdcB, mdcB, mdcB, mdcB, mdcB, mdcB, mdcB, mdcB, mdcB, mdcB, mdcB, mdcB, mdcB, mdcB, mdcB, mdcB, mdcB, mdcB, mdcB, mdcB, mdcB, mdcB, mdcB, mdcB, mdcB, mdcB, mdcB, mdcB, mdcB, mdcB, mdcB, mdcB, mdcB, mdcB, mdcB, mdcB, mdcB, mdcB, mdcB, mdcB, mdcB, mdcB, mdcB, mdcB, mdcB, mdcB, mdcB, mdcB, mdcB, mdcB, mdcB, mdcB, mdcB, mdcB, mdcB, mdcB, mdcB, mdcB, mdcB, mdcB, mdcB, mdcB, mdcB, mdcB, mdcB, mdcB, mdcB, mdcB, mdcB, mdcB, mdcB, mdcB, mdcB, mdcB, mdcB, mdcB, mdcB, mdcB, mdcB, mdcB, mdcB, mdcB, mdcB, mdcB, mdcB, mdcB, mdcB, mdcB, mdcB, mdcB, mdcB, mdcB, mdcB, mdcB, mdcB, mdcB, mdcB, mdcB, mdcB, mdcB, mdcB, mdcB, mdcB, mdcB, mdcB, mdcB, mdcB, mdcB, mdcB, mdcB, mdcB, mdcB, mdcB, mdcB, mdcB, mdcB, mdcB, mdcB, mdcB, mdcB, mdcB, mdcB, mdcB, mdcB, mdcB, mdcB, mdcB, mdcB, mdcB, mdcB, mdcB, mdcB, mdcB, mdcB, mdcB, mdcB, mdcB, mdcB, mdcB, mdcB, mdcB, mdcB, mdcB, mdcB	NT Xyella fastidiosa, sectlon 152 of 229 of the complete genome	HUMAN		EST_HUMAN   wd86f08.x1 NG _CGAP_Lu24 Home capiens cDNA clone IMAGE:2338603 3'			NT Homo sapiens extracellular glycoprotein lactifin precursor, gene, complete cds		EST_HUMAN   UHH-BIS-eko-g-01-0-UI:s1 NCI_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2736940 3	$\neg$		EST_HUMAN EST366723 MAGE resequences, MAGC Homo saplens cDNA				T_HUMAN		,	EST_HUMAN   601855548F1 NIH_MGC_57 Homo saplens cDNA clone IMAGE:4075619 5			EST_HUMAN   EST378191 MAGE resequences, MAGI Homo sapiens cDNA		NT M.musculus gene for geletinase B	Herpesvirus salmiri transformat on-associated protein (STP), and dihydrofolate reductase (DHFR) gene, s  NT complete cds, and small nuclear RNAs (uRNAs)	
	Top Hit Acession Na	2E-02 BE254318.1	2E-02 AE002246.2	2E-02 AW862195.1		2E-02 AF275366.1	1E-02 AB017138.1	1E-02 AE004008.1	1E-02 T11532.1	IE-02 AL163279.2	IE-02 A1692681.1	11426974 NT	11426974 NT	VY005150.1	W 269778.1	1W450487.1	4W450487.1	8.1E-02 AL 163202.2	AW954653.1	J60315.1	J26535.1	J26535.1	3E067219.1	D90915.1	D90915.1	BF246744.1	M23449.1	8.0E-02 AL445067.1	AW966118.1	4503034 NT	8.0E-02 X72794.1	8.0E-02 M28071.1	
	Most Similar (Top) Hit BLAST E Value	8.2E-02	8.2E-02	8.2E-02		8.2E-02	8.1E-02		8.1E-02		8.1E-02	8.1E-02	8.1E-02	8.1E-02/	8.1E-02	8.1E-02				8.0E-02	8.0E-02	8.0E-02	8.0E-02	8.0E-02	8.0E-02	8.0E-02	8.0E-02			<u> </u>	8.0E-02		
	Expression Signal	2.27	3.93	1.43		2.58	96 0	1.03	0.89	0.83	66.0	99.0	0.56	1.83	0.7	0.47	0.47	1.99	7.61	99'0	11.83	11.83	4.4	0.93	0.93	3.21	1.55			0.74	6.87		
-	ORF SEQ ID NO:	36599			<u> </u>		85226	32371	33043			35151	35152			37511	37512	38477	26246	27191			28196		28705							31142	l
	Exan SEQ ID NO:	23004	25318	25458		25875	14877	19063	19674			21616	21616			23891	23891	l	16003	14132	16046		15095	15575	15575	15666	L	L	_	_	L	1	1
	Probe SEQ ID NO:	9962	12454	12686		12909	1524	5873	699	7347	7756	8535	8535	10116	10685	10858	10858	11790	8	. 959	1733	1733	1952	2447	2447	2541	2881	2965	3919	4182	4935	5038	

Page 131 of 550 Table 4 Single Exon Probes Expressed in Placenta

		_	_	_			_	_					_		_	_	_			_	_	_	_	_	т-		_	•	_	
Top Hit Descriptor	Homo sapiens ABCA1 (ABCA1) gene, complete cds	Botrytis cinerea strain T4 cDNA library under conditions of nitrogen deprivation	H.sapiens AGT gene, Intron 4	H.sapiens AGT gene, intron 4	Homo sapiens chromosome 21 segment HS21C009	Home sapiens SCG10 like-protein, helicase-like protein NHL, M68, and ADP-ribosylation factor related protein 1 (ARFRP1) cenes, complete cds.	House position through processes father (lineard) supportantly member 9 (TNFSF9) mRNA	nono septens unitro rectors ractor (rigaria) superiaring mentaci o (111) or o (111)	Drosophila crena hunchback region	Homo saplens cAMP responsive element binding protein-like Z (CKEBLZ) mKNA	600943191F1 NIH_MGC_15 Home sapiens cDNA clone IMAGE::2959510 5	ar86c08.x1 Barstead colon HPLRB7 Homo sapiens cDNA clone IMAGE:2173646 3' strullar to gb:Z26876	60S KIBOSOMAL PRO LEIN LOB (HOWARN);	Mus musculus colony stimulating factor 1 receptor (Cst11), minna	Mus musculus colony stimulating factor 1 receptor (Csf1r), mRNA	Arabidopsis thaliana RXW24L mRNA, partial cds	RC3-GN0042-310800-024-d11 GN0042 Hamo sapiens cDNA	Saccheromyces cerevisiae suppressor of MIF2 Smt4p (SMT4) gene, complete cds	outsb05.s1 NCI_CGAP_Br2 Homo saplens cDNA clone IMAGE:1632465 3' similar to WP:C37A2.2	CE08611;	oue3505.91 NCI_CGAP_Br2 Homo sapiens cDNA clone IMAGE:1632455 3' similar to W.F.;C3/AZ.Z	WESELOT AS STATES IN OF DA P S4 Home seniens cONA clone IMAGE:2370097 3	WOUNDLAST COMPANY OF A PROPERTY OF THE WORK AND THE WORLD AS THE WINDS TO SEE THE WORLD AS THE WORLD AS THE WORLD AS THE WORLD AS THE WORLD AS THE WORLD AS THE WORLD AS THE WORLD AS THE WORLD AS THE WORLD AS THE WORLD AS THE WORLD AS THE WORLD AS THE WORLD AS THE WORLD AS THE WORLD AS THE WORLD AS THE WORLD AS THE WORLD AS THE WORLD AS THE WORLD AS THE WORLD AS THE WORLD AS THE WORLD AS THE WORLD AS THE WORLD AS THE WORLD AS THE WORLD AS THE WORLD AS THE WORLD AS THE WORLD AS THE WORLD AS THE WORLD AS THE WORLD AS THE WORLD AS THE WORLD AS THE WORLD AS THE WORLD AS THE WORLD AS THE WORLD AS THE WORLD AS THE WORLD AS THE WORLD AS THE WORLD AS THE WORLD AS THE WORLD AS THE WORLD AS THE WORLD AS THE WORLD AS THE WORLD AS THE WORLD AS THE WORLD AS THE WORLD AS THE WORLD AS THE WORLD AS THE WORLD AS THE WORLD AS THE WORLD AS THE WORLD AS THE WORLD AS THE WORLD AS THE WORLD AS THE WORLD AS THE WORLD AS THE WORLD AS THE WORLD AS THE WORLD AS THE WORLD AS THE WORLD AS THE WORLD AS THE WORLD AS THE WORLD AS THE WORLD AS THE WORLD AS THE WORLD AS THE WORLD AS THE WORLD AS THE WORLD AS THE WORLD AS THE WORLD AS THE WORLD AS THE WORLD AS THE WORLD AS THE WORLD AS THE WORLD AS THE WORLD AS THE WORLD AS THE WORLD AS THE WORLD AS THE WORLD AS THE WORLD AS THE WORLD AS THE WORLD AS THE WORLD AS THE WORLD AS THE WORLD AS THE WORLD AS THE WORLD AS THE WORLD AS THE WORLD AS THE WORLD AS THE WORLD AS THE WORLD AS THE WORLD AS THE WORLD AS THE WORLD AS THE WORLD AS THE WORLD AS THE WORLD AS THE WORLD AS THE WORLD AS THE WORLD AS THE WORLD AS THE WORLD AS THE WORLD AS THE WORLD AS THE WORLD AS THE WORLD AS THE WORLD AS THE WORLD AS THE WORLD AS THE WORLD AS THE WORLD AS THE WORLD AS THE WORLD AS THE WORLD AS THE WORLD AS THE WORLD AS THE WORLD AS THE WORLD AS THE WORLD AS THE WORLD AS THE WORLD AS THE WORLD AS THE WORLD AS THE WORLD AS THE WORLD AS THE WORLD AS THE WORLD AS THE WORLD AS THE WORLD AS THE WORLD AS THE WORLD AS THE WORLD AS THE WORLD AS THE WORLD AS THE WORLD AS THE WORLD AS THE WORLD AS THE WORLD AS THE WORLD AS THE W	Constitute alament.	Include description 1. E. Dono consister and Alone IMACE 4570467 5; similar to contains   1.3   1	00090002.yo NCI_CGAP_LUS HOMO saptens curva cione invade: 1370407 3 similar to contents critical in	Tokio Entoneo 440700 ONE 600 ENIORS Home caniene c'ONA	L'INCELLINOUS I TOTAL DO CONTRACTOR DE L'ANTICO DE L'ANTIC DE L'ANTIC DE L'ANTIC DE L'ANTIC DE L'ANTIC DE L'ANTIC DE L'ANTIC DE L'ANTIC DE L'ANTIC DE L'ANTIC DE L'ANTIC DE L'ANTIC DE L'ANTIC DE L'ANTIC DE L'ANTIC DE L'ANTIC DE L'ANTIC DE L'ANTIC DE L'ANTIC DE L'ANTIC DE L'ANTIC DE L'ANTIC DE L'ANTIC DE L'ANTIC DE L'ANTIC DE L'ANTIC DE L'ANTIC DE L'ANTIC DE L'ANTIC DE L'ANTIC DE L'ANTIC DE L'ANTIC DE L'ANTIC DE L'ANTIC DE L'ANTIC DE L'ANTIC DE L'ANTIC DE L'ANTIC DE L'ANTIC DE L'ANTIC DE L'ANTIC DE L'ANTIC DE L'ANTIC DE L'ANTIC DE L'ANTIC DE L'ANTIC DE L'ANTIC DE L'ANTIC DE L'ANTIC DE L'ANTIC DE L'ANTIC DE L'ANTIC DE L'ANTIC DE L'ANTIC DE L'ANTIC DE L'ANTIC DE L'ANTIC DE L'ANTIC DE L'ANTIC DE L'ANTIC DE L'ANTIC DE L'ANTIC DE L'ANTIC DE L'ANTIC DE L'ANTIC DE L'ANTIC DE L'ANTIC DE L'ANTIC DE L'ANTIC DE L'ANTIC DE L'ANTIC DE L'ANTIC DE L'ANTIC DE L'ANTIC DE L'ANTIC DE L'ANTIC DE L'ANTIC DE L'ANTIC DE L'ANTIC DE L'ANTIC DE L'ANTIC DE L'ANTIC DE L'ANTIC DE L'ANTIC DE L'ANTIC DE L'ANTIC DE L'ANTIC DE L'ANTIC DE L'ANTIC DE L'ANTIC DE L'ANTIC DE L'ANTIC DE L'ANTIC DE L'ANTIC DE L'ANTIC DE L'ANTIC DE L'ANTIC DE L'ANTIC DE L'ANTIC DE L'ANTIC DE L'ANTIC DE L'ANTIC DE L'ANTIC DE L'ANTIC DE L'ANTIC DE L'ANTIC DE L'ANTIC DE L'ANTIC DE L'ANTIC DE L'ANTIC DE L'ANTIC DE L'ANTIC DE L'ANTIC DE L'ANTIC DE L'ANTIC DE L'ANTIC DE L'ANTIC DE L'ANTIC DE L'ANTIC DE L'ANTIC DE L'ANTIC DE L'ANTIC DE L'ANTIC DE L'ANTIC DE L'ANTIC DE L'ANTIC DE L'ANTIC DE L'ANTIC DE L'ANTIC DE L'ANTIC DE L'ANTIC DE L'ANTIC DE L'ANTIC DE L'ANTIC DE L'ANTIC DE L'ANTIC DE L'ANTIC DE L'ANTIC DE L'ANTIC DE L'ANTIC DE L'ANTIC DE L'ANTIC DE L'ANTIC DE L'ANTIC DE L'ANTIC DE L'ANTIC DE L'ANTIC DE L'ANTIC DE L'ANTIC DE L'ANTIC DE L'ANTIC DE L'ANTIC DE L'ANTIC DE L'ANTIC DE L'ANTIC DE L'ANTIC DE L'ANTIC DE L'ANTIC DE L'ANTIC DE L'ANTIC DE L'ANTIC DE L'ANTIC DE L'ANTIC DE L'ANTIC DE L'ANTIC DE L'ANTIC DE L'ANTIC DE L'ANTIC DE L'ANTIC DE L'ANTIC DE L'ANTIC DE L'ANTIC DE L'ANTIC DE L'ANTIC DE L'ANTIC DE L'ANTIC DE L'ANTIC DE L'ANTIC DE L'ANTIC DE L'ANTIC DE L'ANTIC DE L'AN	600943055F1 NIH_MGC_15 Hamo sapiens CUNA clone iMAGE: 2939093 3	Homo sapiens zinc finger protein 92 (ZFP92), expressed-Xq28STS protein (XQ28ORF), and biglycan (BGN) genes, complete cds; and plasma membrane calclum ATPase isoform 3 (PMCA3) gene, partial cds
Top Hit Database	TN	ΤN	IN	NT	NT	Ę		Z	ΙN	ΝΤ	<b>EST_HUMAN</b>		EST_HUMAN	NT	LΝ	TN	EST_HUMAN	IN		EST_HUMAN	, HOL	NAMOR TO LO	EST HOWAN	144441111111111111111111111111111111111	ESI HOMAN	HOU HOU	NOIN I	ES L HOWAIN	EST_HUMAN	F
Top Hit Acession No.	8.0E-02 AF275948.1	8.0E-02 AL114993.1	<b>474208.1</b>	<74208.1	8.0E-02 AL163209.2	004.7708.4	0.UE-UZ AFZ11790.1	4507608 N	8.0E-02 AJ006376.1	4503034 NT	7.9E-02 BE250008.1		7.9E-02 AI582029.1	6681044 NT	6681044 NT	7.9E-02 AB008019.1	7.9E-02 BF368016.1	7.9E-02 U27832.1		7.9E-02 Al081644.1		7.9E-02/AI081644.1	7.9E-02/AI/61638.1		7.8E-02 AI793275.1	, 2500051	1.8E-02 AI/932/3.1	7.8E-02 BE836331.1	7.8E-02 BE250048.1	7.8E-02 U82695.2
Most Similar (Top) Hit BLAST E Value	8.0E-02	8.0E-02	8.0E-02 X74208.1	8.0E-02 X74208.1	8.0E-02	100	8.UE-02	8.0E-02	8.0E-02	8.0E-02	7.9E-02		7.9E-02/	7.9E-02	7.9E-02	7.9E-02	7.9E-02	7.9E-02		7.9E-02	İ	1	1	i i	7.8E-02	i i	1	ı		
Expression Signal	1.61	2.41	1.38	1.38	0.49	3	7.04	1.69	3.54	1.85	3.37		12.53	4.47	4.47	1.16	1.14	3.1		5.6		2.0	1.27		1.49				2.97	<u>.</u>
ORF SEQ ID NO:	32513			}_	ŀ			38811	32061		28504	L	29240	30110				34824		36859	Ŀ	36860			27457		27458			33504
Exen SEQ ID NO:	19196	1	ı	1	ŧ		- 1	25107	25337	17332	15376		16219	17111	1	18062	1	21303	1	23269	l	J	25664		14396		- 1	18045	17003	20087
Probe SEQ ID NO:	7330	L	9589	9589	10361		11032	12127	12486	13134	2243		3043	3953	3953	4932	6836	8221		10234		10234	13008		1237		1237	4915	5198	7223

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Probe Exon SEQ ID SEQ ID NO: NO:	$\vdash \vdash$	Expression	Most Similar		Top Hit	
	ORF SEO D: ID NO:		BLASTE Value	Top Hit Acession No.	Database Source	i op Hit Descriptor
7223	20087 33505	1.1	7.	8E-02 U82695.2	TN	Homo saplens zinc finger protein 92 (ZFP92), expressed-Xq28STS protein (XQ28ORF), and biglycan (BGN) genes, complete ods: and plasma membrane calcium ATPase isoform 3 (PMCA3) gene, partial ods
		0.93	7.	8E-02 BE897947.1	EST_HUMAN	601440438F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3925449 51
1_	22160 35702	0.69	7	8E-02 X78344.1	LN	S.cerevisiae CAT8 gene
<u> </u>		80	^	BE-02 AF233437.1	-N	Homo sapiens FYVE domain-containing dual specificity protein phosphatase FYVE-DSP1b mRNA, complete ods
┸						Homo sapiens FYVE domain-containing dual specificity protein phosphatase FYVE-DSP1b mRNA, complete
9253 22	22330 35878	8.0	7		$\neg$	αds
L		6.0	1	.8E-02 AA469354.1	EST HUMAN	Incebbo6.r1 NCI_CGAP_Pr1 Homo sapiens cDNA clone IMAGE:771731
L		37 0.56	7	.8E-02 Z99124.1	LN	Becillus subtilis complete genome (section 21 of 21): from 3999281 to 4214814
10901	L	16 2.19	7		IN	Human interleukin-11 receptor alpha chain gene, complete cds
			7	.8E-02 U72847.1	TN	Homo saplens envoplakin (EVPL) gene, exons 15 through 18
l_			7	.7E-02 AF181897.1	LN	Homo sapiens WRN (WRN) gene, complete cds
3677 16			_		TN	Homo sapiens partial AF-4 gene, exons 2 to 7 and Alu repeat elements
						zu53d11.r1 Soares ovary tumor NbHOT Homo sapiens cDNA clone IMAGE:741717 5' similar to
8093 21	21175 34690	5.38	7	.7E-02 AA402949.1	EST_HUMAN	TR:G1173905 G1173905 SPLICEOSOME ASSOCIATED PROTEIN.;
	23078 36679		4	.7E-02 P38080	SWISSPROT	PROBABLE SERINE/THREONINE-PROTEIN RINASE YBROSSO
	23374 36981	84 0.84		7E-02 Al318662.1	EST HUMAN	1280b08.x1 NCI_CGAP_HSC2 Homo squiens cUNA clone IMAGE:2050359 3. Similar to go.z.zoo.195050 RIBOSOMAL PROTEIN L38 (HUMAN);
l					HST HUMAN	ta80b08.x1 NCL_CGAP_HSC2 Homo sapiens cDNA clone IMAGE:2050359 3' similar to gb:Z26876 90S RIBOSOMAL PROTEIN L38 (HUMAN);
	1			1142275	LN	Homo sapiens KIAA0628 gene product (KIAA0628), mRNA
			1	.6E-02 BE514432.1	EST_HUMAN	601316426F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3634903 5
	16661 29673	73 0.98	_	.6E-02 AA296447.1	EST_HUMAN	EST112214 Cerebellum II Homo sapiens cDNA 5' end similar to similar to protocadherin 43
1_	L					Homp sapiens ASCL3 gene, CEGP1 gene, C11ar114 gene, C11ar115 gene, C11ar116 gene and C11ar11
3649	16812 29825	25 0.96	_	.6E-02 AJ400877.1	NT	gene
L			_	.6E-02 A1061275.1	EST_HUMAN	an25g02.x1 Gessler Wilms fumor Homo sapiens cDNA clone IMAGE:1699730 3
<u>J</u>	19653 33015		_	.6E-02 BE379328.1	EST_HUMAN	601236402F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3608401 5
١_		1.11	1	.6E-02 AJ131016.1	IN	Homo saplens SCL gene locus
<u>L</u>		0.99	7	.6E-02 AL139078.2	TN	Campylobacter Jejuni NCTC11168 complete genome; segment 5/6
<u> </u>	23459 37064	64 0.5	2	.6E-02 BE708002.1	EST_HUMAN	RC1-HT0545-020800-017-d06 H10545 Homo saptens cUNA
<u> </u>	L		_	.6E-02 BE959838.2	EST_HUMAN	601654915R1 NIH_MGC_57 Homo saplens oDNA clone IMAGE:3839810 3
┸	23848 37469	169	,	.6E-02 X92656.1	TN	L.esculentum mRNA for triose phosphate translocator

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				Most Similar		ži i	
Probe SEQ ID NO:	SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	(Top) Hit BLAST E Value	Top Hit Acession No.	lop Hit Database Source	Top Hit Descriptor
10815	5 23848	37470	76.0	7.6E-02	7.6E-02 X92656.1		L. esculentum mRNA for triose phosphate translocator
11974	١			7.6E-02	7.6E-02 AW 996645.1	EST HUMAN	QV3-BN0046-150400-151-e04 BN0046 Homo sapiens cDNA
807	13987	27039	1.66	7.5E-02	5902093 NT	NT	Homo sapiens solute carrier (amily 6 (neurotransmitter transporter, glycine), membor 0 (SLC6A9), mRNA
80,	7 13987	27040	1.68	7.5E-02	5902093 NT		Homo sapiens solute carrier family 6 (neurotransmitter transporter, glycine), member 9 (SLC6A9), mRNA
1971	1				7.5E-02 AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
4630	17766	30748	0.74	7.5E-02	7.5E-02 AB015961.1	TN	Homo sapiens IL-18 gene for interleukin-18, intron 1 and exon 2
5974	19159		1.45		7.5E-02 A1948714.1	EST_HUMAN	wq24h09.x1 NC _CGAP_Kid11 Home sapiens cDNA clone IMAGE:2472257 3'
8533	3 21614	35150	1.28		7.5E-02 Al864367.1	EST_HUMAN	wi52b02.x1 NCj_CGAP_Bm26 Homo sapiens cDNA clone IMAGE:2428491 3' similar to gb:M14328 ALPHA ENOLASE (HUMAN);
8705	1	L	1.36		7.5E-02 AU116913.1	EST_HUMAN	AU116913 HEMBA1 Homo sapiens cDNA clone HEMBA1000264 5
10238			0.49		7.5E-02 BF221730.1	EST HUMAN	7c61c05.x1 NCL_CGAP_Pr28 Homo sepiens cDNA clone IMAGE:3578504 3' similar to contains element MER27 repetitive element ;
10711	┸				7.5E-02 BF206809.1	1	601870205F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4100449 5'
10816	L			7.5E-02	7.5E-02 X79460.1	NT	C.fimi DSM 20113 16S rDNA
9	L		1.41	7.4E-02	7.4E-02 AW838547.1	EST_HUMAN	RC5-LT0054-260100-011-H09 LT0054 Homo sapiens cDNA
1489	١.		1.21	7.4E-02	7.4E-02 AF030027.1	NT	Equine herpesvirus 4 strain NS80567, complete genome
2648	1		0.96	7.4E-02	LN 6905579		Mus musculus paired-like homeodomain transcription factor 1 (Pitx1), mRNA
368	1	29854	1.21		7.4E-02 Al807885.1	EST HUMAN	w/43h01.x1 Soares_NFL_T_GBC_S1 Hamo saplens cDNA clone IMAGE:2358385 3'
4826	1				7.4E-02 L78810.1	LN	Homo sapiens ADP/ATP carrier protein (ANT-2) gene, complete cds
491	18044		2.65	7.4E-02	6978442 NT	NT TN	Rettus norvegicus Activin receptor like kinase 1 (Acvrl1), mRNA
5056	ı			7.4E-02	8678492 NT		Mus musculus ubiquintin c-terminal hydrolase related polypeptide (Uchrp), mRNA
6624			1.69		7.4E-02 R17477.1	T HUMAN	yg14g06.r1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:32339 5
671	7 19875	33266		-	7.4E-02 AF030422.1	NT	Electrophorus electricus acetylcholinesterase catalytic subunit precursor gene, complete cds
7636	6 20705	34184	0.64		7.4E-02 AA605132.1	EST_HUMAN	no71d02.s1 NCI_CGAP_AA1 Homo sapiens cDNA clone IMAGE:1112259 3'
8085	5 21167	34683	1.11	7.4E-02	7.4E-02 BE880112.1	EST_HUMAN	601493366F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3895264 5'
8699	l		1.26		7.4E-02 U56089.1	IN	Human periodic tryptophan protein 2 (PWP2) gene, exons 15 to 21, and complete cds
	ı					1477	hh67d11.yi NCI_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2967861 5' similar to SW:SCA2_HUMAN   Oxego secont Topy Capping A SOCIA TED MEMBRANE PROTEIN 2
9367	7 22442	36002	1.08	ļ	7.4E-02 AW629505.1	ESI TOMAN	O DIE SECRETORIO CONTRETATO CONTRETATO CONTRETATO CONTRETATO CONTRETATO CONTRETATO CONTRETATO CONTRETATO CONTRETATO CONTRETATO CONTRETATO CONTRETATO CONTRETATO CONTRETATO CONTRETATO CONTRETATO CONTRETATO CONTRETATO CONTRETATO CONTRETATO CONTRETATO CONTRETATO CONTRETATO CONTRETATO CONTRETATO CONTRETATO CONTRETATO CONTRETATO CONTRETATO CONTRETATO CONTRETATO CONTRETATO CONTRETATO CONTRETATO CONTRETATO CONTRETATO CONTRETATO CONTRETATO CONTRETATO CONTRETATO CONTRETATO CONTRETATO CONTRETATO CONTRETATO CONTRETATO CONTRETATO CONTRETATO CONTRETATO CONTRETATO CONTRETATO CONTRETATO CONTRETATO CONTRETATO CONTRETATO CONTRETATO CONTRETATO CONTRETATO CONTRETATO CONTRETATO CONTRETATO CONTRETATO CONTRETATO CONTRETATO CONTRETATO CONTRETATO CONTRETATO CONTRETATO CONTRETATO CONTRETATO CONTRETATO CONTRETATO CONTRETATO CONTRETATO CONTRETATO CONTRETATO CONTRETATO CONTRETATO CONTRETATO CONTRETATO CONTRETATO CONTRETATO CONTRETATO CONTRETATO CONTRETATO CONTRETATO CONTRETATO CONTRETATO CONTRETATO CONTRETATO CONTRETATO CONTRETATO CONTRETATO CONTRETATO CONTRETATO CONTRETATO CONTRETATO CONTRETATO CONTRETATO CONTRETATO CONTRETATO CONTRETATO CONTRETATO CONTRETATO CONTRETATO CONTRETATO CONTRETATO CONTRETATO CONTRETATO CONTRETATO CONTRETATO CONTRETATO CONTRETATO CONTRETATO CONTRETATO CONTRETATO CONTRETATO CONTRETATO CONTRETATO CONTRETATO CONTRETATO CONTRETATO CONTRETATO CONTRETATO CONTRETATO CONTRETATO CONTRETATO CONTRETATO CONTRETATO CONTRETATO CONTRETATO CONTRETATO CONTRETATO CONTRETATO CONTRETATO CONTRETATO CONTRETATO CONTRETATO CONTRETATO CONTRETATO CONTRETATO CONTRETATO CONTRETATO CONTRETATO CONTRETATO CONTRETATO CONTRETATO CONTRETATO CONTRETATO CONTRETATO CONTRETATO CONTRETATO CONTRETATO CONTRETATO CONTRETATO CONTRETATO CONTRETATO CONTRETATO CONTRETATO CONTRETATO CONTRETATO CONTRETATO CONTRETATO CONTRETATO CONTRETATO CONTRETATO CONTRETATO CONTRETATO CONTRETATO CONTRETATO CONTRETATO CONTRETATO CONTRETATO CONTRETATO CONTRETATO CONTRETATO CONTRETATO CONTRETATO CONTRETATO CONTRETATO CONTRETATO CONTRETATO CONTRETATO CONTRETATO CONTRETATO CONTR
9367	7 22442	36003	1.08		7.4E-02 AW629605.1	EST_HUMAN	hib7d11.01 NC_CGAP_GOT Hamb expens CUNA didne IMANGE.2501801 5 SITTING TO 3V1.3CAZ_TOWANA OD 5127 SECRETORY CARRIER-ASSOCIATED MEMBRANE PROTEIN 2.
9639	ı				7.4E-02 AI672939.1	EST HUMAN	we74d02.x1 Soares_Dieckgraefe_colon_NHCD Homo sapiens cDNA clone IMAGE:2346819 3'
9639	ll			Н	7.4E-02 AI672939.1	EST_HUMAN	we74d02x1 Soares_Dieckgreefe_colon_NHCD Homo sapiens cDNA clone IMAGE:2346d19 3

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23057         36653         1         7.4E-02         L05203.1           23184         36780         0.49         7.4E-02         LA6512678.1           24335         37975         1.48         7.4E-02         AA059107.1           24207         38604         1.42         7.4E-02         A1125063.1           25589         1.22         7.4E-02         AV379431.1           25580         31968         1.44         7.4E-02         BF035099.1           25585         31968         1.44         7.4E-02         BF035099.1           25586         31968         1.44         7.4E-02         BF035099.1           13676         26708         1.15         7.3E-02         BE94491.2           13676         26709         1.15         7.3E-02         BE94491.2           13676         2670         1.15         7.3E-02         BE94491.2           16040         27748         3.26         7.3E-02         AL163302.2           18240         1.02         7.3E-02         AAV990281.1           18240         1.02         7.3E-02         P05143           20702         34180         2.37         7.3E-02         P05143           21442 </th
23057         36653         1         7.4E-02         BF512678.1         EST_HUMAN           24301         38604         1.48         7.4E-02         BF512678.1         EST_HUMAN           24301         38604         1.42         7.4E-02         AN559167.1         EST_HUMAN           25528         1.22         7.4E-02         AN379431.1         EST_HUMAN           25580         31995         2.61         7.4E-02         AN379431.1         EST_HUMAN           25585         31986         1.44         7.4E-02         AN379431.1         EST_HUMAN           25586         31986         1.44         7.4E-02         BF036099.1         EST_HUMAN           25686         31986         1.44         7.4E-02         BF036099.1         EST_HUMAN           13676         2.670         7.3E-02         BF94691.2         EST_HUMAN           13676         2.670         7.3E-02         BE94961.2         EST_HUMAN           14040         2.74         7.3E-02         BF94961.2         EST_HUMAN           16050         1.15         7.3E-02         BR94961.2         BST_HUMAN           16050         1.27         7.3E-02         BF3402.1         BST_HUMAN           <
23057         36653         1         7.4E-02   D62203.1           23184         36780         0.49         7.4E-02   AP659167.1           24335         37975         1.46         7.4E-02   AA059167.1           245283         1.22         7.4E-02   AA059167.1           255283         1.22         7.4E-02   A1125063.1           255284         1.22         7.4E-02   AN379431.1           25585         31996         2.61         7.4E-02   AW379431.1           25586         31996         2.61         7.4E-02   AW379431.1           25586         31996         2.61         7.4E-02   AW379431.1           25586         31996         2.61         7.4E-02   AW379431.1           25680         1.44         7.4E-02   AW379431.1           25680         1.44         7.4E-02   AW379431.1           13676         2.61         7.3E-02   AW379431.1           13676         7.3E-02   AW900281.1           16040         27748         3.26         7.3E-02   AV79977.1           16050         34180         2.37         7.3E-02   AV77997.1           20702         34180         2.37         7.3E-02   P05143           2102         2.37         7.3E-02   P05143
23057         36653         1         7.4E-02   U62283.1           23184         35780         0.49         7.4E-02   BF512675           24335         37975         1.46         7.4E-02   BF512675           24901         38604         1.42         7.4E-02   A125063           25589         1.22         7.4E-02   A125063           25580         31985         2.61         7.4E-02   A125063           25580         31986         1.44         7.4E-02   A125048           13676         26709         1.15         7.3E-02   BF03509           13676         26709         1.15         7.3E-02   A2869496           13876         26709         1.15         7.3E-02   A89002           16040         27748         3.26         7.3E-02   A198002           20702         34180         2.37         7.3E-02   A19806           21030         34180         2.37         7.3E-02   A19806           21030         0.58         7.3E-02   A19806 <t< td=""></t<>
23057         36653         1           23184         36780         0.49           24335         37975         1.46           25288         1.22           26101         3.74           25580         31995         2.61           25586         31989         2.61           25586         31988         1.44           13676         26708         1.15           13676         26708         1.15           13676         26708         1.15           13676         26701         1.15           13677         2631         1.46           13670         37748         3.26           16040         27748         3.26           16040         27748         2.37           20702         34180         2.37           20702         34181         2.37           21442         1.36           21677         0.58           21677         0.58           21677         0.58           21677         0.58
23057 36653 23184 36780 24335 37975 24201 38604 25288 26101 25580 31995 25580 31995 25580 31995 25580 31996 13676 26709 13676 26709 13676 26709 13676 26709 13676 26709 13676 26709 13676 26709 13676 26709 13676 26709 13676 26709 13676 26717 16040 27748 16050 34181 21030 21030 21442 33128 21030 21442
23057 24335 24301 25288 26101 25589 26101 25586 13876 13876 13876 1386 16040 16040 18240 1874 20702 21442 21442 21442 21442
10019 10146 112802 12802 12802 12802 12803 12803 12803 1703 1703 1803 1703 1703 1703 1703 1703 1703 1703 17

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Top Hit Descriptor	602077757F1 NIH_MGC_62 Homo sapiens cDNA clane IMAGE:4251950 5'	Methanococcus jannaschii section 73 of 150 of the complete genome	CALMODULIN	601883905F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4096224 5	601883558F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4095710 51	Streptococcus pneumoniae putetive response regulator (zmpR), putative histidine kinase (zmpṢ), and putative zno metalloprotease (zmpB) genes, complete cds	Strongylocentrotus purpuratus mitochondrion, complete genome	PROLINE-RICH PROTEIN MP-3	PROLINE-RICH PROTEIN MP-3	Lactococcus lactis cspE gene	Human gene for sex hormone-binding globulin (SHBG)	AV712452 DCA Homo sapiens cDNA clone DCAAUG01 5'	Homo saplens plasma membrane calcium ATPase isoform 1 (ATP2B1) gene, alternative splice products, partial cds	601763523F1 NIH_MGC_20 Homo saplens cDNA clone IMAGE:4026436 5	hq24f11x1 NCI_CGAP_Adr1 Homo sapiens cDNA clone IMAGE:3120333 3' similar to TR:Q9Z340 Q9Z340 ATYPICAL PKC SPECIFIC BINDING PROTEIN ;	og62c07.s1 NCI_CGAP_GCB1 Homo saplens cDNA clone IMAGE:1316844 3'	Homo sapiens zinc finger protein 92 (ZFP92), expressed-Xq28STS protein (XQ28ORF), and biglycan (BGN) genes, complete cds; and plasma membrane calcium ATPese Isoform 3 (PMCA3) gerie, partial cds	601343926F1 NIH_MGC_63 Homo sapiens cDNA clone IMAGE:3685951 5'	601065194F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3451559 5'	2/28h05.s1 Soares, fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:451641 3	Rattus norvegicus bHLH transcription factor Mist1 (Mist1) gene, complete cds	af81a04.r1 Soares_NhHMPu_S1 Homo sapiens oDNA done IMAGE:1048398 5'	AJ230796 Homo saplens library (Seranski P) Homo saplens cDNA clone PS13D5 3'	no05h08.s1 NCI_CGAP_Phe1 Homo sapiens cDNA clone IMAGE:1099839 3'	Homo sapiens ataxia telangiectasia (ATM) gene, complete cdo	CW4-NN1009-200300-118-c11 NN1009 Homo sapiens cDNA	zt57c12.r1 Soares_testis_NHT Homo saplens cDNA clone IMAGE:726454 51	Human immunodeficiency virus type 1 (D9) proviral structural capsid protein (gag) gene, partial ods
Top Hit Database Source	EST_HUMAN	NT	SWISSPROT	EST_HUMAN	EST_HUMAN	F	INT	SWISSPROT	SWISSPROT	LN	N	EST HUMAN	FZ	EST HUMAN	EST HUMAN	EST_HUMAN	_ Ľ	EST_HUMAN	EST_HUMAN	EST_HUMAN	NT	<b>EST_HUMAN</b>	EST HUMAN	EST HUMAN	NT	EST_HUMAN	EST_HUMAN	IN
Top Hit Acession No.	7.2E-02 BF572307.1	7.2E-02 U67531.1	P11120	7.2E-02 BF217596.1	7.2E-02 BF216086.1	7 2F-02 AF224128 1	5834897/NT		P05143	7.2E-02 V17217.1	7.2E-02 X16349.1	7.2E-02 AV712452.1	7 25-02   14561 1	7 2E-02 BF125399.1	7.2E-02 AW873187.1	7.2E-02 AA768204.1	7.2E-02 U82695.2	7.2E-02 BE565003.1	7.2E-02 BE539214.1	7.2E-02 AA706897.1	7.2E-02 AF049874.1	7.2E-02 AA773698.1	7.2E-02 AJ230796.1	7.2E-02 AA584465.1	7.2E-02 U82828.1	7.2E-02 AW900962.1	7.2E-02 AA401779.1	7.1E-02 L02290.1
Most Similar (Top) Hit BLAST E Value	7.2E-02	7.2E-02	7.2E-02 P11120	7.2E-02	7.2E-02	7.25-02	7.2E-02	7.2E-02 P05143	7.2E-02 P05143	7.2E-02	7.2E-02	7.2E-02	7 25-02	7 2E-02	7.2E-02	7.2E-02	7.2E-02	7.2E-02	7.2E-02	7.2E-02	7.2E-02	7.2E-02	7.2E-02	7.2E-02	7.2E-02	7.2E-02	7.2E-02	
Expression Signal	3.07	2.73	8.76	1.11	1.32	,	1.5	9.0	0.6	0.67	0.51	2.19	4 88	96 0	234	0.8	21.2	5.57	3.47	0.55	41.4	2.12	3.83	2.05	4.23	7.37	1.63	2.05
ORF SEQ ID NO:	L	31576			33863				34988	L		36430						37331		37492								28197
Exon SEQ ID NO:	17605	18604	18605	19418	İ	1	- 1	1	1		l	•		1		İ	l	L		23870		ı	1	i .	25327	L	25687	
Probe SEQ ID NO:	4465	Ø	5403	4	7318	7225	9 8	8382	118	18	75	9811	1900	1918	10208	10395	10560	10692	10716	10837	11153	15	12350	12411	12474	12488	13048	1953

Page 136 of 550 Table 4 Single Exon Probes Expressed in Placenta

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Top Hit Descriptor		601872281F1 NIH_MGC_63 Homo sapiens cDNA done IMAGE:4092981 5'	qd92a10.x1 Soares_testis_NHT Homo sapiens cDNA done IMAGE:1736922 3'	Homo sapiens chromosome 21 segment HS21C046	601143974F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:3051234 5	COLLAGEN ALPHA 1(XVI) CHAIN PRECURSOR	Martellia Mtcut-1 gene	zl66f04.s1 Stratagene colon (#937204) Homo sapiens oDNA clone IMAGE:509599 3'	UI-H-BI1-acy-c-07-0-UI.s1 NCI_CGAP_Sub3 Homo sepiens cDNA clone IMAGE:2716020 3	al65a12.s1 Soares_testis_NHT Homo sapiens cDNA clone 1375678 3' similar to gb:K03002 60S RIBOSOMAL PROTEIN L32 (HUMAN);	QV4-BT0407-280100-090-e10 BT0407 Homo saplens cDNA	CM0-UM0001-060300-270-e12 UM0001 Homo sapiens cDNA	Canis familiaris inducible nitric oxide synthase mRNA, complote cds	601816291F1 NIH_MGC_56 Homo saplens cDNA clone IMAGE:4050071 5'	Lumbricus rubellus mRNA for cyclophilin B	AV689285 GKC Homo sapiens cDNA clone GKCCAE08 5'	Gallus gallus mRNA for partial aczonin, XL spliced variant (acz gene)	African swine fever virus, complete genome	Rat Ig germline epsilon H-chain gene C-region, 3' end	Human myosin binding protein H (MyBP-H) gene, complete cds	abgea5.s1 Sceres_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1327184 3' similar to gb:L14837   TIGHT JUNCTION PROTEIN ZO-1 (HUMAN);	Homo sapiens hypothetical protein FLJ20116 (FLJ20116), mRNA	Homo saplens chromosome 21 segment HS21C010	Homo saplens chromosome 21 segment HS21C010	Homo sapiens regulator of Gz-selective protein signaling (ZGAP1) mRNA, and translated products	26S PROTEASOME REGULATORY SUBUNIT S3 (NUCLEAR ANTIGEN 2/107)	26S PROTEASOME REGULATORY SUBUNIT S3 (NUCLEAR ANTIGEN 21D7)	H.saplens flow-sorted chromosome 6 HindIII fragment, SC6pA24F7	M.hyorhinls 115 kDa protein (p115) gene, complete cds	Canine distemper virus strain A75/17, complete genome	Human calmodulin (CALM1) gene, exons 2,3,4,5 and 6, and complete cds	601340661F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3683030 5'
Top Hit	Source	EST_HUMAN	EST_HUMAN	۲N	EST_HUMAN	SWISSPROT	NT	EST_HUMAN	EST HUMAN	EST HUMAN	EST HUMAN	EST HUMAN	Z	EST_HUMAN	NT	EST_HUMAN	TN	TN	INT	NT	EST HUMAN	LN	M	F	F	SWISSPROT	SWISSPROT	LN	LN	ΙN	노	EST_HUMAN
Top Hit Acession	o Z	7.1E-02 BF208802.1	7.1E-02 AI125284.1	7.1E-02 AL163246.2	7.1E-02 BE304764.1	207092	K96677.1	7.0E-02 AA056343.1	7.0E-02 AW138152.1	7 0F-02 AA815438 1	7.0E-02 BE070264.1	7.0E-02 AW 792962.1	7.0E-02 AF077821.1	7.0E-02 BF381987.1		7.0E-02 AV689285.1	7.0E-02 Y19187.1	9628113 NT	7.0E-02 K02901.1	7.0E-02 U27266.1	7.0E-02 AA724295.1	11421638 NT	6.9E-02 AL163210.2	6.9E-02 AL163210.2	4507968 NT	1	Q06364	6.9E-02 Z79163.1	8.9E-02 M34956.1	8.9E-02 AF164967.1	6.9E-02 U12022.1	6.9E-02 BE567435.1
Most Similar (Top) Hit	BLAST E Value	7.1E-02	7.1E-02	7.1E-02	7.1E-02	7.0E-02 Q07092	7.0E-02 X96677.1	7.0E-02	7.0E-02	7 OF-02	7.0E-02	7.0E-02	7.0E-02	7.0E-02	7.0E-02	7.0E-02	7.0E-02	7.0E-02	7.0E-02	7.0E-02	7.0E-02	7.0E-02	6.9E-02	6.9E-02	6.9E-02	6.9E-02 Q06364	8.9E-02 Q06364	6.9E-02	6.9E-02	6.9E-02	6.9E-02	6.9E-02
- 5		6.8	1.06	0.53	6.49	1.4	1.28	1.18	2.02	0 65	1.19	1,14	1.19	7.97	0.92	6.0	0.68		1.31	98.0	26	1.2	7.08	7.08	1.58	1.34					1.14	
ORF SEQ	D NO:	28623				26758		L	29286		30301	L	30458		<u> </u>	34107	34331		36415	36791	38424					30051	L					35368
Exon	NO.	15497					1	1_		l _	1	1	1	<u> </u>	L		20838	1	1	23195						L	L		L	L	1	1
Probe	g ë	2366	8091	10866	12193	17	1529	189	3095	7007	155	4268	4330	5045	493	7560	782	9299	797	10158	11654	120	527	52	1384	3893	3893	5302	5316	7793	18	8750

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E- Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
8750	21829	35367	1.01	6.9E-02	6.9E-02 BE567435.1	HUMAN	601340661F1 NIH_MGC_53 Homo saplens cDNA clone IMAGE:3883030 5
9320	1			6.9E-02	8.9E-02 U22967.1	NT	Barbarle duck parvovirus REP protein (rep) and three capsia protein vP (vp) genes, continued cus
44374	1_	38092	1 46	6.9E-02	6.9E-02 S81752.1	Į,	DPH2L=candidate tumor suppressor gene (ovarian cancer critical region or deletion) indinati, 9 woon retaining placental tissues, mRNA, 2233 nt]
12/2	L						DPH2L=candidate turnor suppressor gene (ovarian cancer critical region of deletion) [human, 9 week fetal and
11374	24435	38093	1.46	6.9E-02	6.9E-02 S81752.1		placental tissues, mRNA, 2233 nfj
12346			10.94	6.9E-02	.1		X. kaevis XFD2 mRNA for fork head protein
12524	L		1.56	6.9E-02 P44621		ISSPROT	PROTEIN TRANSPORT PROTEIN HOF CHUMOLUG
12770	1		3.37		6.9E-02 AF195953.1	NT	Homo sapiens membrane-bound aminopepudase P (ANPERZ) gene, complete cus
683	l	28177	1.18	<u> </u>	6.8E-02 AA496759.1	EST HUMAN	ae30f02.r1 Gessler Wilms fumor Homo saplens CINA clone IMAGE:891339 o similar to go.mzzocz. MITOCHONDRIAL MATRIX PROTEIN P1 PRECURSOR (HUMAN);
1905	ı						ae30f02_r1 Gessler Wilms turner Homo saplens cDNA clone IMAGE:897339 5' similar to gb:M22382
1932	15075	28178	1.18			T_HUMAN	MITOCHONDRIAL MATRIX PROTEIN P1 PRECURSOR (HUMAN);
1956	_	l	3.85	6.8E-02	6.8E-02 AF156673.1	N	Homo saplens putative hepatic transcription factor (W BSCR14) gene, compare cus
4675	L		0.64	6.8E-02	6.8E-02 BE141076.1	EST_HUMAN	MR0-HT0069-071089-001-c05 HT0069 Homo sapiens cDNA
6758	19914		0.65		6.8E-02 P20792	SWISSPROT	CELL-SURFACE RECEPTOR DAP-1 PRECURSOR
7040	L		080		6.8E-02 BE061890.1	EST HUMAN	RC1-BT0254-090300-017-d09 BT0254 Hamo sepiens CLINA
7432		33981	8.22		6.8E-02 AL163268.2	TN	Homo sapiens chromosome 21 segment HS21C068
7881	1_		9.0		6.8E-02 U16856.1	NT .	Distyostelium discoldeum myosin heavy chain kinase A (Minon A) inniva, curipped cus
8483	L		6.03		6.8E-02 AJ248287.1	NT	Pyrococcus abyssi complete genome, segment old
8483	L				6.8E-02 AJ248287.1	Ę	Pyrococcus abyssi complete genome, segment 5/0
12141	1_				6.8E-02 T03214.1	EST_HUMAN	FB4A8 Fetal brain, Stratagene Homo Sabiens CDNA clone r D4A6 3 cm Similar D LINE 1
12276	L		1.64	L	6.8E-02 AA758014.1	EST_HUMAN	ah67f05.s1 Soares tests NH1 Homo sapens cuiva digne 1320703.3
12906	L	-	1.34		AW9758	EST_HUMAN	EST387948 MAGE resequences, maken morne sequence contact and contact and contact and contact and contact and contact and contact and contact and contact and contact and contact and contact and contact and contact and contact and contact and contact and contact and contact and contact and contact and contact and contact and contact and contact and contact and contact and contact and contact and contact and contact and contact and contact and contact and contact and contact and contact and contact and contact and contact and contact and contact and contact and contact and contact and contact and contact and contact and contact and contact and contact and contact and contact and contact and contact and contact and contact and contact and contact and contact and contact and contact and contact and contact and contact and contact and contact and contact and contact and contact and contact and contact and contact and contact and contact and contact and contact and contact and contact and contact and contact and contact and contact and contact and contact and contact and contact and contact and contact and contact and contact and contact and contact and contact and contact and contact and contact and contact and contact and contact and contact and contact and contact and contact and contact and contact and contact and contact and contact and contact and contact and contact and contact and contact and contact and contact and contact and contact and contact and contact and contact and contact and contact and contact and contact and contact and contact and contact and contact and contact and contact and contact and contact and contact and contact and contact and contact and contact and contact and contact and contact and contact and contact and contact and contact and contact and contact and contact and contact and contact and contact and contact and contact and contact and contact and contact and contact and contact and contact and contact and contact and contact and contact and contact and contact and contact and conta
12972	L	[	2.3	6.8E-02		L	Mus musculus latent I GF beta binding protein (1grb), marking
13203		31660	1.24	6.8E-02	6978865 NT	Į,	Rattus norvegicus Growth tactor Independent (1911), Illinum
1558	L	L	2.71		6.7E-02 AF115536.1	· LN	Oncorhynchus mydss TAP1 protein (Onmy/AP1) mrkNA, Ormy/AP1 of allete, complete cus
1942	ı	5 28186	2.17	L	6.7E-02 AI220285.1	EST HUMAN	4g79e04.x1 Scares, NFL   GBC_S1 Homo sapiens CUNA crate INVACE. 104 1400 C
3811				L	6.7E-02 P17278	SWISSPROT	HOMEOBOX PROTEIN HOX-D4 (CHOX-A)
4065	L	L	9 0.74			NT	Cyprinus carplo Rap1b mRNA, complete cds
4065	L	L	0.74		6.7E-02 U53783.1	M	Cyprinus carpio Rap1b mRNA, complete cds
	1	L	90		8 7E 02 W/67750 1	EST HUMAN	zd20g11.s1 Soares_feta_heart_NbHH19W Homo sapiens CUNA cione invadE.341202 5 similar to commiss. Alu repetitive element; contains element L1 repetitive element;
7969	- 1			١	Venent 4	TN - IN	H. sardens DNA for cGMP phosphodiesterase (exons 4-22)
8934	4 21117	7 34635	5 . 0.74	١	6./E-UZ A62693.1		

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The recent leaves the recent in recent and the recent and the recent and the recent and the recent and the recent and the recent and the recent and the recent and the recent and the recent and the recent and the recent and the recent and the recent and the recent and the recent and the recent and the recent and the recent and the recent and the recent and the recent and the recent and the recent and the recent and the recent and the recent and the recent and the recent and the recent and the recent and the recent and the recent and the recent and the recent and the recent and the recent and the recent and the recent and the recent and the recent and the recent and the recent and the recent and the recent and the recent and the recent and the recent and the recent and the recent and the recent and the recent and the recent and the recent and the recent and the recent and the recent and the recent and the recent and the recent and the recent and the recent and the recent and the recent and the recent and the recent and the recent and the recent and the recent and the recent and the recent and the recent and the recent and the recent and the recent and the recent and the recent and the recent and the recent and the recent and the recent and the recent and the recent and the recent and the recent and the recent and the recent and the recent and the recent and the recent and the recent and the recent and the recent and the recent and the recent and the recent and the recent and the recent and the recent and the recent and the recent and the recent and the recent and the recent and the recent and the recent and the recent and the recent and the recent and the recent and the recent and the recent and the recent and the recent and the recent and the recent and the recent and the recent and the recent and the recent and the recent and the recent and the recent and the recent and the recent and the recent and the recent and the recent and the recent and the recent and the recent and the recent and the recent and the rece	Top Hit Descriptor	H.sapiens DNA for cGMP phosphodiesterase (exons 4-22)	xb81c11.x1 Soares_NFL_T_GBC_S1 Homo sepiens cDNA clone IMAGE:2580788 3'	UI-H-BI1-acr-g-01-0-UI.s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2715433 3'	LH-BI1-acr-g-01-0-UI.s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMACE:2715433 3'	et12e09.x1 Barstead acrta HPLRB6 Homo sapiens cDNA clone IMAGE:2354920 3' similar to SW-LIN1 NYCCO P08548 LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.;	Mus musculus Capn12 gene for calpain 12, exons 1-21, three alternative transcipts	у18b10.s1 Soares placenta Nb2HP Нотто saplens cDNA clone IMAGE:139579 3'	Homo sapiens mesothelin (MSLN), transcript variant 1, mRNA	Homo sapiens mesothelin (MSLN), transcript variant 1, mRNA	Homo sapiens TESTIN 2 and TESTIN 3 genes, complete cds, alternatively spliced	INTER-ALPHA-TRYPSIN INHIBITOR HEAVY CHAIN HZ PRECURSOR (ITI HEAVY CHAIN HZ)	INTER-ALPHA-TRYPSIN INHIBITOR HEAVY CHAIN H2 PRECURSOR (ITI HEAVY CHAIN H2)	2174807.11 Scares_testis_NHT Homo sapiens cDNA clone IMAGE:728052 5' similar to gb:L04270 TUMOR. NECROSIS FACTOR RECEPTOR 2 RELATED PROTEIN PRECURSOR (HUMAN);	277497.r.1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:728052 5' similar to gb:L04270 TUMOR	NECROSIS FACTOR RECEPTOR 2 RELATED PROTEIN PRECURSOR (HUMAN);	P.vulgaris mRNA for chalcone synthase	MATERNAL EFFECT PROTEIN STAUFEN	MATERNAL EFFECT PROTEIN STAUFEN	MATERNAL EFFECT PROTEIN STAUFEN	MATERNAL EFFECT PROTEIN STAUFEN	Homo sapiens chemokine receptor CXCR4 gene, promoter region and complete cds	Dictyostelium discoideum darlin (darA) gene, complete cds	DNA POLYMERASE ZETA CATALYTIC SUBUNIT (HREV3)	Human respiratory syncytial virus, complete genome	Human respiratory syncytial virus, complete genome	tg7g06x1 NCI_CGAP_Lu24 Homo saplens cDNA clone IMAGE:2149498 3'	Homo sapiens EWS, gar22, rrp22 and bam22 genes	Homo sapiens vinculin (VCL), mRNA	602080608F2 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4245336 5'	MR1-SN0064-010600-006-a12 SN0064 Homo sapiens cDNA	Mus musculus DIPB gene (Dipb), mRNA	Rattus norvegicus cytochrome P450 2E1 (CYP2E1) gene, 5 tianking region
- באסון	Top Hit Database Source	LN.	EST_HUMAN x	EST_HUMAN U	Г	EST HIMAN S	Т	EST_HUMAN y				SWISSPROT	SWISSPROT II	EST HUMAN	Γ	EST_HUMAN N		SWISSPROT	SWISSPROT		SWISSPROT			/ISSPROT			EST_HUMAN	LN LN			EST HUMAN		보
DIBINO.	Top Hit Acession No.		6.7E-02 AW082688.1	6.7E-02 AW 137359.1	Γ	6 6E-02 A1735509 1			7108357 NT	7108357 NT	6.6E-02 AF260225.1		261703	6.6E-02.AA393244.1		6.6E-02 AA393244.1		P25159	P25159	P25159	P25159	6.6E-02 AF052572.1	6.6E-02 AF006055.1	1	9629198 NT	9629198 NT	6.6E-02 AI458752.1	6.6E-02 Y07848.1	11430559 NT	6.6E-02 BF694659.1	6.6E-02 BF374248.1	TN 1697599	6.6E-02 AF167430.1
	Most Similar (Top) Hit BLAST E Vatue	6.7E-02 X62695.1	6.7E-02/	6.7E-02	6.7E-02	A GE-02	8.6E-02/	6.6E-02 R64306.1	6.6E-02	6.6E-02	6.6E-02	6.6E-02 Q61703	6.8E-02 Q61703	6.6E-02		6.6E-02	6.6E-02 X06411.1	6.6E-02 P25159	6.6E-02 P25159	6.6E-02 P25159	6.6E-02 P25159	6.6E-02	6.6E-02	6.6E-02 O60673	6.6E-02	6.6E-02	6.6E-02	١.	6.6E-02				╝
	Expression Signal	0.74	0.73	0.59	0.59	80.0	3.73	12.38	3.11	3.11	1.61	12.07	12.07	29.0		9.0	3.92	0.62	0.62	99'0	0.68	1.51	0.77	0.53	1.28	1.28	0.54	1.5	99.0	0.49	4.95	4.64	1.26
	ORF SEQ. .ID NO:	34636	35250			9750B					30334	31191	31192	31220		31221		33298			33299		35287						L	37349			
	SEQ ID NO:	21117	21713	L	1	1	L		L	16732	17341	18221	_	18258	1	18255	_		19905	19905	19905	L	21749	22058	L	22200	Ļ	L	┖	<u> </u>	L		25733
	Probe SEQ ID NO:	8034	8633	0086	9800	1970	2252	3552	3567	3567	4191	5063	5083	5130		6130	6714	6749	6749	6937	6937	8133	8669	8979	9121	9121	10157	10292	10327	10710	11205	12761	13124

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Top Hit Descriptor	601671046F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3954178 5'	Homo sapiens E2F-like protein (LOC51270), mRNA	Xenopus laevis alpha(E)-catenin mRNA, complete cds	Aquifex aeollous section 96 of 109 of the complete genome	z/46h12.s1 Soares ovary tumor NbHOT Homo sapiens cDNA clone IMAGE:756743 3' similar to gb:M26036 HLA CLASS II HISTOCOMPATIBILITY ANTIGEN, DR-5 BETA CHAIN (HUMAN);	602118687F1 NIH_MGC_66 Homo sapiens cDNA done IMAGE:4276029 5'	Azotobacter vinelandii ATCC 9046 negative regulator MucB (mucB) gene, partfal ods	601656817R1 NIH_MGC_67 Homo saplens cDNA done IMAGE:3865637 3'	601656817R1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:38656373'	601823511F1 NIH_MGC_77 Homo saplens cDNA done IMAGE:4043138 5'	z32g05.s1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:6651443'	Rabbit microsomal epoxide hydrolase	Nectria haematococca kinesin related protein 2 (KRP2) gene, complete cds	A. carterae precursor of peridinin-chlorophylla-protein (PCP) gene	Thermotoga maritima section 89 of 136 of the complete genome	Thermotoga maritima section 89 of 136 of the complete genome	qe07b01.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1738249 3' similar to contains LTR8.b3	LINO ISPONIVE SIGNICIA.	neterouter apydnes beta 1,4-ti boglavarese 1,1-ti boglavarese (110-tilg.1) gotto, om poto od Defooders abytins beta 1,4-tildah inspesa 1 preciiror (HG-eng.1) pena complete cds	was 72-47 of Source Disabetrease colon NHCD Home sariene CDNA clone IMAGE-7346790 3'	ANTERNASSEZ ONE WAS 83 Home saciens a DNA clone IMAGE:3950503 3	Mus musculus chaneroulb sublimit 6a (zeta) (Cct6a), mRNA	K/4/19 sea F Human felal heart. Lambda ZAP Express Homo sapiens cDNA 5'	AF150195 Human mRNA from cd34+ stem cells Homo sepiens cDNA clone CBDAIA10	RC1-OT0083-150600-014-g06 OT0083 Homo sapiens cDNA	Homo sapiens mRNA for KIAA0554 protein, partial cds	Homo sapiens DNA topoisomerace II beta (TOP2B) gene, exons 16, 17, and 18	Homo saplens DNA topoisomerase II beta (TOP2B) gene, exons 16, 17, and 18	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RoRet gene, and sodium phosphate transporter (NPT3) gene, complete ods
Top Hit Database Source	EST_HUMAN		LN	LN	EST_HUMAN	EST_HUMAN	TN	EST_HUMAN	EST_HUMAN		EST_HUMAN	₽		LN	FZ	LN		NOWAIN	Z	TOTAL	Т	NUMP I	H IMAN	Т	Т	T	Ł	LN.	L L
Top Hit Acession No.	6.5E-02 BF027639.1	7706058 NT	6.5E-02 U47624.1	6.5E-02 AE000764.1	6.5E-02 AA443991.1	6.5E-02 BF665340.1	6.5E-02 U22661.1	6.5E-02 BE963200.2	BE963200.2	6.5E-02 BF106300.1	6.5E-02 AA195648.1	6.5E-02 MZ1496.1	6.5E-02 AF102993.1	6.4E-02 X94549.1	6.4E-02 AE001777.1	6.4E-02 AE001777.1			6.4E-02/AF052733.1		0.4E-02 MIO7 2030.1	ETEROSON NIT	8 4E-02 AANGRANE 1	8 4E-02 AF450195 1	6 4F-02 BE834083.1	6.4E-02 AB011126.1	6.4E-02 AF087150.1	6.4E-02 AF087150.1	6.4E-02 U81328.1
Most Similar (Top) Hit BLAST E Vælue	6.5E-02	6.5E-02	6.5E-02	6.5E-02	6.5E-02	6.5E-02	6.5E-02	6.5E-02	6.5E-02	6.5E-02	6.5E-02	6.5E-02	6.5E-02	6.4E-02	6.4E-02	6.4E-02	.,	0.4E-0Z	6.4E-02	0.45-02	9.4E-02	6 45 02	8.4E-02	8 4E 02	6 4F-02	6.4E-02	6.4E-02	6.4E-02	6.4E-02
Expression Signal	1.57	1.3	3.38	2.04	2.07	0.73	1.02	75.0	0.57	0.81	4.45	3.78	3.67	1.49	0.99	66.0		1:13	7.64	\$ 5	37.	100	4.47	80	800	1.87	0.45	0.45	1.86
ORF SEQ ID NO:	26805								36782	·	37589			26799		l					33,00		94778			36545			38697
Exon SEQ ID NO:	13785	14183	14576	14922	18870	L	18539	23185		<u></u>	L	L	ı	13780	14919	14919	Į.	١	1	ı		07707		1			1	1	1
Probe SEQ ID NO:	505	1011	1422	1773	5676	6673	7113	10147	10147	10683	10875	12163	12533	589	1770	1770		2200	6239	6529	6932	/040	1000	9995	078F	9918	10468	10468	12008

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Probe SEQ ID NO:	SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptar
12008	24993	38698		6.4E-02	6.4E-02 U91328.1	TN	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RoRet gene, and sodium phosphate transporter (NPT3) gene, complete cds
12427	26048		2.7	6.4E-02	6.4E-02 AF107890.1	NT	Homo sapiens mucin 5B (MUC5B) gene, partial cds
12479	25331	32056	2.61	6.4E-02	6.4E-02 AJ277174.1	NT	Drosophila melanogaster mRNA for mod(mdg4)51.4 protein
1793	14942	28035	2.51	6.3E-02	6.3E-02 AF109905.1	NT	Mus musculus major histocompatibility locus class III regions Hsc70t gene, partial ods; smRNP, G7A, NG23, MuS homolog, CLCP, NG24, NG25, and NG26 genes, complete ods; and unknown genes
3692	16854			6.3E-02 P37092		SWISSPROT	HEAT SHOCK PROTEIN 70 HOMOLOG
6264	19438	32785	1.12	6.3E-02	6.3E-02 BF210736.1	EST HUMAN	601873316F1 NIH_MGC_54 Homo saplens cDNA clone IMAGE:4097499 5
7391	20469	L	1.64	6.3E-02	6.3E-02 X97869.1	LN	H.sapiens gene encoding La autoantigen
9491	22548	36111	66.0	6.3E-02		IN	Drosophila melanogaster Domina gene, exons 1-3
10218	23264		3.52	6.3E-02	6.3E-02 AB010162.1	ΝŢ	Hepatitis G virus RNA for polyprotoin (NS5A region), partial ods, strain: CMR-152
10478	23513		1.31	6.3E-02		EST_HUMAN	AV698070 GKC Hamo septens cDNA clone GKCAHE01 5
10954	19438	32785	2.36		6.3E-02 BF210736.1	EST HUMAN	601873316F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4097499 5
2549	15874	28797	1,04	6.2E-02		LN L	Arabidopsis thaliana DNA chromosome 4, contig tragment No. 40
4365	17508		4.22	6.2E-02	6.2E-02 AL 161572.2	NT	Arabidopsis thallana DNA chromosome 4, contig tragment No. 65
	1_	L			•	<u> </u>	Rattus norvegicus differentation-associated Na-dependent inorganic phosphate cotransporter (DNPI) mKNA,
4458			1.03		35.1	TODOGOMO	CONTINUES CASE TO BE OF THE ANTIGEN (SS.A)) (ROSS.A)) (ROSS.A)
4705	- 1					SWISSERU	O. NO. TO LETT (CO. O. O. O. O. O. O. O. O. O. O. O. O. O
6935						L	Spiriting platensis LiviA for additivate Cydass, continues dus.
7805		34354				LN	Kamus novogicus P.K. Drindrig protein and substantially designed out
8016	H		0.58		6.2E-02 AL161545.2	NT NT	Arabidopsis thaliana UNA chromosome 4, contiguragment no. 45
9148	26225		0.92		6.2E-02 M61101.1	Į,	Porcine group C rotavirus (strain Cowden) outer membrane protein (YF7) mount, compress co.
9544	22609	36177			AA77845	EST_HUMAN	ar20a06.s1 Soares total fetus Nb2Hr8 9W Home saplens cunha cigne invacine s
9681	ı	36300	1.19	6.2E-02	IN 8687789	LN	Mus musculus stromal cell derived factor receptor 2 (Sdit 2), mKNA
11415	ı	l	1.42		6.2E-02 AF217490.1	IN	Horno sapiens fragile 16D oxido reductase (FOR) gene, exons 8, 9, and partial ods
11629	L	ŀ			6.2E-02 AJ242735.1	LΝ	Metarhizium anisopliae mRNA for Chymotrypsin (chy1 gene)
12263					6.2E-02 AE000750.1	۲	Aquifex aeolicus section 82 of 109 of the complete genome
12617	$\perp$		1,24		ĺ	EST_HUMAN	601583773F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3937842 5
1 2703	l	32024		<u> </u>	6.2E-02 BF112039.1	EST HUMAN	7t37h08.x1 Scares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA done IMAGE:3523815 3' similar to TR:Q874S6 Q974S6 HYPOTHETICAL 30.3 KD PROTEIN. [1];
2000	L				6 1F-02 D16471 1	E	Human mRNA, Xq terminal portion
2007	1		3 6		1 70005	1	Azekidonets thattana K+ Inward ractifixing channel protein (AtKC1) gene, complete ods
4089	17254	=	2.80		6.1E-02 U/3325.1	ż	Nation billion in the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of

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	Top Hit Descriptor	Homo sapiens SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 3 (SMARCA3) mRNA	H.saplens mRNA for B-HLH DNA binding protein	601651086R1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:3934604 3	601651086R1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:3934604 3'	IL3-HT0618-110500-136-C06 HT0618 Hamo sapiens cDNA	Eptatretus burgeri mRNA for RNA polymerase III largest subunit, partial cds	S.japonicum mRNA for serine-enzyme	t259f07.x1 NCI_CGAP_Ov35 Homo sapiens cDNA clone IMAGE:2282801 3	Homo sapiens chromosome 21 segment HS21C007	Thermotoga maritima section 89 of 136 of the complete genome	EST380924 MAGE resequences, MAGJ Homo saplens cDNA	Mesocestoides corti mitochondrial DNA, NADH dehydrogenase subunit 4, tRNA-Gln, tRNA-Phe, tRNA-Met,	ATPase subunit 6, and NADH dehydrogenase subunit 2	zp78c04.r1 Stratagene HeLa cell s3 937216 Homo sapiens cDNA clone IMAGE:626310 5	zp78c04.r1 Stratagene HeLa cell s3 937216 Homo saplens cDNA clone IMAGE:626310 5	EST84266 Colon adenocarcinoma IV Homo sapiens cDNA 5' end similar to tissue-specific protein	EST84266 Colon adenocarcinoma IV Homo sapiens cDNA 5' end similar to tissue-specific protein	601658150R1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3876060 3'	RC3-BT0253-011199-013-b04 BT0253 Homo sapiens cDNA	wf48h05.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2358873 3' sImilar to contains	L1.t1 L1 L1 repetitive element;	Homo sapiens stimulated trans-acting factor (bd KIJA) S I AFDU) mixin A	Homo sapiens stimulated trans-acting factor (50 kDa) (STAF50) mKNA	601815274F2 NIH_MGC_56 Homo sepiens CDNA clone IMAGE: 4049220 3	qf58b08.x1 Soares_testis_NHT Homo sapiens cDNA done IMAGE:1734199 3	Reclinomonas americana mitochondrion, complete genome	ts78a06.x1 NCI_CGAP_GC8 Homo sapiens cDNA clone IMAGE::233/302.3	Is78e06.x1 NCI_CGAP_GC8 Homo sapiens cDNA clone IMAGE:22373623	Actenser baeri partial IGLV gene for Immunoglobulin light chain variable region, exchs 1-2	Acipenser baeri partial IGLV gene for Immunoglobulin light chain variable region, exons 1-2	EST180654 Jurket T-cells V Homo sapiens cDNA 5' end similar to similar to heat shock protein 1, 60 kDa- like
	Top Hit Database Source	N	TN	EST_HUMAN	EST_HUMAN	EST_HUMAN	LN	ΙN	EST HUMAN	ΤN	ΙN	EST_HUMAN		닐	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN		EST_HUMAN	NT	M	EST_HUMAN	EST_HUMAN	INT	EST HUMAN	EST_HUMAN	TN	NT.	EST_HUMAN
6	Top Hit Acession No.	4507070 NT	(99268.1	6.1E-02 BE971853.1	6.1E-02 BE971853.1	6.1E-02 BE179543.1	6.1E-02 AB025333.1	<70969.1	6.1E-02 AI886611.1	6.1E-02 AL 163207.2	6.0E-02 AE001777.1	6.0E-02 AW968848.1		6.0E-02 AB031289.1	6.0E-02 AA188730.1	6.0E-02 AA188730.1	6.0E-02 AA372376.1	6.0E-02 AA372376.1	6.0E-02 BE964443.2	6.0E-02 AW370211.1		6.0E-02 AI807537.1	5174698 NT	5174698 NT	6.0E-02 BF382349.1	6.0E-02 A 1204275.1	11466495 NT	6.0E-02 A1623167.1	6.0E-02 AI623167.1	6.0E-02 AJ245365.1	6.0E-02 AJ245365.1	6.0E-02 AA309797.1
	Most Similar (Τσρ) Hit BLAST E Value	6.1E-02	6.1E-02 X99268.1	6.1E-02	6.1E-02	6.1E-02	6.1E-02	6.1E-02 X70969.1	6.1E-02	6.1E-02	6.0E-02	6.0E-02		6.0E-02	6.0E-02	6.0E-02	6.0E-02	6.0E-02	6.0E-02	6.0E-02		6.0E-02	6.0E-02	6.0E-02	6.0E-02	6.0E-02	6.0E-02	6.0E-02	6.0E-02	6.0E-02	6.0E-02	
	Expression Signal	1.57	3.65	9.0	9.0	3.9	1.66	30.03	1.58	6.43	1.58	1.17		1.43	1.53	1.53	2.07	2.07	0.76	1.01		1	2.86	2.86	2.37	1.78	0.46	1.29	1.29	2	2	0.72
	ORF SEQ ID NO:		35068	35474	35475	37681					27513	28969				26363						32872	31467		33880			36092	36093		L	
	Exen SEQ ID: NO:	19414	21539	21940	21940	24048			$\mathbb{I}_{-}$	25645	1	_	L	15946	1	1_	1_	1_	ı	١.		19515	18553	18553	L.,	L	L		22529		L	Į I
	Probe SEQ (D NO:	6240	8458	8861	8861	10967	12134	12218	12836	12993	1291	2740		2832	3002	3002	3301	3301	3725	5514		6345	7127	7127	7338	7857	8617	9472	9472	9896	9096	10109

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Top Hit Descriptor	Hamo sapiens ABCA1 (ABCA1) gene, camplete cds		601447937F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3851985 5	Xenopus lacvis mRNA for fourth component of complement, complete cds	Xenopus laevis mRNA for fourth component of complement, complete cas	Rattus norvegicus mRNA for potassium channel, alpha subunit (kv9.2 gene)	Mus musculus ect2 oncogene (Ect2), mRNA	on18b09.y1 Normal Human Trabecular Bone Cells Homo sapiens cDNA clone NHTBC_cn18b09 random		Homo saplens chromosome 21 segment HS21C103	Pig DNA for SPAI-2, complete cds	Homo sapiens Xq pseudoautosomal region; segment 1/2	Homo sapiens fragile 16D oxido reductase (FOR) gene, exons 8, 9, and partial cds	Pan troclodytes apolipoprotein-E gene, complete cds	T	repetitive element;	Hydrocotyle rotundifolia ribosomal protein L16 (rp116) gene, intron, chloroplast gene for chloroplast product	601494578F2 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3898610 5	Lycopersicon esculentum LE-ACS6 mRNA for 1-aminocyclopropane-1-carboxylate synthase, complete cds			Г	T	П		_1		nf99d07.s1 NC_CGAP_AlvI Homo saplens cDNA clone IMAGE:923245 similar to 1 K:Grb9859 Gr09859 1 LAMINA ASSOCIATED POLYPEPTIDE 1C.;
Top Hit Database Source	LN	EST_HUMAN	EST HUMAN	N⊤	TN	ΤN	NT	EST_HUMAN	EST_HUMAN	ĽΝ	N.	LZ	μ	FN		EST HOMAN	FZ.	EST_HUMAN	F	EST HUMAN	EST HUMAN		EST HUMAN	EST_HUMAN	EST HUMAN	EST HUMAN	EST HUMAN	EST_HUMAN
Top Hit Acession No.	5.7E-02 AF275948.1	5.7E-02 BE871911.1	5.7E-02 BE871911.1	5.7E-02 D78003.1	5.7E-02 D78003.1	5.7E-02 AJ296090.1	6681260 NT	5.7E-02 AI752685.1	5.7E-02 AI752685.1	5.7E-02 AL 163303.2	5.7E-02 D50320.1	5 7E-02 A.1271735 1	5.7E-02 AF217490.1	E 7E.00 AE281 280 1	A 201200.1	5.7E-02 R48513.1	5.6E-02 AF094455.1	5.6E-02 BE904308.1	5.6E-02 AB013100.1	5.6E-02 AA290599.1	5 6E-02 AW172708.1		5.6E-02 AA866182.1	5.6E-02 BE008001.1	5.6E-02 AI183583.1	5.6E-02 BE542663.1	5.6E-02 BE542683.1	5.6E-02 AA482864.1
Most Stmilar (Top) Hit BLAST E Value	5.7E-02	5.7E-02	5.7E-02	5.7E-02	5.7E-02	5.7E-02	5.7E-02	5.7E-02	5.7E-02	5.7E-02	5.7E-02	5 7E-02	5.7E-02	F 7E.03	3.15-02	5.7E-02	5.6E-02	5.6E-02	5.6E-02	5.6E-02	5 RE-02		5.6E-02	6.6E-02	5.6E-02	5.6E-02	5.6E-02	
Expression Signal	0.67	0.68	0.68	0.72	0.72	1.45	0.82	3.14	3.14	1.68	19.03	212	308	20.0	0.21	1.18	1.1	1.95	1.37		5.87		1.02	3.3		2.52		
ORF SEQ ID NO:		34175	١.			34954		38193	38194						1	31929	27789		30878				33689	33842			L	
Exon SEQ ID NO:	19185	20699	20699	20775	20775	21430	23083	24523		24740	25060	25547	26042	1	20102	25759	14709		<u> </u>	1_	ì _		20167	1	۱.	L.	1	!
Probe SEQ ID NO:	0009	7630	7630	7710	7710	8349	10055	11464	11464	1,4830	1258	00207	12863		13012	13171	1558	2362	4763	4818	0.0	8815	7831	7301	8010	9005	9005	10017

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Top Hit Descriptor	Helicobacter pylori 26695 section 5 of 134 of the complete genome	Helicobacter pylon 26695 section 5 of 134 of the complete genome	Human heparan sulfate proteoglycan (HSPG2) mRNA, complete cds	Lymphocystis disease virus 1, complete genome	Haemophilus Influenzae Rd section 147 of 163 of the complete genome	nuclear protein TIF1 isoform [mice, mRNA, 4053 nt]	HYPOTHETICAL 130.0 KD PROTEIN IN SNF6-SPO11 INTERGENIC REGION	Mus musculus 129/Sv cystatin C (cst3) gene, complete cds	Podospora ansertna mitochondrial epsilon-sen DNA	D.rerio mRNA for xp-23 POU gene, splice variant (neurula, 9-16 hpf and postsomitogenests, 20-28 hpf)	B.rerio pou[c] mRNA for transcription factor	Branchlostome floridae homeodomain-containing protein Hox13 (Hox13) gene, exon 2 and partial cds	Homo saplens meprin A, alpha (PABA peptide hydrolase) (MEP1A) mRNA	Homo sapiens partial LMO1 gene for LIM domain only 1 protein, exon 1	Homo sapiens partial LMO1 gene for LIM domain only 1 protein, exon 1	Arabidopsis thaliana putative dicarboxylate difron protein (Crd1) mRNA, complete cds	Human steroid hormone receptor Ner-I mRNA, complete cds	Rattus narvegicus mRNA for tnyroglobulin, complete cds	Saccharomyces cerevisiae Cdc54p (CDC54) gene, complete cds	wj80e04.x1 NCI_CGAP_Lym12 Homo sapiens cDNA clone IMAGE:2409150 3' similar to contains MER15.b1 MER15 repatitive element;	DNA POLYMERASE PROCESSIVITY FACTOR (POLYMERASE ACCESSORY PROTEIN) (PAP) (DNA- BINDING CENE 18 PROTEIN)	Homo sapiens chromosome 21 segment HS21C004	Turnip moseic virus genomic RNA for Capsid protein, complete cds	Tumin mosaic virus genomic RNA for Capsid protein, complete cds	OXALOACETATE DECARBOXYLASE ALPHA CHAIN	DKFZp547D073_r1 547 (synonym: hfbrt) Homo sapiens cDNA clone DKFZp547D073 5	601653565R2 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:3838361 3'	Campylobacter jejuni NCTC11168 complete genome; segment 4/6	Bacteriophage 80 alpha holin and amidase genes, complete cds	HIV-1 patient 96 from Italy protease (pol) gene, complete cds
Top Hit Database Source	NT	LN	IN				SWISSPROT	NT	NT	NT	LN	NT		IN	NT	LNT	١	NT	TN	EST HUMAN	FOGGGGA	Т	Į.	12	ISSPROT	EST HUMAN	Т	Г	N	NT
Top Hit Acession No.	5.3E-02 AE000527.1	5.3E-02 AE000527.1	5.3E-02 M85289.1	9695413	5.3E-02 U32832.1	5.3E-02 S78221.1	P38742	5.3E-02 U10098.1	5.3E-02 X03127.1	5.3E-02 Y07907.1	5.3E-02 X68432.1	5.3E-02 AF276815.1	5031908 NT	5.2E-02 AJ277661.1	5.2E-02 AJ277681.1	5.2E-02 AF236101.1	5.2E-02 U07132.1	5.2E-02 AB035201.1	5.2E-02 U14731.1	5.2E-02 AI830965.1	000000	5.2E-02 F 30322 5.2E-02 AI 163204.2	5 2E-02   D40027 4	5.2E-02 D10927.1	003030	5.1E-02 AL134071.1	5.1E-02 BE957423.2	5.1E-02 AL139077.2	5.1E-02 U72397.1	5.1E-02 AF280369.1
Most Similar (Top) Hit BLAST E Value	5.3E-02	5.3E-02	5.3E-02	5.3E-02	5.3E-02	5.3E-02	5.3E-02 P38742	5.3E-02	5.3E-02	5.3E-02	5.3E-02	5.3E-02	5.2E-02	5.2E-02	5.2E-02	5.2E-02	5.2E-02	5.2E-02	5.2E-02	5.2E-02	2000	5.2E-02	5 2E-02	5.5E-02	5 25-02 003030	5.1E-02	5.1E-02	5.1E-02	5.1E-02	5.1E-02
Expression Signal	2.39	2.39	1.14	4.02	1.37	2.3	89'0	0.68	1.73	0.61	67.0	1.55	64.04	2.39	2.39	8.0	3,31	99.0	0.64	0.94	8,	0.00	2.16	2.5	9	0.98	0.89	0.96	0.74	0.79
ORF SEQ ID NO:			_		33769		34585		35954		37180	31931				30216					<u> </u>	7/800		36564			31248			33370
Exan SEQ ID NO:	ľ	1	Į	20160	20325	20590	1	21681	22401	23497	L_	L.	15489	16358	16358	ļ.		Ι.	1	19408		24470	ı	L	丄	L	L	Ĺ	L	ľ
Probe SEQ ID NO:	5434	5434	6228	7024	7241	7517	8061	8600	9325	10462	10538	13173	2358	3183	3183	4050	4393	5287	6040	6233		474/		382	10708	2437	5161	5251	5349	6812

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Тор Hit Descriptor	QV0-UM0051-250800-350-b08 UM0051 Homo saplens cDNA	Human hypoxanthine phosphoracyltransterase (HPR I ) gene, complete cos	Human hypoxanthine phosphoribosytransterase (HPKI) gene, complete cus	Spodoptera litteralis mKNA for 3-dehydroecdysone spelaneduciase	KERATIN, TYPE I CYTOSKELE IAL 14 (CYTOKEKATIN 14) (N.14) (ON 14)	KERATIN, TYPE I CYTOSKELETAL 14 (CY I OKERATIN 14) (K14) (CK 14)	Candida abicans protein phosphaiase Ssd1 nomoxeg (SSD1) gene, companie cus	ANTER-SPECIFIC PROLINE-RICH PROTEIN APG (PROTEIN OLA)	Homo sapiens ES18 mKNA, partial cds	Homo sapiens ES18 mKNA, parasi cos	Cucumis melo polygarachtronase precursor (mir co.) Ilinum, cumplicia co.	Mus musculus fatty acid amide hydrotase gene, while	Bacillus subtilis complete genome (section 1 of 21); Iron 1 to 213000 (near 1000 a) (near 21) (near 21)			Mus musculus Unc-51 like kinase 2 (C. elegans) (Uik2), mRNA	Haemophilus influenzae Rd section 97 of 163 of the complete genome	Artheraea pernyi period clock protein homolog mranA, complete cas	CASEIN KINASE II BETA CHAIN (CK II)	Gailus gailus tyrosine kinase JAK1 (JAK1) mKNA, complete cus	Mus musculus Dmp-1 gene, exons 1-9	NEUROPILAMENT TRIPLET LE PROTEIN (NEUROFII AMENT LIGHT POLYPEPTIDE) (NFL)	T	$\top$		Т	_1	NO-ON-TRANSIEN I A PROTEIN binding protein (CaRP, 28) mRNA complete cds	Chicken 28-KDa warmin D-dependent calcium-fullating protating contracting to the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contract	Homo saplens ABCA1 (ABCA1) gene, comprehe cos	Hamo sepiens About I years, whipiers as	Leas mays phytoere sylutates (1.1) gala, company of the company phytoere (1.1) galaxies (1.1) galaxies (1.1) galaxies (1.1) galaxies (1.1) galaxies (1.1) galaxies (1.1) galaxies (1.1) galaxies (1.1) galaxies (1.1) galaxies (1.1) galaxies (1.1) galaxies (1.1) galaxies (1.1) galaxies (1.1) galaxies (1.1) galaxies (1.1) galaxies (1.1) galaxies (1.1) galaxies (1.1) galaxies (1.1) galaxies (1.1) galaxies (1.1) galaxies (1.1) galaxies (1.1) galaxies (1.1) galaxies (1.1) galaxies (1.1) galaxies (1.1) galaxies (1.1) galaxies (1.1) galaxies (1.1) galaxies (1.1) galaxies (1.1) galaxies (1.1) galaxies (1.1) galaxies (1.1) galaxies (1.1) galaxies (1.1) galaxies (1.1) galaxies (1.1) galaxies (1.1) galaxies (1.1) galaxies (1.1) galaxies (1.1) galaxies (1.1) galaxies (1.1) galaxies (1.1) galaxies (1.1) galaxies (1.1) galaxies (1.1) galaxies (1.1) galaxies (1.1) galaxies (1.1) galaxies (1.1) galaxies (1.1) galaxies (1.1) galaxies (1.1) galaxies (1.1) galaxies (1.1) galaxies (1.1) galaxies (1.1) galaxies (1.1) galaxies (1.1) galaxies (1.1) galaxies (1.1) galaxies (1.1) galaxies (1.1) galaxies (1.1) galaxies (1.1) galaxies (1.1) galaxies (1.1) galaxies (1.1) galaxies (1.1) galaxies (1.1) galaxies (1.1) galaxies (1.1) galaxies (1.1) galaxies (1.1) galaxies (1.1) galaxies (1.1) galaxies (1.1) galaxies (1.1) galaxies (1.1) galaxies (1.1) galaxies (1.1) galaxies (1.1) galaxies (1.1) galaxies (1.1) galaxies (1.1) galaxies (1.1) galaxies (1.1) galaxies (1.1) galaxies (1.1) galaxies (1.1) galaxies (1.1) galaxies (1.1) galaxies (1.1) galaxies (1.1) galaxies (1.1) galaxies (1.1) galaxies (1.1) galaxies (1.1) galaxies (1.1) galaxies (1.1) galaxies (1.1) galaxies (1.1) galaxies (1.1) galaxies (1.1) galaxies (1.1) galaxies (1.1) galaxies (1.1) galaxies (1.1) galaxies (1.1) galaxies (1.1) galaxies (1.1) galaxies (1.1) galaxies (1.1) galaxies (1.1) galaxies (1.1) galaxies (1.1) galaxies (1.1) galaxies (1.1) galaxies (1.1) galaxies (1.1) galaxies (1.1) galaxies (1.1) galaxies (1.1) galaxies (1.1) galaxies (1.1) galaxies (1.1) galaxies (1.1) ga	
Top Hit Database Source	EST_HUMAN	LN	F	Ę	SWISSPROT	SWISSPROT	TN	SWISSPROT	F	날	Z	¥	NT	SWISSPROT	LN	NT	NT	NT	SWISSPROT	N	NŢ	SWISSPROT	SWISSERO	EST HUMAN	N	EST HOMAN	\ L	SWISSPROT	Ā	μ	¥	L L	SWISSPROT
Top Hit Acession No.	1E-02 BF378625.1	J26434.1	5.1E-02 M26434.1	4,1131966.1	02533	202533	4F012898.1	P40603	AF083930.1	AF083930.1	AF062467.1	AF098004.1	5.0E-02 Z99104.1	P02810	U72742.1	5.0E-02 7305610 NT	U32782.1	5.0E-02 U12769.2	P40232	5.0E-02 AF096264.1	5.0E-02 AJ242625.1	5.0E-02 P35616	5.0E-02 P35616	5.0E-02 AW062464.1	5.0E-02 AF305238.1	5.0E-02 BF213260.1	5.0E-02 U67600.1	5.0E-02 Q04047	4.9E-02 M14230.1	4.9E-02 AF275948.1	4.9E-02 AF275948.1	4.9E-02 U32636.1	4.9E-02 P54258
Most Similar (Top) Hit BLAST E Value	5.1E-02	5.1E-02 M26434.1	5.1E-02	5.1E-02	5.1E-02	5.1E-02	5.1E-02	5.1E-02	5.1E-02	5.1E-02	6.1E-02	5.0E-02	5.0E-02	5.0E-02 P02810	5.0E-02	5.0E-02	5.0E-02 U32782.		}								)		,			Ì	
Expression Signal	1.73	0.82	0.82	1.42	0.63	0.63	4.27	1.9	1.81	1.81	1.81	2.8	2.82			1.36	1.01	5.9	1.05		1.28					0.55	2.26	4.7	11.82	4.18			1.85
ORF SEQ ID NO:	31508			35160	_			L	37778	37779			27452	<u> </u>	27244		-	29942		32779			34259		3 37045	6	38468		2	8 26623	8 26624		29548
Exan SEQ ID NO:	18516	21528	21528	1	1	L	L	L	1	24143	25487	L	L	1_	]	ļ	1	1	1			!	3 20774				L	L	13452	13588	13588		18532
Probe SEQ (D NO:	6997	8447	8447	8542	9086	9086	10014	10384	11068	11068	12736	495	1231	2047	2879	3418	3684	3775	\$	6258	6436	7128	7705	791	10403	10855	11782	12229	231	380	380	2937	338

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Most Similar  Expression (Top) Hit Top Hit Acession Signal BLASTE No. Source			0.78 4.9E-02 AA400914.1 EST_HUMAN	2.84 4.9E-02 AW167821.1 EST_HUMAN	2.64 4.9E-02 AW167821.1 EST_HUMAN	1.62 4.9E-02 L00122.1 NT	4,9E-02 L00122.1 NT	1.79 4.9E-02 AE000980.1 NT	N	4.9E-02 BE931532.1   EST_HUMAN		0.64 4.9E-02 P19532 SWISSPROT	1.57 4.9E-02 L41161.1 NT	1.57 4.9E-02 L41161.1 NT	38376 3.46 4.9E-02 AF008303.1 INT Homo sepiens prepro placental TGF-beta gene, complete cds	3.23 4.9E-02 M19364.1 NT Human gamma-B-crystalih (gamma 1-2) and gamma-C-crystalih (gamma 2-1) genes, complete cds	26582 1.19 4.8E-02 D16471.1 NT Human mRNA, Xq terminal portion	2.61 4.8E-02 D16471.1 NT	4.8E-02 AF003100.1 INT	2c/49b02.s1 Soares_senescent_fibroblasts_NbHSF Homo sapiens cUNA cione IMAGE:323011 3 similar to la RE-D2/M51983 1 [EST HUMAN [qb:M30938 LUPUS KU AUTOANTIGEN PROTEIN P86 (HUMAN);	4.8E-02 X17144.1 NT	1.06 4.8E-02 Z54280.1 NT	4.8E-02 U91914.1	1.41 4.8E-02 AW388497.1		1.01 4.8E-02/AJ001398.1 NT	1.84 4.8E-02 X61236.1 NT	1.84 4.8E-02 X61236.1 NT	1.46 4.8E-02 9632893 NT	31214 0.74 4.7E-02 6981261 NT Rattus norvegicus Nestin (Nes, mRNA
ORF SEQ Expi		29851	29852	31069	31070	31702	31703	33831			ĺ						L				Ĺ		L	l	۱	1				П
Exan SEQ ID NO:	16823	116844	L	L	L	18685	18685	1	ı	1		23535	1		L	7 25624	L	1	L	7,57	L			L	22405	l.		١.		
Probe SEQ ID NO:	3660	368	3681	4964	4964	848	548	729	8815	89	895	1050	1080	10802	11687	12957	3	341	ន	1	3280	4793	523	833	8	8	11219	11219	12511	5122

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Top Hit Descriptor		yz97f09,r1 Soares melanocyte 2NbHM Homo sapiens cDNA clone IMAGE:291017 5' similar to contains Alu repetitive element,	602143554F1 NIH MGC_46 Homo sapiens cDNA clone IMAGE:4304772 5'	602143554F1 NIH_MGC_46 Homo saplens cDNA clone IMAGE:4304772 5'	Rat statin-related protein (s1) gene, complete CDS	B. taurus mRNA for RF-36-DNA-binding protein	H.saplens DNA for endogenous retroviral like element	Gallus gallus Wokci-8 gene, complete cds	B.taurus mRNA for RF-36-DNA-binding protein	we79c10.x1 Scares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2347314.3'	Bos taurus paired box protein (pax-6) gene, partiel cds	Bos faurus peired box protein (pax-6) gene, partial cds	AV648521 GLC Homo sapiens cDNA clone GLCBKD02 3'	PM0-HT0339-251199-003-g05 HT0339 Homo saplens cDNA	Escherichia coli K-12 MG1655 section 335 of 400 of the complete genome	em50d02.s1 Johnston frontal cortex Homo sapiens cDNA clone IMAGE:1538979 3' similar to TR:P90533	P90533 LIMA ;contains element LTR1 repetitive element;	AV727059 HTC Homo sapiens cDNA clone HTCBW C01 5'	vn24f03.x1 NCI_CGAP_Kid11 Homo sapiens cDNA done INAGE:2694653 3' similar to SW:GRF1_HUMAN   Q12849 G-RICH SEQUENCE FACTOR-1;	PM0-HT0339-251199-003-g05 HT0339 Homo sapiens cDNA	PM0-HT0339-261199-003-g05 HT0339 Homo sapiens cDNA	PM0-HT0339-251199-003-g05 HT0339 Homo saplens cDNA	PM0-HT0339-251199-003-g05 HT0339 Homo sapiens cDNA	Mus musculus nucleolar RNA helicase II/Gu (ddx21) gene, complete cds	Haplochromis burtoni gonadotropin-releasing hormone and GnRH-associated peptide precursor (Gnrh2)	gene, complete cds	C.reinhardtii atp2 (சுந்த) mRNA	С.reinhardtii atp2 (atpВ) mRNA	qc60b06 x1 Soares_placenta_8to9weeks_2NbHP8to9W Homo sapiens cDNA clono IMAGE:1713971 3'	similar to contains L1.t3 L1 repetitive element;	Rattus norvegicus Cathepsin H (Cish), mRNA	PMO-HT0339-060400-009-G12 HT0339 Homo sepiens cDNA	olz7h09.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1524737 3
Top Hit Database	Solitos	EST HUMAN	EST HUMAN	EST_HUMAN	NT	LN	N	TN	TN	EST_HUMAN	IN	F	EST_HUMAN	EST_HUMAN	۲		EST HUMAN	EST_HUMAN	EST HUMAN	EST HUMAN	EST HUMAN	EST HUMAN	EST_HUMAN	NT		TN	N	F		EST HUMAN	N N	EST HUMAN	EST_HUMAN
Top Hit Acession No.		4.7E-02 W01153.1	4.7E-02 BF686625.1	4.7E-02 BF686625.1	4.7E-02 M82752.1	4.7E-02 X15543.1	4.7E-02 X89211.1	4.7E-02 AB026678.1	4.7E-02 X15543.1	4.7E-02 AI873042.1	4.7E-02 U73621.1	4.7E-02 U73621.1	4.7E-02 AV648521.1	4.6E-02 BE153583.1	4.6E-02 AE000445.1		4.6E-02 AI014255.1	4.6E-02 AV727059.1	4.6E-02 AW236023.1	l	Ì	4.6E-02 BE153583.1	4.6E-02 BE153583.1	4.6E-02 AF220365.1		4.6E-02 AF076962.1	4.6E-02 X61624.1	4.6E-02 X61624.1		4.6E-02 AI149574.1	6978720 NT	4.6E-02 BE154006.1	4.6E-02 AA913328.1
Most Similar (Top) Hit BLAST E	Value	4.7E-02	4.7E-02	4.7E-02	4.7E-02	4.7E-02	4.7E-02	4.7E-02	4.7E-02	4.7E-02	4.7E-02	4.7E-02	4.7E-02	4.6E-02	4.6E-02		4.6E-02	4.6E-02	4.6E-02	4.6E-02	4.6E-02	4.6E-02	4.6E-02	4.6E-02		4.6E-02	4.6E-02	4.6E-02		4.6E-02	4.6E-02		
Expression Signal	,	3.34	0.69	0.69	1.71	9.44	1.31	2.97	7.75	0.7	1.43	1.43	4.31	0.69	2.89		1.49	5.39	234	1.78	0.64			0.92		1.57		3.67		1.41	0.63	3.81	
ORF SEQ ID NO:		33623		33582	33527		35777		36068	ŀ	38535	L		26531				27620								32348				33687	34569		7 38377
Exon SEQ ID	Š	20197	2016	20161	20111	21626	22232	22254	l l	i	ı	1	1	13499	13939		14476	L		L	L	16249	L	L	<u>.</u>	19042	L	19529	L	20251	21057	ı	1
Probe SEQ ID	ö	6060	7025	7025	7058	8445	9154	9176	9428	9936	11852	11852	12446	281	758		1320	1390	2557	2869	3073	3410	3585	4239		5852	6329	8359		6938	8007	8856	11689

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	ilit Top Hit Descriptor	Human germline immunoglobulin lambda light chain gene	Γ	Marburg virus strain M/S Africal Johannesburg/1975/Ozolin VP35 gene, complete cds	Marburg virus strain M/S, Africa/Johannesburg/1973/Ozolin VP35 gene, complete cds		Xyiella fastidiosa, section 110 of 229 of the complete genome	Homo saplens chromosome 21 segment HS21C078	Home sapiens ASOL3 gene, CEGP1 gene, C11orf14 gene, C11orf15 gene, C11orf16 gene and C11orf17 gene.	Homo sapiens chromosome 21 segment HS21C080	Methanosardna frisla carbon monoxide dehydrogenase large subunit (cdhiA) gene; carbon monoxide dehydrogenase small subunit (cdhiB) gene, complete cds	Methanosarcina frisia carbon monoxide dehydrogenase lerge subunit (odhIA) gene, carbon monoxide dehydrocenase small subunit (odhIB) gene, complete ods	Arabidopsis thallana CCAAT-box binding factor HAP3 homolog gene, complete cds	AAN EST28167 Cerebellum II Homo sapiens cDNA 5' end similar to similar to neuro-D4 protein	Т	Gallus gallus mRNA for alpha1 Integrin, complete cds	Homo saplens ret finger protein-like 3 (RFPL3), mRNA	П		Drosophila melanogaster extradenticle (EXD) mRNA, complete cds			Myxococcus xantirus serine/threchine kinase Pkn10 (pkn10) gene, complete cds		perfiel cds	Homo sapiens S164 gene, partial cds; PS1 and hypothetical protein genes, complete cds; and S171 gene,	partial cds	Canis familiaris matrix metalloproteinase 9 (MMP-9) mRNA, partial cds	Cants familiaris matrix metalloproteinase 9 (MMP-9) mRNA, pertiel cds		Hepetitis E virus strain HEV-US2 polyprotein (ORF1), (ORF3), and capsid protein (ORF2) genes, complete cds
	Top Hit Database Source	FZ.	SWISSPROT	ΙN	N⊤	SWISSPROT	F	Ν	<u> </u>	L <sub>Z</sub>	L E	F	TN TN	<b>EST HUMAN</b>	μ	Ϋ́	LN	EST_HUMAN	EST_HUMAN	NT	SWISSPROT	EST_HUMAN	NT		LN		LN.	ΔT	NT	EST_HUMAN	Ν
)	Top Hit Acession No.	4.6E-02 X57808.1	P22448	4.5E-02 AF005730.1	4.6E-02 AF005730.1	P32182	4.5E-02 AE003964.1	4.5E-02 AL163278.2	4 5E-02 A 1400877 1	4.5E-02 AL163280.2	4 5E-02   1 28487.1	4 5E-02   28487 1	4.5E-02 AF036684.1	4.5E-02 AA325216.1	4.5E-02 X95508.1	4.5E-02 AB000470.1	11418013 NT	4.5E-02 AA191097.1	4.4E-02 BE972733.1	4.4E-02 L19295.1	P31568	4.4E-02 AW875475.1	4.4E-02 AF159160.1	į	4.4E-02 AF109907.1		4.4E-02 AF109907.1	4.4E-02 AF095824.1	4.4E-02 AF095824.1	4.4E-02 AA736969.1	4.4E-02 AF060669.1
	Most Similar (Top) Hit BLAST E Value	4.6E-02	4.5E-02 P22448	4.5E-02	4.6E-02	4.5E-02 P32182	4.5E-02	4.5E-02	4 5E 00	4.5E-02	4 5E-02	4 5= 02	4.5E-02	4.5E-02	4.5E-02	4.5E-02	4.5€-02	4.5E-02	4.4E-02	4.4E-02	4.4E-02 P31568	4.4E-02	4.4E-02		4.4E-02		4.4E-02	4.4E-02	4.4E-02	4.4E-02	4.4E-02
	Expression Signal	3.14	2.24	1.52	1.52	4.93	2.2	5.04		0.84	0.59	og o	2.24	4.2	0.47	0.79	2.61	3.79	4.35	0.77	6.82	1.81	1.68		1.33		1.33	0.59	0.59	2.34	2.64
	ORF SEQ ID NO:	+	28693	1			28440	29981	00000			22575	35207	36788		37061				27273		58809			30866			33802	L		
	Exon SEQ ID NO:	25708	l.,	1	14404		15312	16977	j	ı	1	1.	21668	L		23456	L	1_	L		15299	15684	16891		17885		17885	L	20350		
	Probe SEQ ID NO:	13079	460	1245	1245	1847	2177	3817	288	9838	7018		8587	10155	10305	10421	12442	12891	227	1050	2163	2559	3730		4750		4750	7267	7267	8952	11326

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	Top Hit Descriptor	ae33f04,r1 Gessler Wilms turnor Homo sapiens cDNA clone IMAGE:897631 5'	Homo sapiens mRNA for KIAA1493 protein, partial cds	601878746F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4107418 5'	Morone saxatilis myosin heavy chain FM3A (FM3A) mRNA, complete ods	AV704878 ADB Homo sapiens cDNA clone ADBAOH08 5'	Homo saplens chromosome 21 segment HS21C010	Homo sapiens promyelocytic leukemia zinc finger protein (PLZF) gene, complete cds	PLECTIN	PLECTIN	Ins69c12.s1 NCI_CGAP_Pr2 Homo sapiens cDNA clone IMAGE:1188886	Homo sapiens desmocollin 3 (DSC3) gene, complete cds, alternatively spliced	H.sapiens NCAM mRNA for neural cell adhesion molecule	H.sapiens NCAM mRNA for neural cell adhesion molecule	Campylobacter Jejuni NCT C11168 complete genome; segment 4/6	AU123327 NT2RM2 Homo sapiens cDNA clone NT2RM2000020 5'	AU123327 NT2RM2 Homo sapiens cDNA clone NT2RM2000020 5	wx34g01 x1 NCL_CGAP_Pitt Horno sepiens cDNA clone IMAGE:2545584 3' similar to TR:Q63291 Q63291   In Detroposon ORF2 MRNA registers 1.13 L1 L1 repetitive element:	Thermostern aridonillim complete genome: segment 4/5	TELEVISION OF CONTRACTOR SOLUTION OF CONTRACTOR SOLUTION OF CONTRACTOR SOLUTION OF CONTRACTOR SOLUTION OF CONTRACTOR SOLUTION OF CONTRACTOR SOLUTION OF CONTRACTOR SOLUTION OF CONTRACTOR SOLUTION OF CONTRACTOR SOLUTION OF CONTRACTOR SOLUTION OF CONTRACTOR SOLUTION OF CONTRACTOR SOLUTION OF CONTRACTOR SOLUTION OF CONTRACTOR SOLUTION OF CONTRACTOR SOLUTION OF CONTRACTOR SOLUTION OF CONTRACTOR SOLUTION OF CONTRACTOR SOLUTION OF CONTRACTOR SOLUTION OF CONTRACTOR SOLUTION OF CONTRACTOR SOLUTION OF CONTRACTOR SOLUTION OF CONTRACTOR SOLUTION OF CONTRACTOR SOLUTION OF CONTRACTOR SOLUTION OF CONTRACTOR SOLUTION OF CONTRACTOR SOLUTION OF CONTRACTOR SOLUTION OF CONTRACTOR SOLUTION OF CONTRACTOR SOLUTION OF CONTRACTOR SOLUTION OF CONTRACTOR SOLUTION OF CONTRACTOR SOLUTION OF CONTRACTOR SOLUTION OF CONTRACTOR SOLUTION OF CONTRACTOR SOLUTION OF CONTRACTOR SOLUTION OF CONTRACTOR SOLUTION OF CONTRACTOR SOLUTION OF CONTRACTOR SOLUTION OF CONTRACTOR SOLUTION OF CONTRACTOR SOLUTION OF CONTRACTOR SOLUTION OF CONTRACTOR SOLUTION OF CONTRACTOR SOLUTION OF CONTRACTOR SOLUTION OF CONTRACTOR SOLUTION OF CONTRACTOR SOLUTION OF CONTRACTOR SOLUTION OF CONTRACTOR SOLUTION OF CONTRACTOR SOLUTION OF CONTRACTOR SOLUTION OF CONTRACTOR SOLUTION OF CONTRACTOR SOLUTION OF CONTRACTOR SOLUTION OF CONTRACTOR SOLUTION OF CONTRACTOR SOLUTION OF CONTRACTOR SOLUTION OF CONTRACTOR SOLUTION OF CONTRACTOR SOLUTION OF CONTRACTOR SOLUTION OF CONTRACTOR SOLUTION OF CONTRACTOR SOLUTION OF CONTRACTOR SOLUTION OF CONTRACTOR SOLUTION OF CONTRACTOR SOLUTION OF CONTRACTOR SOLUTION OF CONTRACTOR SOLUTION OF CONTRACTOR SOLUTION OF CONTRACTOR SOLUTION OF CONTRACTOR SOLUTION OF CONTRACTOR SOLUTION OF CONTRACTOR SOLUTION OF CONTRACTOR SOLUTION OF CONTRACTOR SOLUTION OF CONTRACTOR SOLUTION OF CONTRACTOR SOLUTION OF CONTRACTOR SOLUTION OF CONTRACTOR SOLUTION OF CONTRACTOR SOLUTION OF CONTRACTOR SOLUTION OF CONTRACTOR SOLUTION OF CONTRACTOR SOLUTION OF CONTRACTOR SOLUTION OF CONTRACTOR SOLUTION OF CONTRACTOR SOLUTION OF CONTRACTOR SOLUTION OF CONTRACTOR SOLUTION OF CONTRACT	TRANSTORMING PROJECT WAS	I KANSTURMING FRO EIN WAT	602017105F1 NCI_CGAP_Bmo4 Homo sapiens culva ciona invace 4132072 3	Homo sapiens cytochrome P450 polypeptide 43 (CYP3443) genc, partial cds; cytochrome P450 polypeptide 44 (CYP344) gencs, complete cds; and cytochrome P450 polypeptide 7 (CYP347) gencs, complete cds; and cytochrome P450 polymeptide 5 (CYP3A5) genc, partial cds	Homo sapiens cytochrome P450 polypeptide 43 (CYP3A43) gene, partial cds; cytochrome P450 polypeptide	4 (CYP3A4) and cytochroms P450 polypeptide 7 (CYP3A7) genes, complete cds; and cytochrome P450	polypeptide 5 (CYP3A5) gene, partial cds	601124595F1 NIH_MGC_8 Hamo sapiens cDNA clone IMAGE:2989319 5	Legionella pneumophila catalass-peroxidase (katA) gene, complete cds	AV730347 HTF Homo sapiens cDNA clone HTFAVH04 5	ALPHA-ACTININ 3, NON MUSCULAR (F-ACTIN CROSS LINKING PROTEIN)	[T-BRAIN-1 PROTEIN (1-BOX BRAIN PROTEIN 1) (1BR-1) (1ES-50)
	Top Hit Database Source	EST_HUMAN	LN	EST_HUMAN	ŢŃ	EST_HUMAN	H	NT	SWISSPROT	SWISSPROT	EST_HUMAN	NT	NT	LΝ	LN L	EST_HUMAN	EST_HUMAN	MAMIL TOD	NAME IN LANGE	Z	SWISSPROT	SWISSPROT	EST HUMAN	5		_	NT	EST_HUMAN	NT	EST_HUMAN	SWISSPROT	SWISSPROT
<b>)</b>	Top Hit Acession No.	4.4E-02 AA496739.1	4.4E-02 AB040926.1	4.4E-02 BF241245.1	4.3E-02 AF003249.1	4.3E-02 AV704878.1	4.3E-02 AL163210.2	4.3E-02 AF060568.1	P30427	P30427	4.3E-02 AA652266.1	4.3E-02 AF293359.1	4.3E-02 X55322.1	4.3E-02 X55322.1	4.3E-02 AL139077.2	4.2E-02 AU123327.1	4.2E-02 AU123327.1	24,000,000	AVV003040.1	4.2E-02 AL445066.1	P23091	P23091	4.2E-02 BF342995.1	4 2E-02 AE2804074	201007		4.2E-02 AF280107.1	4.2E-02 BE268285.1	4.2E-02 AF276752.1	4.2E-02 AV730347.1	4.2E-02 P05095	4.2E-02 Q16650
	Most Similar (Top) Hit BLAST E Value	4.4E-02	4.4E-02	4.4E-02	4.3E-02	4.3E-02	4.3E-02	4.3E-02	4.3E-02 P30427	4.3E-02 P30427	4.3E-02	4.3E-02	4.3E-02	4.3E-02	4.3E-02	4,2E-02	4.2E-02	00 10	4.2E-02	4.2E-02												
	Expression Signal	3.08	4.55	1.65	7.25	1.55	9.18	1.21	484	4.94	0.8	0.69	1.32	1.32	12	1.74	2.4	;	10.1	1.37			0.59	72.0			0.74	0.61	4.35	0.61		1.46
	ORF SEQ ID NO:	38206			27034				33172	33173	33433				L	27081			80 L/Z	╛			30982		32224		32225		34244			37013
	SEQ ID NO:	24536	25126	26192		L	ı	l	ı	19785		21791	<u> </u>	Ľ		L	L.	1	- 1	╛	_	16915	17998	1	18970		18928	1	ı	ı		١.
	Probe SEQ ID NO:	11477	12158	12347	802	2634	3516	3749	6625	6625	6871	8711	9001	9001	12412	845	888		200	1758	1819	3754	4865	100	05/6		5735	7122	7695	77/7	9010	10367

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	Top Hit Descriptor	oก33b11.s1 NCI_CGAP_Lu5 Hano seplens cDNA clone IMAGE:1558461 3' similar to gb:M65290 INTERLEUKIN-12 BETA CHAIN PRECURSOR (HUMAN);	PM3-BN0174-250500-009-d10 BN0174 Homo sapiens cDNA	PM3-BN0174-250500-009-010 BN0174 Homo saplens cDNA	PRRS isolate PRRSV36 envelope giycoprotein gelle, comprete cus	W449910.X1 NCI_CGAP_Pen1 Hamo sapiens cultur cone invade	Staphylococcus aureus HSP 10 and HSP 00 genes	Homo sapiens Hron gene, intron 3	Chamydia muridaulm, section ou or or or une complete genome	601177907F1 NIH MGC 17 Homo sapiens cuiva ciare invade. 33330303 3	601177907F1 NIH MGC 1/ Homo septents CLIVA crone livacing	QV1-NN0012-180400-164-106 NN0012 Homo septens cDNA	. monocytogenes type 3 partial lap gene (strain 443)	601107635F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3343636 3	601107535F1 NIH_MGC_16 Home sapiens cDNA cione IMAGE:3343830 3	A.thaliana mRNA for plasma membrane intrinsic protein 1a	Ureaplasma urealyticum section 33 of 59 of the complete genome	Homo sapiens KIAA0867 protein (KIAA0867), mRNA	Mus musculus proviral retroviral insertion in the cGMP-phosphodiesterase (rd beta PDE) gene, intron 1, with the proviral insert encompassing the eny pseudogene (3' end) and 3' LTR	The second sell adhering malestille 1 homolog (11-CAM) gene, complete cds; putative protein 1	Pugu tudipes real a contraction into the contraction of the contraction protein SMC1 homolog (SMC1) gene, (PUT1) gene, partial cds, mitosis-specific chromosome segregation protein SMC1 homolog (SMC1) gene,	complete cds, and calcium channel alpha-1 subunit>	ADAM-TS 1 PRECURSOR (A DISINTEGRIN AND METALLOPROTEINASE WITH THROMBOSPONDIN	MOTIFS 1) (ADAMTS-1) (ADAM-TS1)	CUTICLE COLLAGEN 34	EST84291 Colon edenocarcinoma IV Homo sapiens cDNA 5 end	Brassica napus gin gene for plastid glutamine synthetase, exons 1-12	Homo sapiens mRNA for KIAA1471 protein, partial cds	Human retinoblasioma susceptibility gene exons 1-27, complete cds	Hamo sapiens cytochrome P450 polypeptide 43 (CYP3A43) gene, partial cds; cytochrome P450 polypeptide	4 (CYP3A4) and cytochrome P450 polypeptide 7 (CYP3A7) genes, complete cds; and cytochrome P450	polypeptide o (Circho) gene, par na cuo
	Top Hit Database Source	EST_HUMAN	П	HUMAN	П	T_HUMAN			٦	П	П	I_HUMAN	NT			Ν	NT	N	F	-		Ā		SWISSPROT	SWISSPROT	EST HUMAN	N.	Z	Į.			L.
8	Top Hit Acession No.	.2E-02 AA976118.1	.2E-02 BE815822.1			.2E-02 AI983494.1		.1E-02 AF200629.1	.1E-02 AE002330.2	.1E-02 BE297236.1	.1E-02 BE297236.1	4.1E-02 AW893484.1	.1E-02 X85880.1	1.1	4.1E-02 BE251894.1		4.1E-02 AE002132.1	7662347 NT	, 0,700	4.1E-02 LUZ110.1		4.1E-02 AF026198.1		P97857	P34687	4 1F-02 AA372398.1	4 1E-02 A 1271909 1	4 OE-02 ARDAD904 1	4.05.02   44040 4			4.0E-02 AF280107.1
	Most Similar (Top) Hit BLAST E Value	4.2E-02	4.2E-02	4.2E-02	4.2E-02	4.2E-02 /	4.2E-02	4.1E-02 /	4.1E-02/	4.1E-02	4.1E-02	4.1E-02	4.1E-02	4.1E-02	4.1E-02	4.1E-02	4.1E-02	4.1E-02	L	4.15-02		4.1E-02		4.1E-02 P97857	4.1E-02 P34687	4 1F-02	4 1E.02	4 OF 02	10.10.4	4.0E-02		4.0E-02
	Expression Signal	1.52	2.83	2.83	1.52	6.64	1.17	1.85	1.06	19.0	0.61	8.4	0.61	1.06	1.06	0.98	1.38	1 79		20.08		284		0.74	0.79	78.0	000			90.		5.31
	ORF SEQ ID NO:	38002	38320	38321	Ì	l				30168	30169			32253	32254	_	3477B			34325		34502		35011	L			1	1	SCOOS		31710
	Exon SEQ ID NO:	24361	24640	24640	24785	26109	25705	13716	15858	17162	17162	l	1	1	18051	20158	20334	77777	1	20834		20000		21483	L	L	L	_	-	17059		18694
	Probe SEQ ID NO:	11295	11587	11587	11795	12729	13076	523	2741	4005	4005	4595	5229	5750	5750	2022	27.7	C02L	700/	7778		20,02	74.6	8402	2000		0000	13112	3	3900		5495

Page 152 of 550 Table 4 Single Exon Probes Expressed in Placenta

Exon No: Signal Nors Similar         Most Similar Top Hit Acession Signal Nors Similar         Most Similar Top Hit Acession Database Source Signal         (Top) Hit Top Hit Acession Database Source Nors Nors Nors Nors Nors Nors Nors Nors								
19513         32870         0.98         4.0E-02         BF110434.1         EST_HUMAN           20921         34428         5.99         4.0E-02         L23838.1         NT           20923         34504         0.71         4.0E-02         AL161835.2         NT           20923         34504         0.8         4.0E-02         AF288153.1         NT           21029         34543         0.61         4.0E-02         AF288153.1         NT           21029         34543         0.61         4.0E-02         AF288153.1         NT           22804         36495         2.46         4.0E-02         AF288163.1         NT           22806         36495         2.46         4.0E-02         AF288163.1         NT           22807         36495         2.46         4.0E-02         AF288163.1         NT           22809         36495         2.46         4.0E-02         AF288163.1         NT           22506         31659         16.34         4.0E-02         AF28936.1         NT           22804         31689         16.34         4.0E-02         AF38936.1         NT           2805         31334         1.08         3.9E-02         AH39241			ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.		Top Hit Descriptor
20921         34428         5.99         4.0E-02 AL161535.2         NT           20933         34503         0.71         4.0E-02 AL161535.2         NT           20963         34504         0.8         4.0E-02 AB000381.1         NT           20963         34504         0.61         4.0E-02 AB000381.1         NT           21929         34543         0.61         4.0E-02 AB000381.1         NT           22884         0.63         4.0E-02 BF678376.1         EST HUMAN           22896         36495         2.46         4.0E-02 AJ000941.1         NT           22807         1.08         4.0E-02 AJ0010941.1         NT           2508         2.76         4.0E-02 AJ0010941.1         NT           2509         3.1859         1.52         4.0E-02 AJ0010941.1         NT           2509         3.1859         1.634         4.0E-02 AJ001066.1         NT           14309         2.736         2.79         3.9E-02 AJ001066.1         NT           14530         2.786         2.79         3.9E-02 AJ001066.1         NT           14530         2.736         2.15         3.9E-02 AJ001066.1         NT           14530         3.1366         0.9         3.9E-02 AJ003	8343	19513	32870		4			7n52h07.x1 NCI_CGAP_Lu24 Homo sepiens cDNA clone IMAGE:3568380 3' similar to TR:O75296 O75296 R29124_1 ;
20920         34926         3.59         4.0E-02 AB000381.1         NT           20963         34504         0.8         4.0E-02 AB000381.1         NT           20963         34504         0.8         4.0E-02 AB000381.1         NT           20963         34504         0.8         4.0E-02 AB000381.1         NT           21029         34543         0.61         4.0E-02 AF288163.1         NT           22884         0.63         4.0E-02 BF678378.1         EST_HUMAN           22806         36465         2.46         4.0E-02 AJ001094.1         NT           22507         1.08         4.0E-02 AJ001098.1         NT           22508         31859         16.34         4.0E-02 AJ001098.1         NT           22508         31859         16.34         4.0E-02 AJ00108.1         NT           14309         27366         2.76         3.9E-02 AJ00108.1         NT           14530         27603         2.15         3.9E-02 AJ00108.1         NT           14530         2756         3.9E-02 AJ0047         SWISSPROT           1558         31366         0.9         3.9E-02 AJ00386.1         NT           1616         32482         0.9         3.9E-02 BE98841.1 <td></td> <td></td> <td></td> <td></td> <td></td> <td></td> <td></td> <td>Strongylocentrotus purpuratus homolog of human bone morphogenetic protein 1 (submp) mRNA, complete ode.</td>								Strongylocentrotus purpuratus homolog of human bone morphogenetic protein 1 (submp) mRNA, complete ode.
20993         34504         0.8         4.0E-02 AB000381.1         NT           20993         34504         0.8         4.0E-02 AB000381.1         NT           21029         34513         0.61         4.0E-02 AF288163.1         NT           21029         34543         0.61         4.0E-02 AF288163.1         NT           22884         0.63         4.0E-02 AF288163.1         NT           22809         36495         2.46         4.0E-02 AJ000941.1         NT           22509         36495         2.46         4.0E-02 AJ001094.1         NT           25054         1.52         4.0E-02 AJ001094.1         NT           25059         31859         16.34         4.0E-02 AJ001094.1         NT           14309         2.7366         2.76         3.9E-02 AJ00108.1         NT           14530         2.7603         2.15         3.9E-02 AJ0047         SWISSPROT           156         2.8241         0.67         3.9E-02 AJ00386.1         NT           165         3.1367         0.9         3.9E-02 AJ00388.1         NT           1603         3.246         1.97         3.9E-02 BE675203.1         EST HUMAN           1903         3.2482         0.65	/86/	20927	34428		4.   4			Arabidopsis thaliana DNA chromosome 4, contig fragment No. 35
20993         34504         0.8         4.0E-02 AF288163.1         NT           21029         34543         0.61         4.0E-02 AF288163.1         NT           21929         34543         0.61         4.0E-02 AF288163.1         NT           22884         0.63         4.0E-02 BF678376.1         EST_HUMAN           22209         36495         2.46         4.0E-02 BF678376.1         NT           22207         36495         2.46         4.0E-02 AJ001041.1         NT           22509         31859         16.34         4.0E-02 AJ001041.1         NT           25504         31859         16.34         4.0E-02 AJ001048.1         NT           14530         27366         2.76         3.9E-02 AJ001066.1         NT           14530         277663         2.15         3.9E-02 AJ0047         SWISSPROT           1568         27603         2.15         3.9E-02 AJ0047         SWISSPROT           1568         31364         0.67         3.9E-02 AJ00386.1         NT           1630         31366         0.9         3.9E-02 AJ0041.1         EST_HUMAN           1903         3.246         0.9         3.9E-02 BE68841.1         EST_HUMAN           2006         3.3	7043	20993	34503					Hamo sapiens DNA for GPI-anchared malecule-like protein, complete ads
21029         34543         0.61         4.0E-02 AF288163.1         NT           21983         35532         2.52         4.0E-02 BF678376.1         SWISSPROT           22884         0.63         4.0E-02 BF678376.1         EST HUMAN           22809         36495         2.46         4.0E-02 AJ001941.1         NT           22809         31859         16.34         4.0E-02 AJ001941.1         NT           25505         31859         16.34         4.0E-02 AJ001961.1         NT           14309         27366         2.79         3.9E-02 BF516149.1         BT HUMAN           14530         27563         2.15         3.9E-02 BF516149.1         EST HUMAN           14530         27563         2.15         3.9E-02 BF516149.1         EST HUMAN           1556         28261         3.22         3.9E-02 BF516149.1         EST HUMAN           1568         31334         0.67         3.9E-02 AJ03386.1         NT           18398         31367         0.9         3.9E-02 AJ03386.1         NT           19039         3.246         0.9         3.9E-02 BE675203.1         EST HUMAN           19039         32482         0.65         3.9E-02 BF27437.1         EST HUMAN	7943	20993	34504		Ŀ			Hamo sapiens DNA for GP Fanchared molecule-like protein, complete cds
21933         35532         2.52         4.0E-02 BF678376.1         SWISSPROT           22884         0.63         4.0E-02 BF678376.1         EST HUMAN           22200         36495         2.46         4.0E-02 AJ000941.1         NT           22505         1.08         4.0E-02 DA39491.1         NT           25505         1.52         4.0E-02 DA39491.1         NT           25506         31859         16.34         4.0E-02 DA30401.1         NT           14309         2.7366         2.76         3.9E-02 DA4047         SWISSPROT           14530         2.7603         2.15         3.9E-02 DA4047         SWISSPROT           15884         1.97         3.9E-02 DA4047         SWISSPROT           18398         31366         0.9         3.9E-02 DA4037         SWISSPROT           18398         31366         0.9         3.9E-02 DA4037         SWISSPROT           19039         31366         0.9         3.9E-02 DA336411         EST HUMAN           19039         32462         0.6         3.9E-02 DA336411         EST HUMAN           20068         33478         0.9         3.9E-02 DA336411         EST HUMAN           2106         34823         0.6         3.9E-02	7980	21029	34543		4		LN	Homo sepiens erythrocyte tropomodulin (E-TMOD) gene, exon 7
22884         0.63         4.0E-02         BF679376.1         EST HUMAN           22909         36495         2.46         4.0E-02         DA300941.1         NT           23227         1.08         4.0E-02         DA300941.1         NT           25054         1.52         4.0E-02         DA300941.1         NT           25054         1.52         4.0E-02         DA3001098.1         NT           25054         1.52         4.0E-02         DA3001098.1         NT           25055         2.736         2.78         3.9E-02         BF16149.1         EST HUMAN           14530         2.7863         2.15         3.9E-02         BF16149.1         EST HUMAN           1584         1.97         3.9E-02         BA4036.1         NT           1586         0.67         3.9E-02         A50862.NT         NT           18398         31367         0.9         3.9E-02         B924019         NT           19039         31366         0.9         3.9E-02         B924019         NT           19039         31366         0.9         3.9E-02         B924019         NT           19039         31366         0.9         3.9E-02         B924019	8914	21993	35532		4	P08640		GLUCOAMYLASE S1/S2 PRECURSOR (GLUCAN 1,4-ALPHA-GLUCOSIDASE) (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE)
22500         36495         2.46         4.0E-02 AJ000941.1         NT           23227         1.08         4.0E-02 D43049.1         NT           25054         1.52         4.0E-02 D43049.1         NT           25055         1.859         16.34         4.0E-02 D43040.1         NT           14309         27366         2.79         3.9E-02 BF516149.1         EST_HUMAN           14530         27763         2.15         3.9E-02 BF516149.1         EST_HUMAN           15156         28261         3.22         3.9E-02 BF516149.1         EST_HUMAN           1584         1.97         3.9E-02 AJ403386.1         NT           18398         31366         0.67         3.9E-02 AV392417.1         EST_HUMAN           18398         31366         0.9         3.9E-02 B924018         NT           19039         32346         0.9         3.9E-02 B924018         NT           19162         32482         0.6         3.9E-02 B924018         NT           20068         33478         0.6         3.9E-02 BF296841.1         EST_HUMAN           2106         34829         0.6         3.9E-02 BF29631.1         NT           2107         34828         0.6         3.9E-02 BF2	9844	22884			4			602153884F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4294724 5'
23227         1.08         4.0E-02 AJ001018.1         NT           25654         1.52         4.0E-02 AJ001018.1         NT           25695         3.859         16.34         4.0E-02 AJ001018.1         NT           14309         27366         2.7B         3.9E-02 BF516149.1         EST_HUMAN           14530         27763         2.15         3.9E-02 BF516149.1         EST_HUMAN           15156         28261         3.22         3.9E-02 AJ403386.1         NT           1584         1.97         3.9E-02 AJ403386.1         NT           18398         31366         0.67         3.9E-02 AV392417.1         EST_HUMAN           18398         31367         0.9         3.9E-02 AV392417.1         EST_HUMAN           19039         32346         0.9         3.9E-02 BS24018         NT           19162         32482         0.6         3.9E-02 BS24018         NT           2008         3.246         0.9         3.9E-02 BS24018         NT           19162         3.2482         0.6         3.9E-02 BS24018         NT           2008         3.4820         0.6         3.9E-02 BS24018         NT           21016         3.4820         0.6         3.9E-02 BS24018	6986	22909	36495		L	1	NT	Methanobacterium thermoautotrophicum strain Marburg. Thich:tumarato reductase subunit A
25054         1.52         4.0E-02 AJ001056.1         NT           25909         31859         16.34         4.0E-02 AJ001056.1         NT           14309         27366         2.79         3.9E-02 BF516149.1         EST HUMAN           14530         27603         2.15         3.9E-02 PA1047         SWISSPROT           1584         1.97         3.9E-02 AJ403386.1         NT           18367         31334         0.67         3.9E-02 AW392417.1         EST HUMAN           18398         31366         0.9         3.9E-02 AW392417.1         EST HUMAN           18398         31367         0.9         3.9E-02 AW392417.1         EST HUMAN           19039         3.2346         1         3.9E-02 AW392417.1         EST HUMAN           19039         3.2482         0.9         3.9E-02 AW392417.1         EST HUMAN           19162         3.2482         0.6         3.9E-02 BE968841.1         EST HUMAN           20068         3.9E-02 BE7675203.1         EST HUMAN         ST HUMAN           2106         3.4849         0.6         3.9E-02 BE736041.1         NT           21332         3.4849         0.6         3.9E-02 AJ229041.1         NT           21332         3.4849 </td <td>10190</td> <td>23227</td> <td></td> <td></td> <td></td> <td></td> <td>NT</td> <td>Human mRNA for KIAA0082 gene, partial cds</td>	10190	23227					NT	Human mRNA for KIAA0082 gene, partial cds
25908         31859         16:34         4.0E-02 AJ001056.1         NT           14309         27366         2.7B         3.9E-02 BF516149.1         EST_HUMAN           14530         27603         2.15         3.9E-02 P41047         SWISSPROT           1568         28261         3.22         3.9E-02 AJ403386.1         NT           15884         1.97         3.9E-02 AJ403386.1         NT           18396         31334         0.67         3.9E-02 AW392417.1         EST_HUMAN           18398         31366         0.9         3.9E-02 AW392417.1         EST_HUMAN           19039         31367         0.9         3.9E-02 AW392417.1         EST_HUMAN           19039         31366         0.9         3.9E-02 AW392417.1         EST_HUMAN           19039         31367         0.9         3.9E-02 AW392417.1         EST_HUMAN           19162         32482         0.65         3.9E-02 BE96841.1         EST_HUMAN           2006         3.9E-02 BF675203.1         EST_HUMAN           2106         3.4849         0.67         3.9E-02 BF239613.1         EST_HUMAN           2132         34850         0.6         3.9E-02 BF239613.1         EST_HUMAN           2132         34	12073	25054		1.52		AJ001018.1	TN	Kluyveromyces lactis gene for Ca++ ATP ase
14309         27366         2.78         3.9E-02         BF516149.1         EST_HUMAN           14530         2.7603         2.15         3.9E-02         P41047         SWISSPROT           15684         3.22         3.9E-02         AJ403386.1         NT           18386         31334         0.67         3.9E-02         AW392417.1         EST_HUMAN           18398         31367         0.9         3.9E-02         BB24019         NT           19039         32462         1         3.9E-02         BB24019         NT           19162         32462         1         3.9E-02         BB24019         NT           20068         33478         0.9         3.9E-02         BB24019         NT           20068         3.3478         0.65         3.9E-02         BB24019         NT           2106         3.2482         0.65         3.9E-02         BB24019         NT           2106         3.2482         0.65         3.9E-02         BE271437.1         EST_HUMAN           2106         3.4823         1.44         3.9E-02         BF236041.1         NT           2132         34850         0.6         3.9E-02         BF236041.1         NT	12333	25909	31859			AJ001056.1	ΙN	Ovis aries mRNA for acetyl-coA carboxylase
14530         27603         2.15         3.9E-02 AJ403386.1         NT           15156         28261         3.22         3.9E-02 AJ403386.1         NT           15884         1.97         3.9E-02 AJ403386.1         NT           18367         3.1334         0.67         3.9E-02 AW392417.1         EST HUMAN           18398         31366         0.9         3.9E-02 AW392417.1         EST HUMAN           19039         32346         1         3.9E-02 B924019 NT         EST HUMAN           19162         32462         0.9         3.9E-02 B924019 NT         EST HUMAN           20068         33478         0.65         3.9E-02 BF075203.1         EST HUMAN           21106         34623         1.44         3.9E-02 BF075203.1         EST HUMAN           2132         34480         0.67         3.9E-02 BF075203.1         EST HUMAN           2132         34850         0.6         3.9E-02 BF23663.1         EST HUMAN           2132         34860         0.6         3.9E-02 BF22041.1         NT           21332         34860         0.6         3.9E-02 BF22041.1         NT           21342         0.6         3.9E-02 BF22041.1         NT           2132         3.8E	1144	14309	27366			BF516149.1	EST HUMAN	UI-H-BW1-anx-h-08-0-UI.s1 NCI_CGAP_Sub7 Homo sapiens cDNA clone IMAGE:3084134 3
15168         28261         3.22         3.9E-02         AJ403386.1         NT           1584         1,97         3.9E-02         4506862         NT           1836         0.67         3.9E-02         AW392417.1         EST_HUMAN           18398         31366         0.9         3.9E-02         B824019         NT           18398         31367         0.9         3.9E-02         B824019         NT           19039         32246         1         3.9E-02         BE98841.1         EST_HUMAN           20068         33478         0.66         3.9E-02         BE75203.1         EST_HUMAN           21302         33478         0.87         3.9E-02         BE738013.1         EST_HUMAN           21332         34849         0.87         3.9E-02         BE738013.1         EST_HUMAN           21332         34849         0.6         3.9E-02         BE738041.1         NT           21332         34840         0.6         3.9E-02         BE738041.1         NT           21332         34845         0.6         3.9E-02         BA229041.1         NT           21332         34845         0.6         3.9E-02         BA229041.1         NT <td>1375</td> <td>14530</td> <td>27603</td> <td></td> <td></td> <td></td> <td>SWISSPROT</td> <td>FAS ANTIGEN LIGAND</td>	1375	14530	27603				SWISSPROT	FAS ANTIGEN LIGAND
15884         1.97         3.9E-02         4506862         IT           18367         31334         0.67         3.9E-02         AW392417.1         EST_HUMAN           18398         31366         0.9         3.9E-02         B924019         NT           1939         32346         0.9         3.9E-02         B824019         NT           1962         32346         0.9         3.9E-02         B824019         NT           1962         32462         0.9         3.9E-02         BE08841.1         EST_HUMAN           2008         33478         0.67         3.9E-02         BF278203.1         EST_HUMAN           2132         34849         0.6         3.9E-02         BF238013.1         EST_HUMAN           2132         34849         0.6         3.9E-02         BF238013.1         EST_HUMAN           2132         34845         0.6         3.9E-02         BF238013.1         NT           2132         34850         0.6         3.9E-02         BA223941.1         NT           2107         3.9E-02         PA272941.1         NT         NT           2107         3.9E-02         PA273941.1         NT           2107         3.9E-02 <td>2016</td> <td>15158</td> <td></td> <td></td> <td></td> <td></td> <td>NT</td> <td>M.musculus DNA for desmin-binding fragment DesD7</td>	2016	15158					NT	M.musculus DNA for desmin-binding fragment DesD7
1584         1.97         3.9E-02         450662 NT           18367         31334         0.67         3.9E-02         AW392417.1         EST_HUMAN           18398         31366         0.9         3.9E-02         B824019 NT           18398         31367         0.9         3.9E-02         B824019 NT           19039         32346         1         3.9E-02 BE908841.1         EST_HUMAN           20068         3.9E-02 BE908841.1         EST_HUMAN           2007         3.9E-02 BE908841.1         EST_HUMAN           2106         3.9E-02 BE736203.1         EST_HUMAN           2132         34849         0.87         3.9E-02 BF236613.1         EST_HUMAN           21332         34849         0.6         3.9E-02 BF236613.1         NT           21332         34845         0.6         3.9E-02 BF236613.1         NT           21332         34850         0.6         3.9E-02 B43778         SWISSPROT           21073         3.56         3.9E-02 B48778         SWISSPROT								Homo saplens succinate dehydrogenase complex, subunit C, integral membrane protein, 15kD (SDHC)
18367         31334         0.67         3.9E-02         AW392417.1         EST_HUMAN           18398         31366         0.9         3.9E-02         8924019         NT           18398         31367         0.9         3.9E-02         8924019         NT           19039         32346         1         3.9E-02         BE98841.1         EST_HUMAN           19162         32482         0.65         3.9E-02         BE98841.1         EST_HUMAN           2008         33478         0.97         3.9E-02         BE27437.1         EST_HUMAN           21302         34623         1.44         3.9E-02         BE27437.1         EST_HUMAN           21332         34849         0.6         3.9E-02         BE29041.1         NT           21332         34850         0.6         3.9E-02         BE202041.1         NT           21332         34850         0.6         3.9E-02         BE202041.1         NT           21071         34562         1.56         3.9E-02         BA225041.1         NT           21071         34560         0.6         3.9E-02         BA225041.1         NT	2769	15884		1.97		4506862	N	mRNA
18398         31366         0.9         3.9E-02         8924019 NT           18398         31367         0.9         3.9E-02         8924019 NT           19039         32346         1         3.9E-02 BE968841.1         EST_HUMAN           19162         32482         0.65         3.9E-02 BE975203.1         EST_HUMAN           20068         33478         0.97         3.9E-02 BE739613.1         EST_HUMAN           2130         34623         1.44         3.9E-02 BE739613.1         EST_HUMAN           21332         34849         0.6         3.9E-02 AJ229041.1         NT           21332         34850         0.6         3.9E-02 AJ229041.1         NT           21071         3450         0.6         3.9E-02 Be725961.1         NT           21071         3450         0.6         3.9E-02 AJ229041.1         NT           21071         3450         0.6         3.9E-02 AJ229041.1         NT           21071         3450         0.6         3.9E-02 AJ229041.1         NT           21071         3450         0.6         3.9E-02 AJ229041.1         NT	5246	18367	31334			AW392417.1	EST HUMAN	RC6-ST0258-171199-021-C09 S10258 Homo septens GUINA
18398         31367         0.9         3.9E-02         8024019 NT           19039         32346         1         3.9E-02 BE968841.1         EST_HUMAN           19162         32482         0.65         3.9E-02 BF975203.1         EST_HUMAN           20068         33478         0.97         3.9E-02 BF236913.1         EST_HUMAN           21106         34623         1.44         3.9E-02 BF236913.1         EST_HUMAN           21332         34849         0.6         3.9E-02 AJ229041.1         NT           21332         34850         0.6         3.9E-02 AJ229041.1         NT           21071         3450         0.6         3.9E-02 B42778         SWISSPROT           21071         3450         3.9E-02 B48778         SWISSPROT	5279	18398	31366			8924019	LN⊤	Homo sapiens hypothetical protein PRO1163 (PRO1163), mRNA
19039         32946         1         3.9E-02 BE968241.1         EST_HUMAN           19162         32462         0.65         3.9E-02 BF675303.1         EST_HUMAN           20068         33478         0.97         3.9E-02 BE271437.1         EST_HUMAN           21106         34623         1.44         3.9E-02 BF236041.1         INT           21332         34849         0.6         3.9E-02 AJ229041.1         INT           21071         34560         0.6         3.9E-02 P48778         SWISSPROT           21071         34502         1.56         3.9E-02 P48778         SWISSPROT	5279	18398	31367		3			Homo sapiens hypothetical protein PRO1163 (PRO1163), mkNA
19162         32482         0.65         3.9E-02         BF676203.1         EST_HUMAN           20068         33478         0.97         3.9E-02         BE271437.1         EST_HUMAN           21106         34923         1.44         3.9E-02         BF239613.1         EST_HUMAN           21332         34949         0.6         3.9E-02         AJ229041.1         NT           21332         34950         0.6         3.9E-02         AJ229041.1         NT           21071         34962         1.56         3.9E-02         P49778         SWISSPROT           2607         3.9E-02         AB042553.1         NT	5849	19039		-	3.9E-02	BE968841.1	EST_HUMAN	601649874F1 NIH_MGC_74 Hamo saplens cDNA clone IMAGE:3933642 5
20068         33478         0.97         3.9E-02         BE271437.1         EST_HUMAN           21106         34623         1.44         3.9E-02         BF239613.1         EST_HUMAN           21332         34849         0.6         3.9E-02         AJ229041.1         NT           21332         34850         0.6         3.9E-02         AJ229041.1         NT           21071         34962         1.56         3.9E-02         P48778         SWISSPROT           26073         3.54         3.9E-02         AB042553.1         NT	5977	19162			8		EST_HUMAN	602138132F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4274910 5
21106         3.4623         1.44         3.5E-02         BF239613.1         EST HUMAN           21332         34849         0.6         3.8E-02         AJ229041.1         NT           21332         34850         0.6         3.9E-02         AJ229041.1         NT           21071         34982         1.56         3.9E-02         P48778         SWISSPROT           25053         3.54         3.9E-02         AB042553.1         NT	7203	20068			3		EST_HUMAN	601140729F1 NIH_MGC_9 Home sapiens cDNA clone IMAGE:3049830 5
21332         34849         0.6         3.9E-02 AJ229041.1         NT           21332         34950         0.6         3.9E-02 AJ229041.1         NT           21071         34982         1.56         3.9E-02 P48778         SWISSPROT           25053         3.54         3.9E-02 AB042553.1         NT	8023	21106			3		EST_HUMAN	601906848F1 NIH_MGC_54 Homo saplens cDNA clone IMAGE:4134779 5
21332         34850         0.6         3.9E-02         AJZ29041.1         NT           21071         34582         1.56         3.9E-02         P48778         SWISSPROT           25053         3.54         3.9E-02         AB042553.1         NT	8250	21332			3.	AJ229041.1	μ	Homo sapiens 959 kb contig between AML1 and CBK1 on chromosome 21424, segment 73
21071 34582 1.56 3.9E-02 P48778 SWISSPROT 28058	8250	21332				AJ229041.1	NT	Homo sapiens 959 kb contig between AML1 and CBR1 on chlomosome 21q22, segment 1/3
26059 3.54 3.9E-02 AB042553.1  NT	11695	l i			3	P48778	SWISSPROT	ANTIGEN GOR
	12184	26059		3.54	<u></u>	AB042553.1	N	Fells catus G-CSF gene tor granulocyre colony-summating tector, complete cas

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_					_	_	_	_	_	_		_	_	_			-		_	<del></del>	_	_		_	_	7			$\neg$
	Top Hit Descriptor	Human germline T-cell receptor beta chain TCRBV17S1A1T, TCRBV2S1, TCRBV10S1P, TCRBV29S1P, TCRBV19S1P, TCRBV19S1P, TCRBV19S1, TCRBV19S1, TCRBV19S1, TCRBV3S1, TCRBV3S1, TCRBV3S1, TCRBV3S1, TCRBV3S1, TCRBV4S1A1T, TRY4, TRY6, TRY7, TRY8, TCRBD1, TCRBJ1S1, TCRBV3S1, TCRBV4S1A1T, TRY4, TRY6, TRY7, TRY8, TCRBD1, TCRBJ1S1, TCRBV3S1, TCRBV4S1A1T, TRY4, TRY6, TRY7, TRY8, TCRBV3S1, TCRBV4S1A1T, TRY4, TRY6, TRY7, TRY8, TCRBV3S1, TCRBV4S1A1T, TRY4, TRY8, TRY8, TRY8, TCRBV3S1, TCRBV4S1A1T, TRY4, TRY8, TRY8, TRY8, TRY8, TCRBV3S1, TCRBV4S1A1T, TRY4, TRY8, TRY8, TRY8, TRY8, TRY8, TRY8, TRY8, TRY8, TRY8, TRY8, TRY8, TRY8, TRY8, TRY8, TRY8, TRY8, TRY8, TRY8, TRY8, TRY8, TRY8, TRY8, TRY8, TRY8, TRY8, TRY8, TRY8, TRY8, TRY8, TRY8, TRY8, TRY8, TRY8, TRY8, TRY8, TRY8, TRY8, TRY8, TRY8, TRY8, TRY8, TRY8, TRY8, TRY8, TRY8, TRY8, TRY8, TRY8, TRY8, TRY8, TRY8, TRY8, TRY8, TRY8, TRY8, TRY8, TRY8, TRY8, TRY8, TRY8, TRY8, TRY8, TRY8, TRY8, TRY8, TRY8, TRY8, TRY8, TRY8, TRY8, TRY8, TRY8, TRY8, TRY8, TRY8, TRY8, TRY8, TRY8, TRY8, TRY8, TRY8, TRY8, TRY8, TRY8, TRY8, TRY8, TRY8, TRY8, TRY8, TRY8, TRY8, TRY8, TRY8, TRY8, TRY8, TRY8, TRY8, TRY8, TRY8, TRY8, TRY8, TRY8, TRY8, TRY8, TRY8, TRY8, TRY8, TRY8, TRY8, TRY8, TRY8, TRY8, TRY8, TRY8, TRY8, TRY8, TRY8, TRY8, TRY8, TRY8, TRY8, TRY8, TRY8, TRY8, TRY8, TRY8, TRY8, TRY8, TRY8, TRY8, TRY8, TRY8, TRY8, TRY8, TRY8, TRY8, TRY8, TRY8, TRY8, TRY8, TRY8, TRY8, TRY8, TRY8, TRY8, TRY8, TRY8, TRY8, TRY8, TRY8, TRY8, TRY8, TRY8, TRY8, TRY8, TRY8, TRY8, TRY8, TRY8, TRY8, TRY8, TRY8, TRY8, TRY8, TRY8, TRY8, TRY8, TRY8, TRY8, TRY8, TRY8, TRY8, TRY8, TRY8, TRY8, TRY8, TRY8, TRY8, TRY8, TRY8, TRY8, TRY8, TRY8, TRY8, TRY8, TRY8, TRY8, TRY8, TRY8, TRY8, TRY8, TRY8, TRY8, TRY8, TRY8, TRY8, TRY8, TRY8, TRY8, TRY8, TRY8, TRY8, TRY8, TRY8, TRY8, TRY8, TRY8, TRY8, TRY8, TRY8, TRY8, TRY8, TRY8, TRY8, TRY8, TRY8, TRY8, TRY8, TRY8, TRY8, TRY8, TRY8, TRY8, TRY8, TRY8, TRY8, TRY8, TRY8, TRY8, TRY8, TRY8, TRY8, TRY8, TRY8, TRY8, TRY8, TRY8, TRY8, TRY8, TRY8, TRY8, TRY8, TRY8, TRY8, TRY8, TRY8, TRY8, TRY8, TRY8, TRY8, TRY8,	Mus musculus chromosome X contigB; X-linked lymphocyte regulated 5 gene, zinc finger protein z/5, zinc finger protein 92, mmxq28orf	Human protein C gene, complete cds	HOMEOBOX PROTEIN HOX-84 (HOX-2.6)	Home sapiens ATP-binding cassette, sub-tamily A (ABCT), mentuer o (ABCAO), minuth	Human von Wilebrand factor gene, exons 23 mough 34	Homo sapiens PR00514 protein (PR00514), mRNA	Homo sapiens PELOTA (PELOTA) gene, compiere cas	LAMININ ALPHA-1 CHAIN PRECURSOR (LAMININ A CITALIN )	wr85e08.x1 NCI_CGAP_Kid11 Homo sapiens cUNA cione liviAGE.x494502.5	Homo sapiens mRNA for KIAA0718 protein, partial cds	EOMESODERMIN STATE ASSESSED FOR	601896233F1 NIH_MGC_19 Homo sapiens cUNA dane IMAGE-+12336+ 3	Mus musculus potassium large conductance pH-sensitive channel, sublamily M, alpha member 3 (normas), ImRNA	Aeropynum pernix genomic DNA, section 6/7	Xylella fastidiosa, section 121 of 229 of the complete genome	ai55c09.s1 Soares_parathyroid_tumor_NbHPA Homo septens cDNA clone 1360912.3	601762117F1 NIH_MGC_20 Home sapiens cDNA clone IMAGE:4024973 5	Homo saplens solute carrier family 22 (organic cation transporter), member 1 (SLC22A1), mKNA	Odontella sinensis chloroplast, complete genome	H.wigare Ss1 gene for sucrose synthase	Homo septens genomic region containing hypervariable minisatelittes chromosome 10(10q26.3) or Homo	sapiens	Homo sapiens genomic region containing hypervariable minisatellites chromosome 10[10qzo.5] of maniso	seplens	C.glutamicum gap, pgk and tpl genes for glyceraldehyde-3-phosphate, phosphoglycerate kinase and triceephosphate isomerase	C.glutamicum gap, pgk and tpi genes for glyceraldehyde-3-phosphate, phosphoglycerate kinase and	triosephosphate isomerase
	Top Hit Database Source	TN	TN	LN	SWISSPROT	LZ.	N	LN	LI	SWISSPROT	EST_HUMAN	TN	SWISSPROT	EST_HUMAN	LZ	Þ	LZ.	EST_HUMAN	EST_HUMAN	TN	TN	노		TN		FZ	FZ		NT
	Top Hit Acession No.	J66061.1	3.9E-02 AL049866.2	M11228.1	IJ	6005700 NT		7662563 NT	3.8E-02 AF143952.2		3.7E-02 AI984806.1	3.7E-02 AB018261.1	279944	3.7E-02 BF312963.1	6680541 NT	3.7E-02 AP000063.1	3.7E-02 AE003975.1	3.7E-02 AA782516.1	3.7E-02 BF124974.1	11418392 NT	11467432 NT	3.6E-02 X73221.1		3.6E-02 AL096806.1		3.6E-02 AL096810.1	3 6E-02 X59403 1		3.6E-02 X59403.1
	Most Similar (Top) Hit BLAST E Value	3.9E-02   U66061.1	3.9E-02	3.8E-02	3.8E-02 P10284	3.8E-02	3.8E-02 M60675.	3.8E-02	3.8E-02	3.7E-02 P19137	3.7E-02	3.7E-02	3.7E-02 P79944	3.7E-02	3.7F-02	3.7E-02	3.7E-02	3.7E-02	3.7E-02	3.7E-02	3.7E-02	L							
	Expression Signal	2.35	64.89	0.8	1.04	1.72	1.51	0.64	1.71	4.05	6.19	76.0	1.13	4.33	60	0 95			7.41	3.71	1.23			6.0		0.67	6		0.61
	ORF SEQ ID NO:			31792	32736	34018		37446	37603	27248				L			34430		38837	L		29909	_	29916		31400			31774
	Exon SEQ ID NO:	25595	25979	18754	19387	20546	21943	23822	23972	14187	15442	15768	1		16709	26218	1.	.1_	L	25945		L	1_	16913	١	18430	1	18/40	18740
	Probe SEQ ID NO:	12898	13036	9229	6212	7471	8864	10789	10888	1016	2310	2645	3115	3117	0 110	7000	7880	10210	12227	12961	13069	3744		3752		5313		5543	5543

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Probe SEQ ID SI NO:	Exan SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
5617	18811	31880	99'0		3,6E-02 AF181722.1	NT	Homo saplens RU2AS (RU2) mRNA, complete cds
6846	19999	33406			AW945516.1	EST_HUMAN	CM2-EN0013-110500-192-b10 EN0013 Homo sapiens cDNA
I	19930	33407			3.6E-02 AW945518.1	EST_HUMAN	CM2-EN0013-110500-192-510 EN0013 Homo capiens cDNA
7234	20318			L	Γ	LΝ	Chromatum vinosum sulfur globule protein Cv2 precursor (sgp2) gene, complete ods
7458	20534	34009	2.89	3	6E-02 AA714521.1	EST HUMAN	rw20e05.s1 NCI_CGAP_GCB0 Homo saplens cDNA clone IMAGE:1241024 3' similar to gb:J00314_rna2_TUBULIN BETA-1 CHAIN (HUMAN);
7811	20866	34360		m		EST_HUMAN	MR0-HT0158-030200-003-b08 HT0158 Homo sapiens cDNA
							Dictyostelium discordeum unknown spore germination-specific protein-like protein, orf1, orf2 and orf3 genes,
9591	22646	36216	2.16	65	6E-02 U20608,1	NT	complete cds
9591	22646	36217	2.16	85	6E-02 \U20608.1	IN	Dictyostellum discoldeum unknown spore germination-specific protein-like protein, orf1, orf2 and orf3 genes, complete cds
9812	22852				3.6E-02 BF347586.1	EST_HUMAN	602020453F1 NCI_CGAP_Brn67 Homo saplens cDNA clone IMAGE:4156116 5'
	24516		1.46		BF131609.1	EST_HUMAN	601820416F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4052570 5'
ļ	24516				3.6E-02 BF131609.1	EST HUMAN	601820416F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4052570 5'
918	14093		66.0		3.5E-02 U09506.1	N⊤	Drosophila melanogastar tiggrin mRNA, complete cds
1033	14202	27260	2.43		3.5E-02 AF253417.1	NT	Homo sapiens microsomal epoxide hydrolase (EPHX1) gene, complete cds
1595	14748	27831	1.4		, 1	EST_HUMAN	602085136F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4249377 5/
1595	14748	27832	1.4		3.5E-02 BF678085.1	EST_HUMAN	602085136F1 NIH_MGC_83 Homo saplens cDNA clone IMAGE:4249377 5
4329	17472	30457	1.83			NT	Thermotoga maritima section 85 of 136 of the complete genome
4435	17575	99908	1.11		3.5E-02 P53780	SWISSPROT	CYSTATHIONINE BETA-LYASE PRECURSOR (CBL) (BETA-CYSTATHIONASE) (CYSTEINE LYASE)
6351	19521	32878	1.76		J01238.1	NT	Maize actin 1 gene (MAc1), complete cds
8165	21247		0.94	L	5E-02 H29951.1	EST_HUMAN	yp44a05.r1 Soares retina N2b5HR Homo sapiens cDNA clone IMAGE:190256 5' similar to contains Alu repetitive element;
8824	21903	35443			3.5E-02 BE958970.1	EST_HUMAN	601644701R2 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:3929737 3'
10224	23260		0.94	L	X76642.1	TN	L. lactis MG1383 grpE and dnak genes
10270	23305	į	0.51	L	BE561042.1	EST_HUMAN	601344661F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3677654 5'
11785	24775				AW861641.1	EST_HUMAN	PM1-CT0326-291299-002-h03 CT0328 Homo sapiens cDNA
11785	24775		1.79		AW861641.1	EST_HUMAN	PM1-CT0326-291299-002-h03 CT0326 Homo saplens cDNA
12876	25583		1.31	Ц	5E-02 AF009683.1	Ν	Homo sapiens T cell receptor beta locus, TCRBVBS5P to TCKBV2/1S/2A2 region
12955	25991		2.71	(c)	5E-02 BE276948.1	EST_HUMAN	601178765F1 NIH MGC 20 Horro sapiens cDNA clone IMAGE:3543833 5
592	13783			3	.4E-02 AK024424.1	노	Homo sapiens mRNA for FLJ00013 protein, partial cds
592	13783	26803	Ì	e l	4E-02 AK024424.1	Ę	Homo saplens mRNA for FLJ00013 protein, partial cds
593	13783		3.26	8	4E-02 AK024424.1	닐	Homo sapiens mKNA for FLJ00013 protein, partial cds

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					3		
Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression	Most Similar (Top) Hit BLAST E Value	Top Hit Acession Na	Top Hit Database Source	Top Hit Descriptor
88	13783	26803	3.26	3.4E-02	4E-02 AK024424.1	NT	Homo sapiens mRNA for FLJ00013 protein, partial cds
1078	14242		2.57	3.4E-02	.4E-02 AW 274020.1	EST_HUMAN	xv26d07.x1 Sogres_NFL_T_GBC_S1 Homo septens cDNA ctone IMAGE:2814253 3' similar to SW:C211_HUMAN P53801 PUTATIVE SURFACE GLYCOPROTEIN C210RF1 PRECURSOR;
1233	14392			3.4E-02	11346459 NT	NT	Homo sapiens hypothetical protein FLJ13220 (FLJ13220), mRNA
2465		28717	1.7	3.4E-02	4E-02 T57160.1	EST HUMAN	yo20e06.r1 Stratagene lung (#937210) Homo sepiens cDNA cione IMAGE:81250 5' similar to contains MER29 repetitive element
3517	Ľ			1	3.2	Z	Homo sapiens chromosome 21 segment HS21C008
3875		30032	ľ	ြ		EST HUMAN	RC3-FN0155-060700-011-d10 FN0155 Homo saplens cDNA
4030	l			3.4E-02	.4E-02 AW 794952.1	EST HUMAN	RC6-UM0015-210200-021-A10 UM0015 Homo sapiens cDNA
4720	1		2.77	3.4E-02	.4E-02 X59799.1	NT	M.musculus S-antigen gene promoter region
5172	_		1.9	6	.4E-02 Q26457	SWISSPROT	LA PROTEIN HOMOLOG (LA RIBONUCLEOPROTEIN) (LA AUTOANTIGEN FIUMULUS)
5189	L	31277	1.81	ຶ	.4E-02 AJ012469.1	LN	Ceenorhebditis elegans mRNA for DYS-1 protein, partial
6983	L		4.68	3.4E-02	.4E-02 U24393.1	TN	Human Iysyl oxidase-like protein gene, exon 3
8456				<u>۾</u>	.4E-02 AI869629.1	EST_HUMAN	wiggd04.x1 NCI_CGAP_Bm25 Homo sapiens cDNA clone iMAGE:2433031 3
	1					-	nu70f08.s1 NCI_CGAP_Aiv1 Homo sapiens cDNA clone IMAGE:1216071 similar to contains Au repetitive
8947	22026	35567	1.18	<u>ო</u>	.4E-02 AA664886.1	EST_HUMAN	element contains element MER25 MER25 repetitive element;
	i						zq04f11.s1 Stratagene muscle 937209 Homo sapiens cDNA done IMAGE:628749 3' similar to
							TR.G1017425 G1017425 PRISONEI BRATT SEDANDI KATMBENTEITAENI TINI KESATADAGRYEITAANSSGTTKAFINIVALDRPG
2	22407		5 28		4E-02 AA194306.1	EST HUMAN	PPT GPVVISDITEESVTLKWEPPKYDGGSQVTNYILLKRETSTAVWTEVSATVARTMMKVMKL;
2 68	ı		0.66		3.4E-02 A1092719.1	EST_HUMAN	ozsch08.x1 Scares_parathyroid_tumor_NbHPA Homo sapiens cDNA clone IMAGE:1683519 31
S	L		8.9	L	3.3E-02 AA398735.1	EST_HUMAN	zi75e08.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:728198 3
1193	┸		2	్	.3E-02 AB035867.1	FN	Gricetulus griseus CYP2A17 mRNA for cytochrome P450 2A17, complete cds
1669	上	27904		ြိ	.3E-02 AF110763.1	NT	Homo sapiens skeletal muscle LIM-protein 1 (FHL1) gene, complete cds
1778	L	L	L	.,	1.3E-02 AE000700.1	NT	Aquifex aeolicus section 32 of 109 of the complete genome
2149	15285		2.02		1.3E-02 R09112.1	EST_HUMAN	yr25c09.r1 Soares fetal liver spieen 1NFLS Homo sepiens cDNA clone IMAGE:12/868 3
3445	1	29631			3.3E-02 H02389.1	EST_HUMAN	y35h02.rt Soares placenta Nb2HP Homo sapiens cDNA cione IMAGE:150771 5
4293	1		3.74		3.3E-02 AF110763.1	TN	Homo sapiens skeletal muscle LIM-protein 1 (FHL1) gene, complete cds
4589	1	30709		<u> </u>	EV 55862 NT	TN	Mus musculus tumor rejection antigen gp96 (Traf), mRNA
9290	L				3.3E-02 BF245995.1	EST_HUMAN	601853910F1 NIH_MGC_57 Hono sapiens cDNA clone IMAGE: 40/3/8/ 5
6560	L				3.3E-02 BF245995.1	EST_HUMAN	601853910F1 NIH_MGC_57 Homo saplens cDNA clone IMAGE:4073787 5
7677	L				3.3E-02 AF124162.1	NT	Nicotiana plumbaginifolia molybdopterin synthase sulphurhase (Grixo) gene, partial cus
9523	L.		0.74		3.3E-02 BF115621.1	EST_HUMAN	7m92d04x1 NCI_CGAP_Bm23 Homo saplens cLINA cione IMAGE::3362423 3
9523	L				3.3E-02 BF115621.1	EST_HUMAN	7m92d04.x1 NCI_CGAP_Bm23 Homo saplens cDNA clone IMAGE:3502423 3

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Top Hit Descriptor	L. LIANTEL II II I ANDREAS TO THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF T	ad08f09.s1 Scares_NbHFB Homo sapiens cDNA clone IMAGE:877673 3' similar to gb:X/0944_cds1 MYOBLAST CELL SURFACE ANTIGEN 24.1D5 (HUMAN);	ad08f09.s1 Sogres_NbHFB Homo saplens cDNA clone IMAGE:877673 3' similar to gb:X70944_cds1 MYOBLAST CELL SURFACE ANTIGEN 24.1D5 (HUMAN);	602247171F1 NIH_MGC_62 Homo sapiens cDNA clone IMAGE:4332497 5'	ye49f11.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:121101 5	Mus musculus EIF4H gene, partial cds, LIMK1 gene, complete cds; and ELN gene, partial cds	Human Interleukin 11 (IL11) gene, complete mKNA	Oryctolagus cunicuius gene encoding ileal sodium-dependent pile acid transporter	Drosophila melanogaster heat shock protein 68 (hspos) gene, history allele, comprete cus	Drosophila melanogaster heat shock protein es (nspos) gene, insposo allele, complete cus	Homo sapiens telomerase reverse transcriptase ( IEK I ) gene, exons 7-10 and complete cus	LARGE TEGUMENT PROTEIN	Oryctolagus cuniculus gene encoding ileal sodium-dependent bile acid transporter	601442431F1 NIH_MCC_65 Homo sapiens cDNA clone IMAGE:3845/2/ 5	Homo saplens chromosome 21 segment HS21C003	H.saplens RP3 gene (XLRP gene 3)	Saxifraga nidifica maturase (maik) gene, chloroplast gene encoding chloroplast protein, partial cds	IL3-CT0219-271099-022-C04 CT0219 Homo sepiens cDNA	S.griseocameum whiG-Stv gene	S.griseocameum whiG-Siv gene	Ratipolyomavirus left junction in cell line W98.14	yd33h12.s1 Soares fetal liver spleen 1NFLS Homo sapiens CDNA clone IMAGE:11006/ 3 Similar to contains. Alu repetitive element;contains LTR1 repetitive element;	Saguinus oedipus tissue kalilifrein gene, complete cds	Homo sapiens cytochrome P450, subfamily IIB (phenobarbital-Inducible) (CYP2B), mKNA	Mus musculus kinesIn family member 3c (Kif3c), mRNA	Homo sapiens chromosome 3 subtelomeric region	qm17b04.x1 NCi_CGAP_Lu5 Homo saptens cDNA clore IMAGE:1882063 3'	qm17b04.x1 NCI_CGAP_Lu5 Homo saplens cDNA clone IMAGE:1882063 3	zg54b12.s1 Soares_pineal_gland_N3HPG Homo sapiens cDNA clone IMAGE:397151 3' similar to gb:L08441 CYTOCHROME C OXIDASE POLYPEPTIDE III (HUMAN);	Macaca mulatta chemokine receptor CCR5 mRNA, complete cds
Top Hit Database Source		EST_HUMAN	EST HUMAN	П		NT	NT	NT NT	L	NT	NT	SWISSPROT	NT	EST HUMAN	LN	LN	TN	EST_HUMAN	ΝŢ	LN L	NT	EST HUMAN	LN.	Ŋ	N	N	EST HUMAN	EST HUMAN	EST HUMAN	NT
Top Hit Acession No.		3.3E-02 AA488202.1	3E-02 AA488202 1	3.3E-02 BF691107.1	T96545.1	4F289665.1	VI81890.1	4,1002005.1	3.2E-02 AF096275.1	AF096275.1	AF128894.1	P28955	AJ002005.1	BE867353.1	AL163203.2	3.2E-02 X94768.1	3.2E-02 AF114182.1	2E-02 AW850159.1	.2E-02 X68709.1	.2E-02 X68709.1	2E-02 M32437.1	2E-02 T89367.1	2E-02 AF173845.1	11424049 NT		2E-02 AF109718.1	2E-02 AI278971.1	2E-02 A 278971.1	. 2E-02 AA719795.1	3.2E-02 U96762.1
교 국 국 교	Value	3.3E-02	3.3F-02	3.3E-02	3.3E-02	3.3E-02	3.3E-02	3.2E-02	3.2E-02	3.2E-02	3.2E-02	3.2E-02	3.2E-02	3.2E-02	3.2E-02	3.2E-02	3.2E-02	3.2E-02	3.2E-02	3.	8	3.2E-02	3.2E-02	9		"		3		
Expression Signal		0.67	75.0	3.28	3.1	1.6	1.85	1.79	6.32	6.32	1.08	1.09	0.87	13.21	0.94	16.42	3.85	0.93	1.49	1.49	2.4	30.91			8.04					
ORF SEQ ID NO:		36248	36240	38104				26394	27370	27371	28054		26394				31005						33290				36065			37207
SEQ ID	 j	22679	22670	24444	25303	25379	25398	13360	14314	14314	14961	15322	1	<u> </u>	<u> </u>	L	1	١.	L		19812	l	1	1	1_	1	1	22500	1	23601
Probe SEQ ID	į	9624	59	11383	12428	12557	12591	134	1150	1150	1812	2187	2902	3204	3806	4334	4890	5310	5652	5652	6653	REFE	6743	2020	8008	2 2	90426	672	10363	10566

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Top Hit Descriptor	Homo sepiens dual specificity phosphatase 4 (DUSP4) mRNA	NEURONAL ACETYLCHOLINE RECEPTOR PROTEIN, ALPHA-3 CHAIN PRECURSUK (GF-ALPHA-3)	Mus musculus adaptor-related protein complex AP-3, delta subunit (Ap3d), mRNA	Human leukernia inhibitory factor receptor (LIFR) gene, promoter and partial exon 1	2581a06.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:703858 5	602066783F1 NIH_MGC_57 Hamo saplens cDNA clone IMAGE:4065789 5	AV695098 GKC Homo saplens cDNA clone GKCAVH09 5	601658879R1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3886291 3	wm57d09x1 NCI_CGAP_Ut2 Homo saplens cDNA clone IMAGE:2440049 3	Enterococcus faecalls surface protein precursor, gene, complete cds	Pityokteines minutus cytochrome œidese I gene, partial cds; mitochondrial gene for mitochondrial product	zr65h03.r1 Scares_testis_NHT Homo septens cDNA clone IMAGE:727253 5'	Pseudomonas fluorescens family II aminotransferase gene, complete cds	QV2-ST0296-150200-040-e09 ST0296 Hamo sapiens cDNA	EST74530 Pineal gland II Homo sapiens cDNA 5' end	Homo sapiens neuropiiin 2 (NRP2) gene, complete cds, alternatively spliced	Homo sapiens neuropilin 2 (NRP2) gene, complete cds, alternatively spliced	Homo saplens mRNA for KIAA1573 protein, partial cds	za39a10.r1 Scares fetal liver spieen 1NFLS Homo sapiens cDNA done IMAGE:294808 5' similar to contains element TAR1 repotitive element;	2a39a10.r1 Soares fetal liver spleen 1NFLS Homo sepiens cDNA clone IMAGE:294906 5' similar to contains	element TAR1 repetitive element;	Cyprinus carplo mRNA for Inducible nitric oxide synthase (INOS gene)	601512206F1 NIH_MGC_71 Homo saplens cDNA clone IMAGE:3913848 b	601512206F1 NIH_MGC_71 Home septems cDNA clone IMAGE:3913848 5	Homo sapiens nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 (NFKB1) gene, complete	loas	חסווים משוופונים ומסופים ומסופים ומסופים ומסופים ביות המשווים מסופים מסופים ביות מסופים ביות מסופים ביות מסופים ביות מסופים ביות מסופים ביות מסופים ביות מסופים ביות מסופים ביות מסופים ביות מסופים ביות מסופים ביות מסופים ביות מסופים ביות מסופים ביות מסופים ביות מסופים ביות מסופים ביות מסופים ביות מסופים ביות מסופים ביות מסופים ביות מסופים ביות מסופים ביות מסופים ביות מסופים ביות מסופים ביות מסופים ביות מסופים ביות מסופים ביות מסופים ביות מסופים ביות מסופים ביות מסופים ביות מסופים ביות מסופים ביות מסופים ביות מסופים ביות מסופים ביות מסופים ביות מסופים ביות מסופים ביות מסופים ביות מסופים ביות מסופים ביות מסופים ביות מסופים ביות מסופים ביות מסופים ביות מסופים ביות מסופים ביות מסופים ביות מסופים ביות מסופים ביות מסופים ביות מסופים ביות מסופים ביות מסופים ביות מסופים ביות מסופים ביות מסופים ביות מסופים ביות מסופים ביות מסופים ביות מסופים ביות מסופים ביות מסופים ביות מסופים ביות מסופים ביות מסופים ביות מסופים ביות מסופים ביות מסופים ביות מסופים ביות מסופים ביות מסופים ביות מסופים ביות מסופים ביות מסופים ביות מסופים ביות מסופים ביות מסופים ביות מסופים ביות מסופים ביות מסופים ביות מסופים ביות מסופים ביות מסופים ביות מסופים ביות מסופים ביות מסופים ביות מסופים ביות מסופים ביות מסופים ביות מסופים ביות מסופים ביות מסופים ביות מסופים ביות מסופים ביות מסופים ביות מסופים ביות מסופים ביות מסופים ביות מסופים ביות מסופים ביות מסופים ביות מסופים ביות מסופים ביות מסופים ביות מסופים ביות מסופים ביות מסופים ביות מסופים ביות מסופים ביות מסופים ביות מסופים ביות מסופים ביות מסופים ביות מסופים ביות מסופים ביות מסופים ביות מסופים ביות מסופים ביות מסופים ביות מסופים ביות מסופים ביות מסופים ביות מסופים ביות מסופים ביות מסופים ביות מסופים ביות מסופים ביות מסופים ביות מסופים ביות מסופים ביות מסופים ביות מסופים ביות מסופים ביות ביות מסופים ביות מסופים ביות מסופים ביות מסופים ביות מסופים ביות מסופים ביות מסופים ביות מסופים ביות מסופים ביות מסופים ביות מסופים ביות מסופים ביות מסופים ביות מסופים ביות מסופים ביות מסופים ביות מסופים ביות מסופים ביות מסופים ביות מסופים ביות מסופים ביות מסופים ביות מסופים ביות מסופים ביות מסופים ביות מסופים ביות מסופ	Himan distroblings	Transmission by April 1900 83 Home capiene c'UNA clene IMAGE 4296654 5	60/2104364F1 Nith_MCC_35 Floring septietts CDNA clone IMAGE:3545647 5	11 FITTON I MINI MINI TO AN ENTRY MANN Series ANA	1L5-H   0704-290600-108-504 H   0704 H amb septens alive
Top Hit Database Source	NT	SWISSPROT	LN.	ΝΤ	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	LN.	·	EST_HUMAN	LΝ	EST_HUMAN	EST_HUMAN	TN	TN	LN	FST HUMAN		EST_HUMAN	ΝΤ	EST_HUMAN	EST_HUMAN	ļ	z	LN.		I LOL	EST HUMAN	EST HUMAN	EST_HUMAN
Top Hit Acession No.	4503416 NT	P18845	6871564 NT	178104.1	3.1E-02 AA278478.1	3.1E-02 BF687742.1	3.1E-02 AV696098.1	3.1E-02 BE965092.2	3.1E-02 AI872302.1	3.1E-02 AF034779.1	3.0E-02 AF187125.1	3.0E-02 AA402242.1	3.0E-02 AF247644.1	3.0E-02 AW820223.1	3.0E-02 AA364003.1	3.0E-02 AF281074.1	3.0E-02 AF281074.1	3.0E-02 AB046793.1	3 OE-02 N99615 1		3.0E-02 N99615.1	3.0E-02 AJ242906.1	3.0E-02 BE889948.1	3.0E-02 BE889948.1		3.0E-02 AF213884.1	1 700 AE343004 4	9.0E-02 At 213004.1	M80524.1	3.0E-02 BF679706.1	3.0E-02 BE512670.1	3.0E-02 BF353889.1
Most Similar (Top) Hit BLAST E Value	3.1E-02	3.1E-02	3.1E-02	3.1E-02 U78104.1	3.1E-02	3.1E-02	3.1E-02	3.1E-02	3.1E-02	3.1E-02	3.0E-02	3.0E-02	3.0E-02	3.0E-02	3.0E-02	3.0E-02	3.0E-02	3.0E-02	3 DE-02		3.0E-02	3.0E-02	3.0E-02	3.0E-02		3.0E-02	000	9.0E-02	3.05-02		1	
Expression Signal	1.92	1.46	1.28	1.29	2.6	77.0	0.58	0.48	0.46	2.67	2.41	1.08	2.82	0.93	46.0	8.17	8.17	3.21	78.0		0.67	2.87	2.9	2.9		1.92		28.1	1.22			0.74
ORF SEQ ID NO:		27559	28184	31449		32259		35784		36864		28888				31250			32040		32911	33677		Ì.		33497			33921			35459
Exon SEQ ID NO:	14445	14490	15083	18580	18675	18956	21204	122221	22415	23272	14805		16904	L		18286	I	18706			19553		L	20100	1	20083		-1	┙	- 1	- 1	21921
Probe SEQ ID NO:	1289	1333	1940	5378	5476	5764	8122	9142	9339	10237	1652	2852	3743	3839	4058	5164	5164	5507	7000	3	6384	6929	7047	7047		7218		/218	7380	8317	8821	8842

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Top Hit Descriptor	Omithorhynchus anatinus coagulation factor X mRNA, complete cds	Thermotoga maritima section 109 of 136 of the complete genome	HSAAADTHS TEST1, Human adult Testis tissue Homo sapiens cDNA clone cam test244 (b)	Human coagulation factor VII (F7) gene exon 1 and factor X (F10) gene, exon 1	ne87f04.s1 NCI_CGAP_Kid1 Homo sapiens cDNA clone IMAGE:911263	yh63d04.s1 Soares placenta Nb2HP Homo saplens cDNA clone IMAGE:134407 3	QV4-NN0038-270400-187-h05 NN0038 Homo sapiens cDNA	Rattus norvegicus UDP-Caligiucosylceramide beta-1,4-galactosyltransferase mRNA, complete cds	Sheep gene for ultra high-sulphur keratin protein	yu07e10.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE::233130 5	Sus scrofa deoxynibonuclease II mRNA, complete cds	601452661F1 NIH_MGC_66 Homo sepiens cDNA clane IMAGE:3856598 5	601140729F1 NIH_MGC_9 Homo saplens cDNA clone IMAGE:3049830 5	HUMNK262 Human epidermal kerathocyte Homo sapiens cDNA clone 262	Buchnera aphidicola natural-host Schlechtendalla chinensis gluconate-8-phosphate dehydrogenase (gnd)	gene, partial cds	Buchnera aphidicola natural-host Schlechtendalla chinensis gluconate-6-phosphate dehydrogenase (gnd) nene, partial cds	CM3-PT0014-071299-051-c04 PT0014 Homo sapiens cDNA	CM3-PT0014-071299-051-c04 PT0014 Homo saplens cDNA	EST388706 MAGE resequences, MAGN Homo sepiens cDNA	Aeropyrum pernix genomic DNA, section 7/7	Sheep gene for ultra high-sulphur keratin protein	AU135817 PLACE1 Homo sepiens cDNA done PLACE1002362 5'	EST382234 MAGE resequences, MAGK Homo sapiens cDNA	Homo saplens retinal fascin (FSCN2) gene, expn 2	Homo sapiens ratinal fascin (FSCN2) gene, exon 2	Rattus norvegicus microtubule associated protein tau (Mapt), mRNA	601594078F1 NIH_MGC_9 Homo sapiens cDNA done IMAGE:3948067 5	yd21b08.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:108855 5	Craterostigma plantagineum mRNA for homeodomain leucine zipper protein (hb-1)	zs95c06,r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:711466 5	Cavia porcellus inwardly-rectifying potassium channel Kir2.1 (KCNJ2) gene, complete cas
Top Hit Database Source	NT	LΝ	EST_HUMAN	L	EST_HUMAN	EST_HUMAN	EST_HUMAN	LΝ	⊥N	EST_HUMAN	뒫	EST_HUMAN	EST_HUMAN	EST HUMAN		LN⊤	FN	EST HUMAN	EST HUMAN	EST HUMAN	LN	۲N	EST_HUMAN	EST_HUMAN	ΤN	눌	ΙN	EST_HUMAN	EST_HUMAN	ΤN	EST_HUMAN	LN
Top Hit Acession No.	3.0E-02 AF275654.1				1.1	3.0E-02 R32019.1	3.0E-02 AW895565.1	3.0E-02 AF048687.1	X55294.1	2.9E-02 H72805.1	2.9E-02 AF060221.1	2.9E-02 BF032233.1	2.9E-02 BE271437.1	2.9E-02 D29214.1		2.9E-02 AF129279.1	2 05 02 1 5120270 1	2 0F-02 AWR75979 1	2 9F-02 AW875979.1	2 9E-02 AW976597.1	2.9E-02 AP000064.1	2.9E-02 X55294.1	2.9E-02 AU135817.1	2.8E-02 AW970153.1	2.8E-02 AF066063.1	2.8E-02 AF066063.1	8393751 NT	2.8E-02 BE741083.1	2.8E-02 T78960.1	2.8E-02 AJ005820.1	2.8E-02 AA280762.1	2.8E-02 AF187872.1
Most Similar (Top) Hit BLAST E Value	3.0E-02	3.0E-02	3.0E-02	3.0E-02	3.0E-02	3.0E-02	3.0E-02	3,0E-02	2.9E-02 X55294.1	2.9E-02	2.9E-02	2.9E-02	2.9E-02			2.9E-02	2000	2.9E-02	2 BE-02				١								L	
Expression Signal	1.93	2.03	0.47	2.26	7.11	1.95	11.62	4.97	6.0	0.81	1.39	6.58	9.95	0.65		0.82	6	2 44	2 14	0.65	1.25			0.76		1.2	ľ		1.08		0.75	1.41
ORF SEQ ID NO:		37319	37425	38243		31556			29826		32712	32055	33943	_		34793		Cavas			37196					29840		31866	L	L	35840	
Exon SEQ ID NO:	22072	23711	23803	24566	24974	26168	25621	26161		l	19364	1	ı			21269		20717	32800	L	1	L		L			L	1		L.	1	22483
Probe SEQ ID NO:	8993	10677	10770	11508	11989	12536	12943	12989	3650	4039	6188	6421	7398	7584		8187		8167	2020	10078	10553	11303	12538	579	3453	3453	4430	5095	6948	8523	9219	9409

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Top Hit Descriptor	Archaeoglobus fulgidus section 15 of 172 of the complete genome	T.thermophila calcium-binding 25 kDa (TCBP 25) protein gene, complete cds	T.thermophila calcium-binding 25 kDa (TCBP 25) protein gane, complete cds	Human germline T-cell receptor beta chain Dopamine-beta-hydroxylase-like, TRY1, TRY2, TRY3,	TORBV27S1P, TORBV22S1A2N1T, TORBV9S1A1T, TORBV7S1A1N2T, TORBV5S1A1T, TORBV13S3,	IGRBV6S7P, TGRBV7S3AZ1, IGRBV13S2A11, IGRBV9S2AZP1, IGRBV7SZA1N41,	TCRBV13S9/13S>				Т	y/33d09.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:128657 5' similar to SP.JC2284 JC2284 TISSUE FACTOR PATHWAY INHIBITOR - RHESUS;	Т	A.bisporus pgkA gene	<ul> <li>ot96h03.s1 Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:1624661 3'</li> </ul>		1	transmembrane secretory component Intman, leukocytes, Genomic, 337 m, segment 4 of 11]	┑			Mus musculus histidine rich calcium binding protein (Hrc), mRNA	Mus musculus histidine rich calcium binding protein (Hrc), mRNA	Mus musculus MHC class III region RD gene, partial cds, Bf, C2, G9A, NG22, G9, HSP70, HSP70, HSC704,	and smRNP genes, complete cds, G7A gene, partial cds; and unknown genes	Chicken dorsalin-1 mRNA, complete cds	Deinococcus radiodurans R1 section 151 of 229 of the complete chromosome 1	xa52b04 x1 NCI_CGAP_Sar4 Homo sepiens cDNA clone IMAGE:2570383 3' similar to SW:Y069_HUMAN		Arabidopsis thaliana DNA chromosome 4, contig fragment No. 63			
Top Hit Database Source	Ę	L	TN			!	LN.	۲	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST HUMAN	LZ	LN LN	EST_HUMAN	HOU HOU	בין ופואטו	Z	LN	EST_HUMAN	EST HUMAN	NT	ΙN		TN	노	NT		EST_HUMAN	LN	EST_HUMAN	EST_HUMAN	FN
Top Hit Acession No.	2.8E-02 AE001092.1	J05109.1	105109.1				2.7E-02 U66059.1	2.7E-02 AL161494.2	2.7E-02 N47258.1	2.7E-02 N47258.1	2.7E-02 BF245672.1	2 7E-02 R12245 1	2.7E-02 X61670.1	2.7E-02 X97580.1	2.7E-02 AA993571.1	A DOOR FOL	4.7E-02 AIST 1030.1	2.7E-02 \$43442.1	2.6E-02 AL163282.2	2.6E-02 AW 850515.1	2.6E-02 AA490021.1	6754241 NT	6754241 NT		2.6E-02 AF109906.1	2.6E-02 L12032.1	2.6E-02 AE002014.1		2.6E-02 AW241154.1	2.6E-02 AL161563.2	2.6E-02 Al206030.1	2.6E-02 BE621748.1	2.6E-02 Z99064.1
Most Similar (Top) Hit BLAST E Value	2.8E-02	2.8E-02 J05109.1	2.8E-02 J05109.1				2.7E-02	2.7E-02	2.7E-02	2.7E-02	2.7E-02	2 75-02	2.7E-02	2.7E-02	2.7E-02	Ļ	4.1E-02	2.7E-02	2.6E-02	2.6E-02	2.6E-02	2.6E-02	2.6E-02		2.6E-02	2.6E-02	2.6E-02		2.6E-02	2.6E-02	2.6E-02	2.6E-02	2.6E-02
Expression Signal	0.76	0.47	0.47				96.0	1.99	1.93	1.93	9.0	1 43	8	1.02	1.92	90	05.1	0.55	2.52	0.99	2.6	4.45	4.45		2.07	3.89	1.22		2.54	2.94	6.85	2	0.83
ORF SEQ ID NO:	36144	36207	l				27753	28682	30447	30448	31432	21703			33491			35434	26796		28694	28696				31131	1		31283			33083	
SEQ ID	22578		l				- 1	16684	17462	17462	18565	18755	19205	19890	1		21030	- 1	13776	14563	15567	15569	15569		16158	18154		1	18324	19195		١.	
Probe SEQ ID NO:	9513	9674	9674				1518	3518	4319	4319	5362	5557	8022	6734	7213	3	808	8816	585	1399	2439	2441	2441		2982	5025	5176		5203	6011	6349	6555	9969

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Top Hit Descriptor	Vaccinia virus ORF1L, strain Wyeth	Raitus norvegicus Nerve growth factor receptor, fest (Ngfr), mRNA	ALANYL-TRNA SYNTHETASE (ALANINETRNA LIGASE) (ALARS)	ak22704,s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1406719 3'	Homo sapiens KIAA1070 protein (KIAA1070), mRNA	Saccharomyces dairenensis NRRL Y-12639(T) ATP synthase subunit 9 (ATP9) gene, mitochondrial gene percodian mitochondrial protein complete cds	Saccharomyces dairenensis NRRL Y-12639(T) ATP synthase subunit 9 (ATP9) gene, mitochondrial gene	encoding mitochondrial protein, complete cds	Homo sapiens chromosome 21 segment HS21C103	zs84c02.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:704162 5	UI-HF-BN0-akj-e-10-0-UI.r1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3077466 5	602015501F1 NCI_CGAP_Brn64 Homo sapiens cDNA clone IMAGE:4150944 5	Homo sapiens hypothetical protein FLJ10724 (FLJ10724), mRNA	yc86f07.s1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:22845 3' shrilar to contains DBR	repetitive element;	on 26f06.y5 NCI_CGAP_Lu5 Homo saplens cDNA clone IMAGE:155/82/ 5	on26f08.y5 NCI_CGAP_Lu5 Hamo sapiens cDNA clone IMAGE:1557827 5	601680305R2 NIH_MGC_83 Homo sapiens cDNA done IMAGE:3950665 3'	601680305R2 NIH_MGC_83 Hamo sepiens cDNA clone IMAGE:3950665 3	Raffus norvegicus rabphilin-3A mRNA, complete cds	H.carterae mRNA for fucoxanthin chlorophyll a/c binding protein, Fcp1	H.carterae mRNA for fucoxanthin chlorophyll a/c binding protein, Fcp1	PM2-NN0128-080700-001-a12 NN0128 Homo sapiens cDNA	PM2-NN0128-080700-001-412 NN0128 Homo sapiens cDNA	H36h08.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2934015 3	2x83c10.x5 Soares ovary tumor NbHOT Homo sapiens cDNA clone IMAGE:810354 3	7e30e09x1 NCI_CGAP_Lu24 Hamo sapiens cDNA clone IMAGE:3284008 3' similar to contains L1.t1 L1	repetitive element;	601579393F1 NIH_MGC_9 Homo sepiens cDNA clone IMAGE:3928054 5	Chlamydomonas reinhardtii VSP-3 mRNA, complete cds	602070562F1 NCI_CGAP_Bm64 Homo sapiens cDNA clone IMAGE:4213406 5	602070552F1 NCI_CGAP_Bm64 Homo sapiens cDNA clone IMAGE:4213406 5	Chlamydomonas reinhardti class II DNA photolyase (PHK2) gene, complete cds
Top Hit Database Source	Z		SWISSPROT	T_HUMAN		Ŀ		LN	NT	EST_HUMAN	EST_HUMAN	EST_HUMAN	LN LN		EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	۲	LN L	L L	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN		EST_HUMAN	EST HUMAN	NT	EST HUMAN	EST_HUMAN	N.
Top Hit Acession No.	799064.1	6981271 NT	221894	2.6E-02 AA860946.1	11432020 NT	0 00 00 00 00 00	1.20%	2.6E-02 AF114952.1	2.6E-02 AL163303.2	2.6E-02 AA279351.1	2.6E-02 AW 500547.1	2.6E-02 BF343827.1	11422936 NT		2.6E-02 R43678.1	2.5E-02 AI793130.1	2.5E-02 AI793130.1	2.5E-02 BE974314.1	2.5E-02 BE974314.1	2.5E-02 U12571.1	2.5E-02 X99697.1	2.5E-02 X99697.1	2.5E-02 BE701165.1	2.5E-02 BE701165.1	2.5E-02 AW592114.1	2.5E-02 AI732776.1		2.5E-02 BE670128.1	2.5E-02 BE746888.1	2.5E-02 L29029.1	2.5E-02 BF526722.1	2.5E-02 BF526722.1	2.5E-02 AF129458.1
Most Similar (Top) Hit BLAST E Value	2.6E-02 Z99064.1	2.6E-02	2.6E-02 P21894	2.6E-02	2.6E-02	LO CO	Z.OE-702/	2.6E-02	2.6E-02	2.6E-02	2.6E-02	2.6E-02	2.6E-02		2.6E-02	2.5E-02	2.5E-02	2.5E-02	2.5E-02	2.5E-02	2.5E-02	2.5E-02	2.5E-02	2.5E-02							Ĺ		
Expression Signal	0.83	5.63	0.65	0.73	1.24	9	0	0.78	5.37	1.59	1.35	1.43	1.32		1.39	1.75	1.75	9.54		2.53			0.92	0.92		0.72		4.88	3.72	9.0	1.72	1.72	
ORF SEQ ID NO:	33620				l		+cos		37257		38547					26762				l	29219		_		l.	32327				32994	34400		Ш
Exon SEQ ID NO:	20194	8	20526	21783	22702		COSTZ	22955	ı	1	24849	ı	1		25658	13738	L			L	L	L	ı	1		L		19494	L	1	I_	L	
Probe SEQ ID NO:	9969	7050	7449	B703	9560		CLES .	9915	10614	11670	11861	12480	12583		12947	545	545	832	892	2821	3021	3021	4156	4156	4322	5830		6322	6338	6466	7843	7843	8008

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Top Hit Descriptor	801108291F1 NIH MGC_16 Hamo sapiens cDNA clone IMAGE:334278 5'	OHORDIN PRECURSOR (OKGANIZEK-SPECIFIC SECURIC SECURIOS CALIFORNIZETA)	wu08c10.x1 NCI_CGAP_GC8 Hamo sapiens cDNA clone IMAGE: 2519370 3	Dradicum 28S ribosomal RNA, D2 domain	qb22a08.x1 Soeres_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:1090962 3	HYPOTHETICAL 46.7 KD PROTEIN C19G10.05 IN CHROMOSOME I	HYPOTHETICAL 46.7 KD PROTEIN C19G10.05 IN CHKOMOSUME I	Mus musculus major histocompatibility locus class II region: major histocompatibility proten class ii aipria chah (IAalpha) and major histocompatibility protein class II beta chain ('Ebeta) genes, complete ods;	butyrophilin-like (NG9), butyrophilin-li>	Homo sapiens gene for LECT2, complete cds	Homo sapiens similar to ALEX3 protein (H. sapiens) (LOCoso344), mKNA	Homo sapiens mitogen-activated protein kinase kinase kinase (War on 13), minus	Dictyostelium discoideum putative protein kinase MkcA (mkcA) gene, comprete cos	601652365R2 NIH_MGC_82 Hamp sapiens cDNA clone IMAGE:3936513 3	tc72c07.x1 Soares_NhHMPu_S1 Home sapiens cDNA clone IMAGE:20/0130 3	yr/5f1 f.r1 Scares fetal liver spicen Tinne, and in Saprens course some liver Spicen (H-2K(B))	H-2 CLASS I HIS I OCCUMPATIBILITY ANTIGEN, KIR AI DHA CHAIN PRECURSOR (H-2K(B))	H-2 CLASS   HIS LOCATIVE IDILITY AND A CONTROL OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE 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KC3-510186-230300-0184100 5101001100100 separate security	Human retrotransposon 5 tong terminal repress	yu12c05.s1 Scares fetal liver spieen 1\rightarrows sapiens count durie introduced of commentations and preparative element;	za35g11.s1 Soares fetal liver spleen 1NFLS Home saplens cDNA clone IMAGE:294596 3' similar to	gbjK02909jK415K7K Kat (rKNA),contains Abr. 51 Abr. 51 Abr. 51 Abr. 51 Abr. 51 Abr. 51 Abr. 51 Abr. 51 Abr. 51 Abr. 51 Abr. 51 Abr. 51 Abr. 51 Abr. 51 Abr. 51 Abr. 51 Abr. 51 Abr. 51 Abr. 51 Abr. 51 Abr. 51 Abr. 51 Abr. 51 Abr. 51 Abr. 51 Abr. 51 Abr. 51 Abr. 51 Abr. 51 Abr. 51 Abr. 51 Abr. 51 Abr. 51 Abr. 51 Abr. 51 Abr. 51 Abr. 51 Abr. 51 Abr. 51 Abr. 51 Abr. 51 Abr. 51 Abr. 51 Abr. 51 Abr. 51 Abr. 51 Abr. 51 Abr. 51 Abr. 51 Abr. 51 Abr. 51 Abr. 51 Abr. 51 Abr. 51 Abr. 51 Abr. 51 Abr. 51 Abr. 51 Abr. 51 Abr. 51 Abr. 51 Abr. 51 Abr. 51 Abr. 51 Abr. 51 Abr. 51 Abr. 51 Abr. 51 Abr. 51 Abr. 51 Abr. 51 Abr. 51 Abr. 51 Abr. 51 Abr. 51 Abr. 51 Abr. 51 Abr. 51 Abr. 51 Abr. 51 Abr. 51 Abr. 51 Abr. 51 Abr. 51 Abr. 51 Abr. 51 Abr. 51 Abr. 51 Abr. 51 Abr. 51 Abr. 51 Abr. 51 Abr. 51 Abr. 51 Abr. 51 Abr. 51 Abr. 51 Abr. 51 Abr. 51 Abr. 51 Abr. 51 Abr. 51 Abr. 51 Abr. 51 Abr. 51 Abr. 51 Abr. 51 Abr. 51 Abr. 51 Abr. 51 Abr. 51 Abr. 51 Abr. 51 Abr. 51 Abr. 51 Abr. 51 Abr. 51 Abr. 51 Abr. 51 Abr. 51 Abr. 51 Abr. 51 Abr. 51 Abr. 51 Abr. 51 Abr. 51 Abr. 51 Abr. 51 Abr. 51 Abr. 51 Abr. 51 Abr. 51 Abr. 51 Abr. 51 Abr. 51 Abr. 51 Abr. 51 Abr. 51 Abr. 51 Abr. 51 Abr. 51 Abr. 51 Abr. 51 Abr. 51 Abr. 51 Abr. 51 Abr. 51 Abr. 51 Abr. 51 Abr. 51 Abr. 51 Abr. 51 Abr. 51 Abr. 51 Abr. 51 Abr. 51 Abr. 51 Abr. 51 Abr. 51 Abr. 51 Abr. 51 Abr. 51 Abr. 51 Abr. 51 Abr. 51 Abr. 51 Abr. 51 Abr. 51 Abr. 51 Abr. 51 Abr. 51 Abr. 51 Abr. 51 Abr. 51 Abr. 51 Abr. 51 Abr. 51 Abr. 51 Abr. 51 Abr. 51 Abr. 51 Abr. 51 Abr. 51 Abr. 51 Abr. 51 Abr. 51 Abr. 51 Abr. 51 Abr. 51 Abr. 51 Abr. 51 Abr. 51 Abr. 51 Abr. 51 Abr. 51 Abr. 51 Abr. 51 Abr. 51 Abr. 51 Abr. 51 Abr. 51 Abr. 51 Abr. 51 Abr. 51 Abr. 51 Abr. 51 Abr. 51 Abr. 51 Abr. 51 Abr. 51 Abr. 51 Abr. 51 Abr. 51 Abr. 51 Abr. 51 Abr. 51 Abr. 51 Abr. 51 Abr. 51 Abr. 51 Abr. 51 Abr. 51 Abr. 51 Abr. 51 Abr. 51 Abr. 51 Abr. 51 Abr. 51 Abr. 51 Abr. 51 Abr. 51 Abr. 51 Abr. 51 Abr. 51 Abr. 51 Abr. 51 Abr. 51 Abr. 51 Abr. 51 Abr. 51 Abr. 51 Abr. 51 Abr. 51 Abr. 51 Abr. 51 Abr. 51 Abr. 51 Abr. 51 Abr. 51 Abr. 51 Abr. 51	Borrella buigaorien (section 11 di 70) di de Comprete Serionio	2191008 s1 Soares_lests. NH I nome septens cours out environment of the septent of the septent of the septent of the septent of the septent of the septent of the septent of the septent of the septent of the septent of the septent of the septent of the septent of the septent of the septent of the septent of the septent of the septent of the septent of the septent of the septent of the septent of the septent of the septent of the septent of the septent of the septent of the septent of the septent of the septent of the septent of the septent of the septent of the septent of the septent of the septent of the septent of the septent of the septent of the septent of the septent of the septent of the septent of the septent of the septent of the septent of the septent of the septent of the septent of the septent of the septent of the septent of the septent of the septent of the septent of the septent of the septent of the septent of the septent of the septent of the septent of the septent of the septent of the septent of the septent of the septent of the septent of the septent of the septent of the septent of the septent of the septent of the septent of the septent of the septent of the septent of the septent of the septent of the septent of the septent of the septent of the septent of the septent of the septent of the septent of the septent of the septent of the septent of the septent of the septent of the septent of the septent of the septent of the septent of the septent of the septent of the septent of the septent of the septent of the septent of the septent of the septent of the septent of the septent of the septent of the septent of the septent of the septent of the septent of the septent of the septent of the septent of the septent of the septent of the septent of the septent of the septent of the septent of the septent of the septent of the septent of the septent of the septent of the septent of the septent of the septent of the septent of the septent of the septent of the septent of the septent of the septent o	XTR repetitive element ;
Top Hit Database Source	EST_HUMAN	SWISSPROT	EST_HUMAN	F	EST_HUMAN	SWISSPROT	SWISSPROT		NT	NT.	NT	TN	FN	EST_HUMAN	EST_HUMAN	EST_HUMAN	SWISSPROT	SWISSPROT	LZ.	EST HUMAN	EST_HUMAN	Į.	Z	EST_HUMAN	Į	EST HUMAN		EST HUMAN	LN L		EST_HUMAN
Top Hit Acessian No.	2.5E-02 BE252469.1		l				Π			П	11420078 NT	11433220 NT	Γ		2.4E-02 Al378582.1	165884.1	201901	201801	105110.1	W86680.1	Z20573.1	-	١	7.1	4E-02 M16780.1	4E-02 H78376 1		.4E-02 N69442.1	.4E-02 AE001125.1		2.4E-02 AA625660.1
Most Similar (Top) Hit BLAST E Value	2.5E-02	2.5E-02 C	2.5E-02	2.5E-02	2.5E-02/	2.5E-02 (	2.5€-02		2.5E-02	2.5E-02	2.5E-02	2.5E-02	2.5E-02	2.5E-02	2.4E-02	2.4E-02	2.4E-02	2.4E-02	2.4E-02	2.4E-02	2.4E-02	2,4E-02	2.4E-02	2.4E-02	2.4E-02	0.45.02		7	2		
Expression Signal	0.5	0.92	0.57	0.63	0.65	171	1.71		2.93	1.87	2.17	52.1	8.	1.58	44.1	8.	1.38	1.38	1.69	0.86	1.2	1.11	1.11	0.75	0.57	0.67	0.0	11.69	0.78		0.81
ORF SEQ ID NO:	34768	35845	35785		37466	١	37760							32032	Ĺ			28364		32871	33912		33929					35344	32806		35831
Exon SEQ ID NO:	21249	22104	22242	22.20	23843	1		1	24192	25046	26072	1	1.	25497	┸	l	l	16054	١.	19514	20449		20464	1	ł	1	21/16	21808	1		22289
Probe SEQ ID NO:	8167	9025	9464	10274	10840	9 6	11048	2	11120	12065	12410	12821	12716	12750	178	1628	2102	2102	4488	8344	7370	7386	7386	8074	8129		8636	8728	9187		9211

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Probe SEQ ID NO:	Exan SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
9893	22933	36516	0.55	2.4E-02		NT	Arabidopsis thaliana motybdopterin synthase sulphurylase (cnx5) gene, complete cds
9893			0.55	2.4E-02	2.4E-02 AF124160.1	NT	Arabidopsis thallana molybdopterin synthase sulphurylase (cnxb) gene, complete cds
1001	L			2.4E-02	2.4E-02 AV692954.1	EST_HUMAN	AV692954 GKC Homo sapiens cDNA clone GKCDSC03 6
80,00	<u>i</u>		282	2.4E-02		EST HUMAN	nh07b12.s1 NCI_CGAP_Titv/I Homo sapiens cDNA clone IMAGE:943583 similar to contains Alu repetitive element; contains dement PTR5 repetitive element;
10839	$\perp$					EST HUMAN	601274962F1 NIH_MGC_20 Hamo saplens cDNA clone IMAGE:3615902 5
11874	24862	38557	2.45		2.4E-02 AF109905.1	. TN	Mus musculus major histocompatibility locus class III regions Hsc70t gene, partial ods; smRNP, G7A, NG23, MutS homolog, CLCP, NG24, NG25, and NG28 genes, complete cds; and unknown genes
11874	l	38658	2.45		2.4E-02 AF109905.1	NT	Mus musculus major histocompatibility locus class III regions Hsc70t gene, partial cds; smRNP, G7A, NG23, MutS homolog, CLCP, NG24, NG25, and NG26 genes, complete cds; and unknown genes
12210	1				TN 60627909	TN	Bacteriophage bIL97, complete genome
12362	١	32116	4.45	2.4E-02		TN	Mus musculus DinB homolog 1 (E. coli) (Dinb1), mRNA
12478	<u> </u>	Ì	1.38		2.4E-02 U78167.1	LΝ	Rattus norvegicus cAMP-regulated guanine nucleotide exchange factor I (cAMP-GEFI) mRNA, complete cds
12478	25330	32096	1.38		2.4E-02 U78167.1	TN	Rettus norvegicus cAMP-regulated guantne nucleotide exchange factor I (cAMP-GEFI) mRNA, complete cds
12668	25445		10.87		2.4E-02 AB008569.1	ΗN	Caenorhabditis elegans mRNA tor iron-sulfur subunit of mitochortatial succinate uen yu ogenase, comprese ods
12697	L		1.28		2.4E-02 N42980.1	EST_HUMAN	lyy08a06.r1 Soares melanocyte 2NbHM Homo sapiens cDNA clone IMAGE:2/0610 5
12883	L	31858		L	2.4E-02 AA179693.1	EST HUMAN	zp13h01.r1 Stratagene fetal retina 937202 Homo saplens cDNA clone IMAGE:009301 3
1921	L		6.25		2.3E-02 W05340.1	EST HUMAN	Za84g08.r1 Soares fetal lung NbHL19W Homo sapiens CUNA cione Invider. 259259-5
1936			16.26		2.3E-02 U94165.1	LN.	4 Homo sapiens mammaly tumor-associated protein intro (artic) and the sapient of the sapient of the sapient of the sapient of the sapient of the sapient of the sapient of the sapient of the sapient of the sapient of the sapient of the sapient of the sapient of the sapient of the sapient of the sapient of the sapient of the sapient of the sapient of the sapient of the sapient of the sapient of the sapient of the sapient of the sapient of the sapient of the sapient of the sapient of the sapient of the sapient of the sapient of the sapient of the sapient of the sapient of the sapient of the sapient of the sapient of the sapient of the sapient of the sapient of the sapient of the sapient of the sapient of the sapient of the sapient of the sapient of the sapient of the sapient of the sapient of the sapient of the sapient of the sapient of the sapient of the sapient of the sapient of the sapient of the sapient of the sapient of the sapient of the sapient of the sapient of the sapient of the sapient of the sapient of the sapient of the sapient of the sapient of the sapient of the sapient of the sapient of the sapient of the sapient of the sapient of the sapient of the sapient of the sapient of the sapient of the sapient of the sapient of the sapient of the sapient of the sapient of the sapient of the sapient of the sapient of the sapient of the sapient of the sapient of the sapient of the sapient of the sapient of the sapient of the sapient of the sapient of the sapient of the sapient of the sapient of the sapient of the sapient of the sapient of the sapient of the sapient of the sapient of the sapient of the sapient of the sapient of the sapient of the sapient of the sapient of the sapient of the sapient of the sapient of the sapient of the sapient of the sapient of the sapient of the sapient of the sapient of the sapient of the sapient of the sapient of the sapient of the sapient of the sapient of the sapient of the sapient of the sapient of the sapient of the sapient of the sapient of the sapient of the sapient of
2065					2.3E-02 AW 797355.1	EST HUMAN	CMZ-UMUU39-Z8U40U-17 Z-D I TUNO028 TUITO september VIII
2426	ı				2.3E-02/2/4293.1	NAME OF THE PERSON	HSAAACADH P Human foetal Brain Whole tissue Homo saplens cDNA
3773	16934	78840	7.02		2.3E-02 (2037).1		Canis beta-galactosides-binding lectin (LGALS3) mRNA, 3'end
4267	L	30398		L	2.3E-02 L24799.1	TN	Gallus gallus connexin 46.8 (Cx45.6) gene, complete cds
4267	┸				2.3E-02 L24799.1	NT	Gallus gallus connexin 45.6 (Cx45.6) gene, complete cds
4540	上	L		L	2.3E-02 AW899107.1	EST_HUMAN	CM4-NN0080-290400-160-b04 NN0080 Homo sapiens cDNA
4571	L				2.3E-02 BE935225.1	EST HUMAN	CM3-MT0/18-0/0900-318-g07 MT0/18 Homo sapiens cDNA
4571	١	ן ו		Н	2.3E-02 BE935225.1	EST HUMAN	CM2-MT0118-010900-318-g07 M10118 Homo espiens cDNA
4572	18469	9 30691	1.2		2.3E-02 AW593693.1	EST_HUMAN	XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX

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Top Hit Descriptor	xs25d08.x1 NCI_CGAP_Ut2 Homo sapiens cDNA done IMAGE:2770671 3'	601672279F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3955386 5	601872279F1 NIH_MGC_20 Homo sepiens cDNA clone IMAGE:3955386 51	RC2-CN0051-290100-011-407 CN0051 Homo saplens cDNA	Rattus norvegicus guanine nucleotide binding protein gamma subunit 11 mRNA, complete cds	Raitus norvegicus guanine nucleotide binding protein gamma subunit 11 mRNA, complete cds	Caulobacter crescentus topolsomerase IV ParE subunit (parE) gene, complete cds, and propionyl-CoA carboxylase beta chain (pccB) homolog gene, partial cds	601822921R1 NIH_MGC_77 Homo sapiens cDNA clone (MAGE:40428293'	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 17	MR0-HT0080-011099-002-c09 HT0080 Homo saplens cDNA	Horno sapiens chromosome 21 segment HS21C103	Human plectin (PLEC:) gene, exons 3-32, and complete cds	Homo sapiens PDX1 gene for lipoyl-containing component X exons 1-11	Homo sapiens PDX1 gene for lipoyl-containing component X, exons 1-11	wa76h10.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2302147 3'	wa76h10.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2302147 3	HYPOTHETICAL 55.6 KD PROTEIN B0280.5 IN CHROMOSOME III PRECURSOR	CHROMOSOME ASSEMBLY PROTEIN XCAP-C	Escherichia coli K-12 MG1635 section 89 of 400 of the complete genome	Escherichia coli K-12 MG1655 section 89 of 400 of the complete genome	GLUCOAMYLASE S1/S2 PRECURSOR (GLUCAN 1,4-ALPHA-GLUCOSIDASE) (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE)	601179958F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3546567 5	602043629F1 NCI_CGAP_Brn67 Homo saplens cDNA clone IMAGE:4181454 5'	602043629F1 NCI_CGAP_Brn67 Homo sapiens cDNA clone IMAGE:41814545'	Streptomyces sp. alpha-1,3/4-fucosidase precursor gene, complete cds	Dictyostelium discoideum extracellular signal-regulated protein kinase (ERK1) mRNA, complete cds	Columba livia nucleoside diphosphate kinase (NDPK) gene, nuclear gene encoding mitochondrial protein,	complete ods	Homo sapiens chromodomain helicase DNA binding protein 2 (CHU2) mKNA	MYOSIN LIGHT CHAIN KINASE, SKELETAL MUSCLE (MLCK)	MYOSIN LIGHT CHAIN KINASE, SKELETAL MUSCLE (MLCK)
Top Hit Database Source	EST_HUMAN		EST_HUMAN	LHUMAN		NT	LN.	EST_HUMAN	LN	T HUMAN	TN	TN	LN				П	ISSPROT	NT	NT	SWISSPROT	EST_HUMAN	EST_HUMAN	EST_HUMAN	NT	TN		NT	ΝŢ	SWISSPROT	SWISSPROT
Top Hit Acessian No.	2.3E-02 AW593693.1	2.3E-02 BF026487.1	2.3E-02 BF026487.1	2.3E-02 AW844307.1	2.3E-02 AF257110.1	2.3E-02 AF257110.1	2.3E-02 U86303.1	2.3E-02 BF106464.1	2.3E-02 AL161505.2	2.3E-02 BE141475.1	2.3E-02 AL163303.2	2.3E-02 U63610.1	2.3E-02 AJ298105.1	2.3E-02 AJ298105.1	2.3E-02 AI685380.1	2.3E-02 AI685380.1	P41996	P50532	2.3E-02 AE000199.1	2.3E-02 AE000199.1	P08640	2,3E-02 BE278331.1	2.3E-02 BF528462.1	2.3E-02 BF528462.1	2.3E-02 U39394.1	2.3E-02 U11077.1		2.2E-02 AF018267.1	4557448 NT	P07313	P07313
Most Similar (Top) Hit BLAST E Value	2.3E-02	2.3E-02	2.3E-02	2.3E-02	2.3E-02	2.3E-02	2.3E-02	2.3E-02	2.3E-02	2.3E-02	2.3E-02	2.3E-02	2.3E-02	2.3E-02	2.3E-02	2.3E-02	2.3E-02 P41996	2.3E-02 P50532	2.3E-02	2.3E-02	2.3E-02 P08640	2.3E-02									2.2E-02 P07313
Expression Signal	1.2	3.01	3.01	6.0	0.62	0.62	3.86	0.62	4	69.0	.0.63	4.52	1.12	1.12	0.75	0.75	0.84	76.0	1.4	1.44	2.38	3.61	1.78	1.78	2.47	1.88		3.59	1.79	2,94	
ORF SEQ ID NO:	30692	l	30836				31707		33306						35509	L				36863	37739			İ	31974			26982			
Exon SEQ ID NO:	18469	17852	17852		1	1	18690	19535	19911		١.	21143		ı	21973	21973	1	23101	l_		l	1_	_	L	25604		ı	13937	14935	14949	14949
Probe SEQ ID NO:	4572	4717	4717	5144	5265	5265	5491	6365	6755	7119	7619	8060	8667	8667	8894	8894	9338	10063	10236	10236	11022	12338	12801	12801	12919	12975		756	1786	1800	1800

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Top Hit Descriptor	S.pneumoniae pcpA gene and open reading frames	nn24e04.s1 NCI_CGAP_Gas1 Homo sapiens cDNA clone IMAGE:1084782 3'	Infectious bursal disease virus segment B strain IL4 VP1 gene, complete ods	PM0-BT0340-170100-004-b03 BT0340 Homo saplens cDNA	S.cerevisiae chromosome IV reading frame ORF YDL245c	S.cerevisiae chromosome XVI reading frame ORF YPL241c	AV699721 GKB Homo sapiens cDNA clone GKBAND03 3	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 27	Arabidopsis thallana DNA chromosome 4, contig fragment No. 27	P.vulgata alpha tub 2 mRNA	Mus musculus partial FBPase 2 gene for Fructose-1,6-bisphosphalase, exon 5 and intron 5	Mus musculus partial FBPase 2 gene for Fructose-1,6-bisphosphatase, exon 5 and intron 5	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes,	complete cds)	Mus musculus Sjogren syndrome antigen A1 (Ssa1), mRNA	ne47h07.s1 NCI_CGAP_Cc3 Hamo sapiens cDNA clone IMAGE:900541 3' similar to contains Alu repetitive	element	AV761502 MDS Homo sapiens cDNA clone MDSADG01 5'	Dictyostellum discoideum histidine kinase C (dhkC) mRNA, complete cds	Bacilius subtilis cotKLM cluster, CotK (cotK), CotL (cotL), and spore coat protein CottM (cottM) genes,	complete cas	Mus musculus macrophage mgradon Inhibitory (Air.) gene, o iranning region and partial cos	Mus musculus macrophage migration inhibition/ factor (MIF) gene, 5 tranking region and partial cos	KERATIN, HIGH-SULFUR MATRIX PROTEIN, B2A	KERATIN, HIGH-SULFUR MATRIX PROTEIN, B2A	KERATIN, HIGH-SULFUR MATRIX PROTEIN, B2A	Tegula aureotincta major acrosomal protein precursor (TMAP) mRNA, complete cds	PM2-BT0546-120100-001-f11 BT0546 Homo sapiens cDNA	PM2-BT0548-120100-001-f11 BT0546 Homo sapiens cDNA	yx43h07.r1 Soares melanocyte 2NbHM Homo sapiens cDNA clone IMAGE:264541 5	2x63b09.r1 Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:796121 5	S.cerevisiae chromosome IV reading frame OKH YDL245c
Top Hit Database Source	FN	EST_HUMAN		EST_HUMAN	IN	IN	EST_HUMAN	NT	NT		IN	F	TN		NT	INT			T_HUMAN	NT		L	LN	NT	SWISSPROT	SWISSPROT	SWISSPROT	N N	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	LN.
Top Hit Acession No.	282001.1	2.2E-02 AA577785.1	AF083094.1	4W601317.1	274293.1	273597.1	AV699721.1	AL161515.2	AL161515,2	X79468.1	AJ243025.1	AJ243025,1	2E-02 AB026898.1		2E-02 AB026898.1	6678140 NT		2.2E-02 AA503553.1	AV761502.1	AF029726.1		U72073.1	AF204395.1	AF204395.1	P02438	P02438	P02438	AF190899.1	1E-02 BE072546.1	1E-02 BE072546.1	N29266.1	2.1E-02 AA461271.1	274293.1
Most Similar (Top) Hit BLAST E Value	2.2E-02	2.2E-02	2.2E-02	2.2E-02	2.2E-02	2.2E-02	2.2E-02	2.2E-02	2.2E-02	2.2E-02	2.2E-02	2.2E-02	2.2E-02		2.2E-02	2.2E-02		2.2E-02	2.1E-02	2.1E-02		2.1E-02	2.1E-02	2.1E-02	2.1E-02	2.1E-02	2.1E-02	2.1E-02	2.1E-02	2.1E-02	2.1E-02	2.1E-02	2.1E-02
Expression Signal	2.17	2.03	4.09	0.98	0.99	1.37	3.43	1.41	1.41	0.82	0.45	0.46	2.73		2.73	125		6.8	4.48	6.62		6.65	1.31	1.31	76.0	0.97					3.12		0.68
ORF SEQ ID NO:	28329			30116	30195	31262	33941		35189					L	36512								27644	27645	L		L	28264			L		5 30384
Exon SEQ ID NO:	15212	L	16897		17185	18299	20474	L	21647	1	L			1	22928	L	1	25421	<u> </u>	L		14448	14571	14571		1	L	L	1		L	1 1	17395
Probe SEQ ID NO:	2072	3521	3736	3956	4029	5177	7396	8566	8566	6006	9856	9856	8888		9888	10409		12625	432	482		1292	1418	1418	1823	1823	1823	2019	2092	2092	2877	3674	4249

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Top Hit Descriptor		602015306F1 NCI_CGAP_Brn64 Homo sapiens cDNA clone IMAGE:4151161 5'	Borrelia burgdorferi plasmid cp32-2, erpC and erpD genes, complete cds; and unknown genes	wg81d11.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2371509.3'	A. thaliana mitochondrial genome, part A	ag55g12.s1 Gessler Wilms tumor Homo sapiens cDNA clone IMAGE:1126918 3'	wh54a05,x1 NCI_CGAP_Kid11 Hamo saplens cDNA clone IMAGE:2384528 3'	601671411F1 NIH_MGC_20 Hano sapiens cDNA clone IMAGE:3954410 6	CM4-HT0244-111199-040-h05 HT0244 Homo sapiens cDNA	QV3-GN0058-120900-329-a12 GN0058 Homo sapiens cDNA	Mus musculus scriing nexin 1 (Snx1), mRNA	am83e07.s1 Stratagene schizo brain S11 Homo saplens cDNA done IMAGE:1629732 3' stmilar to contains Alu repetitive element;contains e/ement MER11 repetitive element ;	Homo sapiens partial 5-HT4 receptor gene, exons 2 to 5	Hama sapiens partial 5-HT4 receptor gene, exons 2 to 5	Streptococcus pneumoniae integrase, excisionase, repressor protein, relaxase, UmuC MucB homolog, and	UmuD MucA homolog genes, complete cds; and unknown genes	атк89e07.s1 Stratagene schizzo brain S11 Homo sapiens cDNA clone IMAGE:1629732 3' similar to contains. Alu repetitive element;contains element MER11 repetitive element ;	Bacillus halodurans genomic DNA, section 13/14	Mus musculus heat shock protein, 74 kDa, A (Hspa9a), mRNA	RC4-CN0050-130200-012-h04_1 CN0050 Homo saplens cDNA	Homo sapiens putative psihHbA pseudogene for hair keratin, exons 2 to 7	Human germline UBE1L gene similar to the gene for ubiquitin-activating enzyme, exons 1-22	Azospirilum brasilense major outer membrane protein OmaA precursor (omaA) gene, complete cds	7g51c08.x1 NCI_CGAP_Pr28 Homo saplens cDNA clone IMAGE:3309998 3' similar to contains MER1.t3	MER1 repetitive element;	QV4-NN0038-270400-187-h05 NN0038 Homo saplens cDNA	Mus musculus DinB homolog 1 (E. coli) (Dinb1), mRNA	aa15510.r1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:813307 5	Mus muscutus DinB hamalog 1 (E. coli) (Dinb1), mRNA	Homo sapiens genomic region containing hypervariable minkatellites chromosome 1[1p36.33] of Homo sepiens	Homo saciens hypothetical protein FLJ10379 (FLJ10379), mRNA	
Top Hit Database	Source	EST_HUMAN		EST_HUMAN				EST_HUMAN (		EST_HUMAN		EST HUMAN		NT.		- LN	EST HUMAN	Γ		T_HUMAN	TN	NT	TN		П	T_HUMAN		EST_HUMAN	ΝΤ	ĽN	TN	
Top Hit Acessian	ž	2.1E-02 BF343656.1		2.1E-02 AI768127.1		7.1		2.1E-02 BF026405.1	2.1E-02 AW379529.1	2.1E-02 BF086199.1	9790238 NT	2.1E-02 AA984288.1	2.1E-02 AJ243213.1	2.1E-02 AJ243213.1		2.1E-02 L29324.1	21F-02 AA984288.1	AD004540 4	2.1E-02 AF 00 13 13.1	2.1E-02 AW844320.1	2.1E-02 Y19213.1	2.1E-02 L34170.1	2.1E-02 AF183913.1		2.0E-02 BF002932.1	AW8955	6753635 NT	2.0E-02 AA456538.1	6753635 NT	2.0E-02 AL096805.1	TIM POSCOOR	
Most Similar (Top) Hit	Value	2.1E-02	2.1E-02 U44914.1	2.1E-02/	2.1E-02 Y08501.1	2.1E-02	2.1E-02	2.1E-02	2.1E-02	2.1E-02	2.1E-02	2.1E-02	2.1E-02	2.1E-02			ļ	241	2.1E-02	2.1E-02		2.1E-02		i_	i		2.0E-02		2.0E-02		١	2.05-02
Expression	3,500	0.89	2.14	1.64	5.95	0.75	0.89	16:0	9.0	0.73	99.0	0.54	2.49	2.49		1.15	0.75	9	1.48	1.42	11.16	1.22	3.82	]   	1.28	14.95	5.03	2,95				
ORFSEQ		30549					l	31402					١	36454		36820			38474		L	31862	31938		26257		26518		27054			27448
Exen SEQ ID	Ö	17567	17705	17714	17964	L	L	1					1	1		23226		1	23888		1	1	25712	L	13257			13622	L		ı	14386
Probe SEQ ID	ö	4427	4667	4577	4831	4852	4940	5315	5756	7212	8716	0703	9831	9831		10189	10.266	0700	10855	12063	12602	12647	13091		19	8	269	88	821	111		1226

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Top Hit Descriptor	Homo sapiens hypothetical protein FLJ10379 (FLJ10379), mRNA	Homo sapiens hypothetical protein FLJ10486 (FLJ10486), mRNA	Homo sapiens hypothetical protein FLJ10486 (FLJ10486), mRNA	Arabidopsis thaliana DNA chromosome 4, contig fregment No. 32	7g51c08.x1 NCI_CGAP_Pr28 Homo sapiens cDNA clone IMAGE:33099998 3' similar to contains MEX1.t3 MFB1 repositive element :	Mile misculus sems domain, transmembrane domain (TM), and cytoplasmic domain, (semaphorin) 6B	(Semabb) mRNA	Arabidopsis thaliana C2H2 zinc finger protein FZF mRNA, complete cds	P. vulgaris hydraxyproline-rich glycaprotein (HRGP) mRNA, 3' end	qi83e03.xf NCI_CGAP_Kid3 Home sapiens cunna done invade: 1600u70 3	Dictyostellum discoldeum class VII unconventiona myosin (myol) gene, comprae cus	Pyrococcus harkashii OT3 genamic DNA, 777001-994000 nt position (4/7)	Pyrococcus harikashii OT3 genomic DNA, 777001-994000 nt position (4/7)	Japanese encephalitis virus envelope protein mRNA, partial cds	wa17b02.x1 NCI_CGAP_Kid11 Homo sapiens cUNA clone liwa GE. 22363 ip 3	Mycobacterium tuberculosis H37Kv complete genome, segment 93/102	Equus cabalius DNA for 17alpha-hydroxylase17,20-ryase, complete cos	Homo sapiens ankyrin 3, node of Ranvier (ankyrin G) (ANK3), transcript variant 1, miniv	Homo sapiens ankyrin 3, node of Ranvier (ankyrin G) (ANK3), transcript variant 1, mr. N.A.	aa15510.r1 Soares NhHMIPu S1 Homo sapiens curva cione invareno 13307 3	Arabidopsis thaliana UNA chromosome 4, contig itaginent no. 32	yd04c09.r1 Spares infant brain 1NIB Homo sapiens dury conto infanto confant 1 1111	nf19a07.s1 NC_CGAP_Pr1 Home saptens cUINA Gone IMAGE: 914.130 similia to contains E E. repetitive element :	Home saplens chromosome 21 segment HS21C103	Homo sapiens chromosome 21 segment HS21C103	nwo4f05.s1 NCI CGAP SS1 Homo sapiens cDNA clone IMAGE:1238337 3'	AVIGABRES OF C. Homo seriens of NA clone GLOBLH07 3	Avotovo Curo roma separa oznako osnako postako karantaria karantaria da karantaria karantaria da karantaria karantaria karantaria karantaria karantaria karantaria karantaria karantaria karantaria karantaria karantaria karantaria karantaria karantaria karantaria karantaria karantaria karantaria karantaria karantaria karantaria karantaria karantaria karantaria karantaria karantaria karantaria karantaria karantaria karantaria karantaria karantaria karantaria karantaria karantaria karantaria karantaria karantaria karantaria karantaria karantaria karantaria karantaria karantaria karantaria karantaria karantaria karantaria karantaria karantaria karantaria karantaria karantaria karantaria karantaria karantaria karantaria karantaria karantaria karantaria karantaria karantaria karantaria karantaria karantaria karantaria karantaria karantaria karantaria karantaria karantaria karantaria karantaria karantaria karantaria karantaria karantaria karantaria karantaria karantaria karantaria karantaria karantaria karantaria karantaria karantaria karantaria karantaria karantaria karantaria karantaria karantaria karantaria karantaria karantaria karantaria karantaria karantaria karantaria karantaria karantaria karantaria karantaria karantaria karantaria karantaria karantaria karantaria karantaria karantaria karantaria karantaria karantaria karantaria karantaria karantaria karantaria karantaria karantaria karantaria karantaria karantaria karantaria karantaria karantaria karantaria karantaria karantaria karantaria karantaria karantaria karantaria karantaria karantaria karantaria karantaria karantaria karantaria karantaria karantaria karantaria karantaria karantaria karantaria karantaria karantaria karantaria karantaria karantaria karantaria karantaria karantaria karantaria karantaria karantaria karantaria karantaria karantaria karantaria karantaria karantaria karantaria karantaria karantaria karantaria karantaria karantaria karantaria karantaria karantaria karantaria karantaria karantaria karantaria karantaria karantaria karantaria ka	Undifficilly Billiouise Indiana Benis or systemic or promise or promise INACE - 284331 3	VZZ8b0Z.51 Soares mulippe sciences. 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Joseph 37 cimilar to contains All repetitive	qn04c07.x1 NC_CGAP_Lib Hamo septens culva cone livrace. Iosr 200 5 surina la comana radio pagas element;
Top Hit. Database Source				١	November 1	בסו בוסומשוא	Į.	NT	NT	EST_HUMAN	ΝΤ	LN	TN	TN	EST_HUMAN	N	TN	TN	TN	EST HUMAN	LN	EST HUMAN	MAN HIMAN	LN	FZ -	EST HIMAN	TOT TOT	ESI HUMAN	NT.	EST_HUMAN	EST_HUMAN	EST_HUMAN
Top Hit Acesson No.	R922391 NT	8922453 NT	8922453 NT	2.0E-02 AL161532.2		2.0E-02 BF002832.1	7305474 NT	2.0E-02 AF095588.1	20E-02 M18095.1	2.0E-02 AI271995.1	2.0E-02 L35321.2	2.0E-02 AP000004.1	2.0E-02 AP000004.1	2.0E-02 U70408.1	2.0E-02 AI640342.1	2.0E-02 Z73966.1	2.0E-02 D88184.1	10947055 NT	10947055 NT	2.0E-02 AA456538.1	2.0E-02 AL161532.2	2.0E-02 T80037.1	4 OF 00 AAE70784 4	1.9E-02 A012/04:1	4 OE 02 A1 463203 2	4 OF 02 A A 2430E8 4	1,0000.1	1.9E-02 AV648669.1	1.9E-02 AB033611.1	1.9E-02 N52250.1	1.9E-02 BE738088.1	1.9E-02 Al301183.1
Most Similar (Top) Hit BLAST E Value	2.0E-02	20E-02	2.0E-02	2.0E-02	1	Z.0E-0Z	2.0E-02	2.0E-02	20E-02	2.0E-02	2.0E-02	2.0E-02	2.0E-02	2.0E-02	2.0E-02	2.0E-02	2.0E-02	2.0E-02	2.0E-02	2.0E-02	2.0E-02	2.0E-02				1		ا				
Expression Signal	0.91	28.	\$	2.09		1.56	1.13	1.99	1.57	0.74	0.59	0.95	0.95	2.39	1.84	1.65	1.9r	2.04	2.04	1.8	2.26	5.63	9	2.42 4 95	201	100.4			0.72	1.12	8.1	0.83
ORF SEQ ID NO:	27449		l			26257			30267		32520	34275		١.	37210			L	L	L				20929	1	1		29217	2	_		3 29971
Exen SEQ ID NO:	14386	15065	15065	15973		13257	16387	16473	17267	18341	19201	20787	20787	23119	23605	1	١_	L	L	_	L	25771	<u> </u>	ᆚ	/6761			16194	16505	16860	16954	16968
Probe SEQ ID NO:	1226	1022	1922	28.50	3	3148	3243	3289	4113	5219	8018	7723	77.23	10081	10570	10879	11653	11978	11978	12149	12644	13186		711	ŝ	2087	2970	3018	3332	389	3793	3808

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Top Hit Descriptor	Mycoplasma Imitans VIhA1 precursor (vhA1) and VIhA2 precursor (vihA2) genes, partial cds	HOMEOTIC BICOID PROTEIN (PRD-4)	HOMEOTIC BICOID PROTEIN (PRD-4)	iyed04.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sepiens cDNA clone IMAGE:2144551 3' similar to	Officialis And Telegraphy equations,	Arabdopsis thallana UNA chromosome 4, contiguration to the	Mus musculus T cell receptor gamma locus, 1 CR gamma 1 and gamma 3 gane crusters	Meleagris gallopavo paraoxonase-2 (PON2) mRNA, complete cds	Drosophila kanekoi gene for glycerol-3-phosphate denydrogenase, complete cos	Homo sapiens interferon-gamma receptor alpha chain gene, exon 1	Homo sapiens interferon-gamma receptor alpha chain gene, exon 1	Neisseria meningitidis serogroup A strain Z2491 complete genome; segment 3//	601896130F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4125462 5	Nicctiana tabacum type II phytochrome (phyB) gene, complete cds	601852385F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4076253 5	Synechocystis sp. PCC6803 complete gename, 20/27, 2539000-2644/94	Vibrio cholerae V86 phage putative replication protein gene, complete cds	Hirudo medicinalis intermediate filament gilarin mRNA, complete cds	Candida albicans lambda Ca3/B fragment	hn52co6.x1 NCI_CGAP_Co17 Homo sapiens cDNA clone IMAGE:3027274 3' similar to contains element	MEXASSET SILL 1100 TO Describe the second of the STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE	2018943.29-1 NIH MIGC 17 HOME Sapiers COINT ORDER INTO ELL'A 100000 O	H. francisci mknA tor mydin basic protein (Mbr.)	Urosophila meanogaster cytopasmic protein en compression and carlo migracian	Pseudomonas aeruginosa PAU1, section 105 of 529 of the Confidence of	te52e09.x1 Soares_NFL_T_GBC_S1 Homo sapiens CUNA cione invisue: 2050250 3	MR1-0T0011-280300-009-g04 010011 Homo septens cUNA	MR1-OT0011-280300-009-g04 OT0011 Home saplens cDNA	ak24h04.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1406935 3'	QV4-DT0021-301299-071-b11 DT0021 Homo sapiens cDNA	HYPOTHETICAL PROTEIN DJ845024.2	HYPOTHETICAL 7.9 KD PROTEIN IN FIXW S'REGION	601763268F1 NIH_MGC_20 Homo sepiens dDNA done IMAGE:4026280 5	601763268F1 NIH_MGC_20 Homo sapiens cDNA done IMAGE:4026260 5
Top Hit Database Source	П		SWISSPROT		HOMAIN			LΝ	Z,	NT	NT	IN	EST_HUMAN	님	EST_HUMAN	LN	LN	NT	LN		EST_HUMAN	EST_HUMAN	L	L L	NT	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST HUMAN	EST HUMAN	SWISSPROT	SWISSPROT	EST_HUMAN	EST HUMAN
Top Hit Acession No.	1.9E-02 AF141940.1	P09081	P09081		1.9E-02 AI452999.1	1.9E-02 AL161560.2	1.9E-02 AF037352.1	1.9E-02 L47572.1	1.9E-02 AB019507.1	1.9E-02 U19241.1	1.9E-02 U19241.1	1.9E-02 AL162754.2	1.9E-02 BF316129.1	1.9E-02 L10114.1	1.9E-02 BF695832.1	1.9E-02 D64001.1	1.9E-02 AF008938.1	1.9E-02 AF101065.1	1.9E-02 L11068.1		1.8E-02 AW771104.1	1.8E-02 BF308122.1	1.8E-02 X17664.1	1.8E-02 AF243382.1	1.8E-02 AE004544.1	1.8E-02 AI805829.1	1.8E-02 AW879122.1	1.8E-02 AW879122.1	1.8E-02 AA861446.1	1.8E-02 AW 936363.1	1.8E-02 O60810	1.8E-02 P14310	1.8E-02 BF125690.1	1.8E-02 BF125690.1
Most Similar (Top) Hit BLAST E Value	1.9E-02	1.9E-02 P09081	1.9E-02 P09081		1.9E-02	1.9E-02	1.9E-02	1.9E-02	1.9E-02	1.9E-02	1.9E-02	1.9E-02	1.9E-02	1.9E-02	1.9E-02	1.9E-02	1.9E-02	1.9E-02	1.9E-02		1.8E-02	1.8E-02	1.8E-02	1.8E-02	1.8E-02	1.8E-02	1.8E-02	1.8E-02	1.8E-02	1.8E-02	1.8E-02			1.8E-02
Expression Signal	1.3	1.58	1.58		279	4.22	96.0	1.25	0.93	1.1	1.1	1.33	121	0.67	1.24	0.67	1.91	4.41	1.46		1.67	1.81	1.43	1.38	1.74	0.94	1.09	1.09	1.01	1.52	2.02	4.44		0.61
ORF SEQ ID NO:	30305	30440	30441			28822	31609	L		33780			36169			_			L					27704	28972		30156			30669		ľ		
Exon SEQ ID NO:	17309	17453	17453	<u> </u>	17798	15701	18631	18780		l	L			1		L			1_					14621	15860	L	17150	L	L		L	<u> </u>		ı
Probe SEQ ID NO:	4158	4310	4310		4663	5125	5431	5585	5908	7250	7250	8769	9532	9914	10251	10458	11021	12372	13008		358	203	1186	1467	2743	3282	3993	3993	4197	4550	2069	6949	7624	7650

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
8322	21404	34931	0.88	1.8E-02	1.8E-02 U37091.1	NT	Mus musculus carbonic anhydrase IV gene, complete ods
8983	1		0.46	1.8E-02	1.8E-02 AW905327.1	EST_HUMAN	QVZ-NN 1073-220400-159-H09 NN 1073 Homo sapiens cDNA
8710	l		0.76	1.8E-02	6678943 NT	NT	Mus musculus microtubule-associated protein 2 (Mtap2), mRNA
9693	1		0.57	1.8E-02	1.8E-02 BF241924.1	EST HUMAN	601877025F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4105303 5
888				1.8E-02	1.8E-02 BF241924.1	EST_HUMAN	601877025F1 NIH_MGC_55 Homo septens cDNA clone IMAGE:4105303 5
0872	1		2.23	1.8E-02	1.8E-02 AA897543.1	EST HUMAN	aj62f09.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1394921 3' similar to go:L11672 ZINC FINGER PROTEIN 91 (HUMAN);
10268		36900		1.8E-02		EST_HUMAN	601463545F1 NIH_MGC_67 Homo saplens cDNA clone IMAGE:3866963 5'
10431	1		1.29	1.8E-02	1.8E-02 X96933.1	IN	L. stagnalis mRNA for myomodulin neuropeptide precursor
11721	1			1.8E-02	1.8E-02 AB002337.2	IN	Homo sapiens mRNA for KIAA0339 protein, partial cds
11721	23907	L	1.76	1.8E-02	1.8E-02 AB002337.2	NT	Horno sepiens mRNA for KIAA0339 protein, partial cds
11912	_			1.8E-02	1.8E-02 AP000006.1	NT	Pyrococcus harikoshii OT3 genamic DNA, 1166001-1485000 nt. position (6/7)
11926		l		1.8E-02	1.8E-02 U62749.1	TN	Zea mays acidic ribosomal protein P2a-3 (rpp2a-3) mRNA, partial cds
13096			1.78		1.8E-02 AF202180.1	뒫	Plasmodium falciparum enythrocyte membrane-associated giant protein antigen 332 (Ag332) gene, partial cds
800	L	27167			1.7E-02 BE394869.1	EST HUMAN	601310626F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE::3632190 6'
				<u>.</u>			hr34a03.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2833740 3' similar to contains
1831	14979	28075	2.12		1.7E-02 AW573183.1	EST HUMAN	L1.t1 L1 repetitive element;
						H	hr34a03.x1 Soares_NFL_T_GBC_S1 Hamo sapiens cuiva cione imacezess740 s sirilita in contains
1831		28076			1.7E-02 AW573183.1	ES HOMAIN	List I reposition desirent,
1920	15063		2.85	١	1.7E-02 AL163204.2	Į.	Hamo sapiens chiamesante zi sayinenti in za const
2181	15316		13.13		1.7E-02 AB004816.1	LN.	Oryctolagus cunculus mixiva for misuguriniza, curipius cus
2705	15823		1.36		7657495 NT	NT	Homo sapiens putative Kabb GDP/G IP Socienties racio nomogue (NADEZA) in vivo
3062	16238	29259	0.89		1.7E-02 AI147615.1	EST HUMAN	db22a08.X1 Soares pregnant uterus Nontro name septens convenient in Note 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and
			101		4 7E 02 MM 027289 4	NAMIN HOR	hm45a04.x1 NCI_CGAP_RUF1 Homo sapiens cUNA done IN/AGE.3013334.3 similar to currents MER19.b1 MER19 reactitive element :
3002	_1_		*O:*		004000	CWISCOBOT	HISTIDINE-RICH GLYCOPROTEIN PRECURSOR
3/16	8		60.0		67640		ac19f04.s1 Stratagene overy (#937217) Homo sapiens cDNA clone IMAGE:856927 3' similar to contains Alu
4284	17429		123		1.7E-02 AA669618.1	EST_HUMAN	repetitive element;contains element MER24 repetitive element;
4317	i		2.02		1.7E-02 R02506.1	EST HUMAN	ye86f08.r1 Scares fetal liver spleen 1NFLS Homo sapiens cDNA clane IMAGE:124647 5
4576	J	30607			1 7E-02 Al305279.1	EST HUMAN	qm08g07.x1 NCI_CGAP_Lu5 Hamo sapiens cDNA clone IMAGE:1881276 3' similar to go.X52359 ZINC FINGER PROTEIN 30 (HUMAN);
É	i i						hf34a03.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA done IMAGE:2933740 3' similar to contains
4649	9 17785	30768	1.32		1.7E-02 AW573183.1	EST_HUMAN	L1.ft L1 repetitive element;

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Top Hit Descriptor	Messenger RNA for anglerfish (Lophlus americanus) somatostatin II	ov51e02.s1 Soares_testis_NHT Homo saplens cDNA clone IMAGE:16408583	wg35f09.xt Soares_NSF_F8_SW_OT_PA_P_S1 Homo sepiens cDNA clone IMAGE:2367113 3' similar to comains Atu moetitive element:	ov85h03.xf Soares fetal liver spleen_1NFLS_S1 Homo sapiens cDNA done IMAGE:1672661 3'	Macaca fascicularis protain tyrosine phosphatase (PRL-1) mRNA, complete cds	Homo sapiens nebulin (NEB), mRNA	Human apolipoprotein (a) gene, exon 1	Human apolipoprotein (a) gene, exon 1	Homo sapiens hyperion gene, exchs 1-50	Caenorhabditis elegans cCAF1 protein gene, complete cds	DKFZp434l0314_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434l0314 5	Homo saplens serum constituent protein (MSE66), mRNA	CM4-NN1030-040400-130-f06 NN1030 Homo sapiens cDNA	oe08d04.s1 NCI_CGAP_0v2 Homo sapiens cDNA clone IMAGE:1385287 similar to contains element MSR1	repetitive element;	Mycobacterium tuberculosis H37Rv complete genome; segment 13/102	Treponema mattophilum flaB2, flaB3 and fliD genes for flagellin subunit proteins and CAP protein homologue	LIVER CARBOXYLESTERASE 22 PRECURSOR (EGASYN) (ESTERASE-22)	LIVER CARBOXYLESTERASE 22 PRECURSOR (EGASTN) (ESTERASE-22)	Homo eapiens KVLQ I 1 gene	ne81d06.s1 NCI_CGAP_Ew1 Homo sapiens cDNA clone IMAGE:91056/	Hamo sepiens mRNA for KIAA0634 protein, partial cds	II.3-CT0219-160200-063-C07 CT0219 Homo sapiens cDNA	Mus musculus major histocompatibility complex region NG27, NG28, RPS28, NADH oxdoreductase, NG29, VIEC4 Exact hadron matein RINC4 fenesin ReKDS-like, KE2 BING4, beta 1,3-dalactosyl transferase, and	RPC18 genes complete cds: Sacm21 gene, partial>	OVICE DETAILS AND AND AND ADDITIONS OF THE ADDITIONS OF THE ADDITIONS OF THE ADDITIONS OF THE ADDITIONS OF THE ADDITIONS OF THE ADDITIONS OF THE ADDITIONS OF THE ADDITIONS OF THE ADDITIONS OF THE ADDITIONS OF THE ADDITIONS OF THE ADDITIONS OF THE ADDITIONS OF THE ADDITIONS OF THE ADDITIONS OF THE ADDITIONS OF THE ADDITIONS OF THE ADDITIONS OF THE ADDITIONS OF THE ADDITIONS OF THE ADDITIONS OF THE ADDITIONS OF THE ADDITIONS OF THE ADDITIONS OF THE ADDITIONS OF THE ADDITIONS OF THE ADDITIONS OF THE ADDITIONS OF THE ADDITIONS OF THE ADDITIONS OF THE ADDITIONS OF THE ADDITIONS OF THE ADDITIONS OF THE ADDITIONS OF THE ADDITIONS OF THE ADDITIONS OF THE ADDITIONS OF THE ADDITIONS OF THE ADDITIONS OF THE ADDITIONS OF THE ADDITIONS OF THE ADDITIONS OF THE ADDITIONS OF THE ADDITIONS OF THE ADDITIONS OF THE ADDITIONS OF THE ADDITIONS OF THE ADDITIONS OF THE ADDITIONS OF THE ADDITIONS OF THE ADDITIONS OF THE ADDITIONS OF THE ADDITIONS OF THE ADDITIONS OF THE ADDITIONS OF THE ADDITIONS OF THE ADDITIONS OF THE ADDITIONS OF THE ADDITIONS OF THE ADDITIONS OF THE ADDITIONS OF THE ADDITIONS OF THE ADDITIONS OF THE ADDITIONS OF THE ADDITIONS OF THE ADDITIONS OF THE ADDITIONS OF THE ADDITIONS OF THE ADDITIONS OF THE ADDITIONS OF THE ADDITIONS OF THE ADDITIONS OF THE ADDITIONS OF THE ADDITIONS OF THE ADDITIONS OF THE ADDITIONS OF THE ADDITIONS OF THE ADDITIONS OF THE ADDITIONS OF THE ADDITIONS OF THE ADDITIONS OF THE ADDITIONS OF THE ADDITIONS OF THE ADDITIONS OF THE ADDITIONS OF THE ADDITIONS OF THE ADDITIONS OF THE ADDITIONS OF THE ADDITIONS OF THE ADDITIONS OF THE ADDITIONS OF THE ADDITIONS OF THE ADDITIONS OF THE ADDITIONS OF THE ADDITIONS OF THE ADDITIONS OF THE ADDITIONS OF THE ADDITIONS OF THE ADDITIONS OF THE ADDITIONS OF THE ADDITIONS OF THE ADDITIONS OF THE ADDITIONS OF THE ADDITIONS OF THE ADDITIONS OF THE ADDITIONS OF THE ADDITIONS OF THE ADDITIONS OF THE ADDITIONS OF THE ADDITIONS OF THE ADDITIONS OF THE ADDITIONS OF THE ADDITIONS OF THE ADDITIONS OF THE ADDITIONS OF THE ADDITIONS OF THE ADDITIONS OF THE ADDITIONS OF T	VZ-P1001Z-14010Q-030-107 P1001Z TOTAL SEQUENS COLVA	qu42b09.x1 NCI_CGAP_Lymb Home sapiens curviv cione invalcia. 1907 * 17 3	Mus musculus CD5 antigen (Cd5), mRNA	Candida albicans CaGCK3 gene, complete cds	Saccharomyces cerevisiae CAD2 gene for cadmium resistance protein, compact cas	Saccharomyces cerevisiae CAD2 gene for cadmium resistance protein, compare cus
Top Hit Databese Source	NT.	EST_HUMAN o	W NAMI II FOR	Т	Т			TN.			EST HUMAN [		EST_HUMAN C	$\overline{}$	EST_HUMAN "	$\neg$	ĽΝ		SSPROT		T HUMAN		EST_HUMAN		1		7	T_HUMAN				LN.
Top Hit Acession No.	.7E-02 V00641.1	.7E-02 AI015076.1	7 TYC02714 CO 37	1.7E-02 AIN38280 1		00716	1.7E-02 L07899.1	1.7E-02 L07899.1	1.7E-02 AJ010770.1	1.7E-02 U21854.1	1.7E-02 AL040554.1	5902007 NT	1.7E-02 AW903482.1	ļ		1.6E-02 AL021929.1	1.6E-02 Y18889.1	Q64176	Q64176	1.6E-02 AJ006345.1	1.6E-02 AA484872.1	1.6E-02 AB014534.1	1.6E-02 AW850652.1		4 00000	1.6E-02 AF110320.1	1.6E-02 AW875407.1	1.6E-02 AI281385.1	6671715 NT	1.6E-02 AB015281.1	1.6E-02 AB027571.1	1.6E-02 AB027571.1
Most Similar (Top) Hit BLAST E Value	1.7E-02	1.7E-02	7 7	1./E-02	4 75 00	1.7E-02	1.7E-02	1.7E-02	1.7E-02	1.7E-02	1.7E-02	1.7E-02	1.7E-02		1.7E-02	1.6E-02	1.6E-02	1.6E-02 Q64176	1.6E-02 Q64176	1.6E-02	1.6E-02	1.6E-02	1.6E-02									
Expression Signal	191	5.98		- 08	92.1	0	1.08	1.08	1.71	0.89	1.28	1.66	2.35		1.46	4.05	1.37	1.81	1.81	76.0	1.75	1.01	5.33		,	1.96		65.0	1.42	2.16	1.14	1.14
ORF SEQ ID NO:	30957			32773	33230			34061		34591					31928		27926						29793					31438	32234	33331		
Exen SEQ ID NO:	17969	18064		19427	П	1	20587	20587	20972	1	1	1	26111		25757	13717	14841		L	15754			16778	ı	_		17556	18570	18934	19935	20124	L
Probe SEQ ID NO:	4836	4934		6253	80/0	7252	7513	7513	7921	9636	0066	12093	12001		13166	524	1989	2323	2323	2631	2708	2758	3614			4291	4415	5367	5741	6780	707	707

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
7888	20940	34446	0.98	1.6E-02	.6E-02 AL161508.2	Ę	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 20
8312	21394	34919	0.74	_	.6E-02 AJZ77662.1	NT	Homo sapiens partial TUB gene for tubby (mouse) homolog and LMO1 gene for LIM domain only 1 protein
8372				1.6E-02		LN	Human spoC-II gene for preprospolipoprotein C-II
10246	23281		2.97	1.6E-02	.6E-02 AF079764.1	NT	Drosophia melanogaster enhancer of polycomb (E(PC)) mixink, complete cus
10833	23667	37276	1.61	1.6E-02	.6E-02 AA572818.1	EST_HUMAN	nf19g03.s.1 NCI_CGAP_Pr1 Homo sapiens cDNA done IMAGE:914260 similar to SW:1ELO_KABI1 P29294 TELOKIN. [1];
10633	<u> </u>			_		EST HUMAN	nf19g03.s.1 NCI_CGAP_Pr1 Homo sapiens cDNA cione IMAGE:914260 similar to SW:1 ELO_KABI I P29294 TELOKIN. [1]:
11149		37848	2.9	_	.6E-02 Z94828.1	NT	G.gallus microsatellite DNA (LEi0260 (=716lilE11))
11488	L		2.11			NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 20
11488	1		2.11			NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 20
11801	ı			_		EST_HUMAN	qz98e10.x1 Soares_pregnant_uterus_NbHPU Homo capiene cUNA clone IMAGE:2042442.3
12348	L	<u> </u>		Ī	.6E-02 Q64176	SWISSPROT	LIVER CARBOXYLESTERASE 22 PRECURSOR (EGASYN) (ES I EKASE-22)
12348	L				.6E-02 Q64176	SWISSPROT	LIVER CARBOXYLESTERASE 22 PRECURSOR (EGASYN) (ESTERASE-22)
770	L		9.38	1.5E-02	8923734	NT	Homo sapiens transcription factor (HSA130894), mKNA
2209	15343	28469	3.58	Ì	1.5E-02 N39521.1	EST_HUMAN	y/27b07.s1 Soares fetal liver spieen 1/NFLS Homo sapiens culna ciona livrace. 240920 3
2244	L		1.6			NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 90
3128	16304		1.04	-	.5E-02 AJ006216.1	NT	Homo sapiens CACNA1F gene, exons 1 to 48
3128	١.				1.5E-02 AJ006216.1	ΤN	Homo sapiens CACNA1F gene, exons 1 to 48
3818			1.14			EST HUMAN	MR4-TN0115-080900-201-b12 TN0115 Homo sapiens CLIVA
4590	<u> </u>		0.72	٠	25.1	ĻΝ	Homo sapiens TESTIN 2 and LESTIN 3 genes, complete cas, attentalively spilical
6423	l	32957			Q09711	SWISSPROT	HYPOTHETICAL CALCIUM-BINDING PROTEIN CT8811.04 IN CHROWING I
7472		,	1.69			IN	Cyanophora paradoxa cyanelle, complete genome
7561	١_	34108			2 11418713 NT	卜	Homo sapiens KIAA1009 protein (KIAA1009), mrvkA
8658	١.	34660			AL1633	N	Homo saplens chromosome 21 segment HSZTC10103
8065	ŀ	L		3 1.5E-02	2 11417739 NT	NT	Homo sapiens valyf-#RNA synthetase 2 (VARSZ), mRNA
9030	ı		1.42		1.5E-02 BF345554.1	EST_HUMAN	602019135F1 NCI CGAP Brn6/ Homo sapiens cluiva cione liviace: 413-304 3
8996	١.				1.5E-02 AF096774.1	NT	Homo sapiens kinase-related protein isotorm 1 mKiNA, complete cos
9770	L	36337	1.59		1.5E-02 D44606.1	Į,	Saccharomydes cerewisiae chromosome VI plasmid Cepo
10016	_		1.3	3 1.5E-0;	1.5E-02 R32667.1	EST HUMAN	WEG4510.11 Soares placefita NDZHF Home sepiens CDINA clone living CL. 1990.11
1001	١	36650	1.3	1.5E-0;		EST_HUMAN	yr64b10.r1 Soares placenta NDZHP nomo septens contra cione invo.c. 130001.2
10860		L				EST_HUMAN	yet 7(10.st Stratagene lung (#35/210) mamo sapitatis con A cione involutional
11056		3	1.78		1.5E-02 D26547.1	<u>k</u>	Kee gene for undredown it, complete cus

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_			_							_	_		_					_							_	_	_	_	-,	_	_	
	Top Hit Descriptor	Plasmodium falciparum (strain FCR3) variant-specific surface protein (var-2, var-3) genes, complete ods's	RC4-CN0048-140100-011-c11 CN0049 Horna saplens cDNA	Chlamydophila pneumoniae AR39, section 58 of 94 of the complete genome	Homo sapiens NESH protein (LOC61225), mRNA	Haemophilus influenzae Rd section 115 of 163 of the complete genome	Xenopus laevis neurogenin related 1b (X-NGNK-1b) mKNA, complete cas	Bifidobacterium longum Na+/H+ antiporter (nhaB), cytosine deaminase, and alpha-galactosidase (agil.)	genes, complete cds; and N-acetylglucosamine/xylose repressor protein (neg./xylrx) gene, partial cds	xb09d09.x1 NCI_CGAP_GU1 Home sapiens cUNA clone liMAGE_2073783.3	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 62	Arabidopsis thaliana DNA chromosome 4, contig tragment No. 62	Homo saplens coagulation factor XII (Hageman factor) (F12), mKNA	Mus musculus histocompatibility 2, complement component factor B (H2-5f), mKNA	EST374761 MAGE resequences, MAGG Homo saplens cDNA	EST374761 MAGE resequences, MAGG Homo saplens cDNA	601567403F1 NIH_MGC_21 Homo saplens cDNA clone IMAGE:3842280 5	601587403F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3842280 5	H.sapiens La/SS-B pseudogene 3	ni11c04.s1 NCI_CGAP_Br2 Homo sapiens cDNA done IMAGE:1026890 3: similar to contains Alu repeutive in communications and support to the contains and repeutive indicates the contains and repeutive indicates the contains and repeutive indicates the contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contai	PIGATOR OF INC. COAP Rro Homo saniens CDNA clone IMAGE:1029990 3' similar to contains Alu repetitive	element;	Mycobacterium fuberculosis H37Rv complete genome; segment 88/162	Candida boldinii methanol oxidase (AOD1) gene, complete cds	Homo sapiens SPP2 gene for secreted phosphoprotein 24 precursor, exons 1-8	601078239F1 NIH_MGC_12 Homo sapiens cDNA done IMAGE:3464241 5	Homo sapiens chromosome 21 segment HS21C018	Human IFNAR gene for interferon alpha/beta receptor	Arabidopsis thaliana F21J9.2 mRNA, complete cds	Home canians snarm associated entiden 7 (SPAG7), mRNA	Profito Septems Specification associated an agent ( ).  Repend to the partial cds, chloroplast gene for chloroplast	Mituali X calaci alli 1970 i Gengaloga alla Gengaloga alla Gengaloga alla Gengaloga alla Gengaloga alla Gengaloga alla Gengaloga alla Gengaloga alla Gengaloga alla Gengaloga alla Gengaloga alla Gengaloga alla Gengaloga alla Gengaloga alla Gengaloga alla Gengaloga alla Gengaloga alla Gengaloga alla Gengaloga alla Gengaloga alla Gengaloga alla Gengaloga alla Gengaloga alla Gengaloga alla Gengaloga alla Gengaloga alla Gengaloga alla Gengaloga alla Gengaloga alla Gengaloga alla Gengaloga alla Gengaloga alla Gengaloga alla Gengaloga alla Gengaloga alla Gengaloga alla Gengaloga alla Gengaloga alla Gengaloga alla Gengaloga alla Gengaloga alla Gengaloga alla Gengaloga alla Gengaloga alla Gengaloga alla Gengaloga alla Gengaloga alla Gengaloga alla Gengaloga alla Gengaloga alla Gengaloga alla Gengaloga alla Gengaloga alla Gengaloga alla Gengaloga alla Gengaloga alla Gengaloga alla Gengaloga alla Gengaloga alla Gengaloga alla Gengaloga alla Gengaloga alla Gengaloga alla Gengaloga alla Gengaloga alla Gengaloga alla Gengaloga alla Gengaloga alla Gengaloga alla Gengaloga alla Gengaloga alla Gengaloga alla Gengaloga alla Gengaloga alla Gengaloga alla Gengaloga alla Gengaloga alla Gengaloga alla Gengaloga alla Gengaloga alla Gengaloga alla Gengaloga alla Gengaloga alla Gengaloga alla Gengaloga alla Gengaloga alla Gengaloga alla Gengaloga alla Gengaloga alla Gengaloga alla Gengaloga alla Gengaloga alla Gengaloga alla Gengaloga alla Gengaloga alla Gengaloga alla Gengaloga alla Gengaloga alla Gengaloga alla Gengaloga alla Gengaloga alla Gengaloga alla Gengaloga alla Gengaloga alla Gengaloga alla Gengaloga alla Gengaloga alla Gengaloga alla Gengaloga alla Gengaloga alla Gengaloga alla Gengaloga alla Gengaloga alla Gengaloga alla Gengaloga alla Gengaloga alla Gengaloga alla Gengaloga alla Gengaloga alla Gengaloga alla Gengaloga alla Gengaloga alla Gengaloga alla Gengaloga alla Gengaloga alla Gengaloga alla Gengaloga alla Gengaloga alla Gengaloga alla Gengaloga alla Gengaloga alla Gengaloga alla Gengaloga alla Gengaloga alla Gengalo
	Top Hit Database Source	LN	EST_HUMAN	TN	TN	NT	LN		NT	EST_HUMAN	M	ΝŢ	TN	TN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	TN	EOT LUMAN	LO LICINOIS	EST_HUMAN	F	N⊤	N F	EST_HUMAN	Ę	LN	LN		Z	Ā
26	Top Hit Acession No.	40609.1	1.5E-02 AW 750834.1	1.4E-02 AE002230.2	TV05980 NT	J32800.1	1.4E-02 U67779.1		1.4E-02 AF160969.2	1.4E-02 AW074212.1	1.4E-02 AL 161586.2	1.4E-02 AL161586.2	4503628 NT	R996918 NT	1.4E-02 AW96268B.1	1.4E-02 AW982688.1	1.4E-02 BE733142.1	1.4E-02 BE733142.1	1.4E-02 X91338.1	7 0000	1.45-02 Andreadon.	1.4E-02 AA559030.1	1.4E-02 AL022073.1	1.4E-02 M81702.1	1.4E-02 AJ272265.1	1.4E-02 BE544561.1	1.4E-02 AL163218.2	1 4E-02 X60459 1	4 AE 02 AE324085 1	1,024500.1	11426968 N	1.4E-02 AF238059.2
	Most Similar (Top) Hit BLAST E Value	1.5E-02 L40609.1	1.5E-02	1.4E-02	1.4E-02	1.4E-02 U32800.1	1.4E-02		1.4E-02	1.4E-02	1.4E-02	1.4E-02	1.4E-02	1.4年-02	1.4E-02	1.4E-02	1.4E-02	1.4E-02	1.4E-02	ŗ	1.45-02	1.4E-02	1.4E-02	1.4E-02	1.4E-02	1.4E-02					1.4E-02	
	Expression Signal	221	2.38	1.54	3.81	2.12	2.49		1.83	1.23	6.6	6.9	0.75	12.14	9.97	26.6	6.22	6.22	0.74		70.4	4.52	1.86	1 44	141	1,86	0.89	8 05	70,4	70.	1.45	1.57
	ORF SEQ ID NO:	38171			27363				29478	29668	29753		l	29911		١		31103			33083	33084		35722		36227		29258				
	Exon SEQ ID NO:	24503			14307	l_			16458	16653		<u> </u>	L	1_	L	L		L	L		19707	19707	1	1		1	1_	1	L	-1	25625	25704
	Probe SEQ ID NO:	11442	12576	430	1142	1285	1326		3284	3485	3573	3573	3608	3746	4612	4612	4004	4998	201		8545	6545	8333	0000	8888	888	1078	40050	0077	12640	12959	12075

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					,		
Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
1913	15056		1.19	1.3E-02	.3E-02 BE739263.1	L HUMAN	601556462F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:3826335 5'
2010	15150	28254	2.13	1.3E-02	.3E-02 AL163201.2		Hono sapiens chromosome 21 segment HS21C001
2512	ì	١.	0.98	1.3E-02		FZ	Nelsseria meningitidis serogroup B strain MC58 section 87 of 206 of the complete genome
3285	ì.	29479	2.41	1.3E-02	.3E-02 BF697081.1	EST_HUMAN	602129475F1 NIH_MGC_56 Homo saplens cDNA clone IMAGE:4286203 5'
3285	1			1.3E-02		EST_HUMAN	602129475F1 NIH_MGC_56 Homo sapiens cDNA ctone IMAGE:4286203 51
4076	i			1.3E-02		NT	Mus musculus beta-sarcoglycan gane, complete cds
5275	18394		3.02	1.3E-02	.3E-02 D26547.1	LN	Rice gene for thioredaxin h, complete cds
		L.		10.1		Ŀ	Mus musculus chromosome X contigB; X-linked lymphocyle regulated 5 gene, Zinc finger protein 275, Zinc finger protein 275, Zinc finger protein 27 mmxq28nf
2360	18563	314/8	1.61	1.35-02	3E-02 AL.049866.2	Z	High piceni ac, illinatedour
5360	18563	31479	1.61	1.3E-02	.3E-02 AL049866.2	ΝΤ	Mus musculus chromosome X contigib: X-linked lymphocyte regulated 3 gene, zinc ringer protein z/ 3, z.inc finger protein 92, mmxq28orf
	1						Homo sapiens basic transcription factor 2 p44 (btf2p44) gene, partial cds, neuronal apoptosis inhibitory
6233	_1	Ì				Z	botton (1981) and administration region of programmer of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of
6327	19499			- `	.3E-02 M62962.1	IZ Z	C. reinhardii ribulose 1,3-dispirospirate calboyyasia dyygenase dyygenase duli v.A. Compress dos Arabidansis thallana DNA chromosome 4 contin fragment No. 46
7101	18528	Ì			Ī	Z	A Little On the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Contr
7101	18528	31482	1.3	-	.3E-02 AL161546.2	LN	Arabidopsis thatiana UNA chromosome 4, contig tragitient two. 40
7752	20812	34303	4.9	Ì	1.3E-02 Al031593.1	EST HUMAN	იო06g05.x1 Soares_parattyroid_tumor_NbHPA Homo sapiens cDNA cione IMAGE:1646072 3 similar to contains Alu repetitive element
8678	L					NT.	Homo sapiens human endogenous retrovirus W gagC3.37 G gag (gag) gene, complete cds
10411	<u> </u>					ĽΖ	Mouse kidney androgen-regulated protein (KAP) gene, complete cds
10485	1	37129	0.95		1.3E-02 AE001304.1	LΝ	Chlamydia trachomatis section 31 of 87 of the complete genome
11239	ı				1.3E-02 AW268563.1	EST_HUMAN	xv34e03.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2815036 3
11239	ı				1.3E-02 AW 268563.1	EST_HUMAN	xv34e03.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:28150363'
12645	26127		1.7		1.3E-02 Z99117.1	LΝ	Bacillus subtilis complete genome (section 14 of 21): from 2599451 to 2812870
12753	l_		2.56	1.3E-02	TN 6905596	TN	Human herpesvirus 6B, complete genome
12965	L		30.16		1.3E-02 AF152238.1		Homo sapiens V1b vasopressin receptor (VPR3) gene, complete cds
							H.sapiens DMA, DMB, HLA-Z1, IPP2, LMP2, TAP1, LMP7, TAP2, DOB, DQB2 and RING8, 9, 13 and 14
219	13441		0.82		1.2E-02 X87344.1	TN	genes
	l						zf65g01,r1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:381840 5' similar to contains element
366	13575		4.38		1.2E-02 AA059299.1	EST_HUMAN	L1 repetitive element;
465	13660	L	1,43		1.2E-02 P38898	SWISSPROT	HYPOTHETICAL 17.1 KD PROTEIN IN PUR5 3'REGION
					4 DO TO 4	EOT LIMAN	qd68e12x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1734670 3' similar to contains L1.t1 L1 provotitius element :
767	- 1				1	ESI_HOMAN	Ideas earliers,
2246	15379	28507	7 2.03		1.2E-02JAL163213.2	Z	Trong sapreis of office at seasons at the seasons at the seasons at the seasons at the seasons at the seasons at the seasons at the seasons at the seasons at the seasons at the seasons at the seasons at the seasons at the seasons at the seasons at the seasons at the seasons at the seasons at the seasons at the seasons at the seasons at the seasons at the seasons at the seasons at the seasons at the seasons at the seasons at the seasons at the seasons at the seasons at the seasons at the seasons at the seasons at the seasons at the seasons at the seasons at the seasons at the seasons at the seasons at the seasons at the seasons at the seasons at the seasons at the seasons at the seasons at the seasons at the seasons at the seasons at the seasons at the seasons at the seasons at the seasons at the seasons at the seasons at the seasons at the seasons at the seasons at the seasons at the seasons at the seasons at the seasons at the seasons at the seasons at the seasons at the seasons at the seasons at the seasons at the seasons at the seasons at the seasons at the seasons at the seasons at the seasons at the seasons at the seasons at the seasons at the seasons at the seasons at the seasons at the seasons at the seasons at the seasons at the seasons at the seasons at the seasons at the seasons at the seasons at the seasons at the seasons at the seasons at the seasons at the seasons at the seasons at the seasons at the seasons at the seasons at the seasons at the seasons at the seasons at the seasons at the seasons at the seasons at the seasons at the seasons at the seasons at the seasons at the seasons at the seasons at the seasons at the seasons at the seasons at the seasons at the seasons at the seasons at the seasons at the seasons at the seasons at the seasons at the seasons at the seasons at the seasons at the seasons at the seasons at the seasons at the seasons at the seasons at the seasons at the seasons at the seasons at the seasons at the seasons at the seasons at the seasons at the seasons at the seasons a

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Top Hit Descriptor	xj37e09.x1 Soares_NFL_T_GBC_S1 Homo saplens cDNA clone IMAGE::2659432 3'	xj37e09.x1 Soares_NFL_T_GBC_S1 Homo saplens cDNA done IMAGE:2659432 3	zm88e03.r1 Stratagene ovarian cencer (#937219) Homo cepiens cDNA clone IMAGE:545020 5	y11b08 s1 Soares placenta Nb2HP Homo sapiens cDNA done IMAGE:138903 3'	zb68e07.x5 Soares_fetaj_lung_NbHL19W. Homo sapiens cDNA clane IMAGE:308532 3' similar to contains element MER22 repetitive element ;	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RoRet gene, and sodium phosphate transporter (NPT3) gene, complete ods	Cynops pyrrhogaster CpUbiqT mRNA, partial cds	AV731704 HTF Homo sapiens cDNA clone HTFBHG11 5'	Rana rugosa mRNA for calreticulin, complete cds	Homo sapiens wbscr1 (WBSCR1) and wbscr5 (WBSCR5) genes, complete cds, alternatively spliced and replication factor C subunit 2 (RFC2) gene, complete cds	Mus musculus DNA methyltransferase (Dnmt1) gene, exons 2, 3, 4, and 5	y/34h12.s1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:150695 3'	AV732093 HTF Homo sapiens cDNA clone HTFBJC09 5	601882949F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4095253 5'	CMP-N-ACETYLNEURAMINATE-BETA-GALACTOSAMIDE-ALPHA-23-SIALYLTRANSFERASE (BETA- GALACTOSIDE ALPHA-2,3-SIALYLTRANSFERASE) (ALPHA 2,3-ST) (GAL-NAC6S) (GAL-BETA-1,3- GAINAC-AIPHA-2-3-SIALY TRANSFERASE) (ST3-GALA-2) (SIAT4-B)	V43706.s1 Soares placenta Nb2HP Homo sapiens dDNA done IMAGE:142019 3'	y43106.s1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:1420193'	Homo sapiens fringe protein mRNA, partial cds	Homo sapiens fringe protein mRNA, partial cds	yd72c08.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:113774 3'	Norwalk-like virus genogroup 2 gene for capsid protein, complete cds	Homo sapiens Spast gene for spastin protein	COLLAGEN ALPHA 1(IV) CHAIN PRECURSOR	C18119 Human placenta cDNA (TFujiwara) Homo sapiens cDNA done GEN-557G06 5	zm69e11.s1 Stratagene neurospithelium (#837231) Homo sapiens cDNA clone IMAGE:530924 3	H.sapiens LIPA gene, exon 4	H.sapiens LIPA gene, exon 4	602018037F1 NCI_CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4153505 5
Top Hit Database Source	EST_HUMAN			EST_HUMAN	EST_HUMAN	LN		EST_HUMAN		ΤN	Ę	EST_HUMAN	EST_HUMAN	EST_HUMAN	TOGGOOMS	Т	Τ	N	Z	EST_HUMAN	NT	NT	SWISSPROT		HUMAN	NT	LΝ	EST_HUMAN
Top Hit Acession No.	1.2E-02 AW172350.1	1.2E-02 AW172350.1	1.2E-02 AA075418.1	1.2E-02 R62805.1	1.2E-02 A1668694.1	J91328.1	1.2E-02 AB019786.1		1,2E-02 D78589.1	1.2E-02 AF045555.1	1.2E-02 AF175412.1	1.2E-02 H02197.1	1.2E-02 AV732093.1	1.2E-02 BF216650.1	30000	1.2E-02 Q11200	1.2E-02 R68831.1	1.2E-02 AF193612.1	1.2E-02 AF193612.1	1.2E-02 T76987.1	1.2E-02 AB031013.1	1.2E-02 AJ246003.1	P17139	1.2E-02 C18119.1	1.1E-02 AA070364.1	1.1E-02 X75491.1	1.1E-02 X75491.1	1.1E-02 BF345263.1
Most Similar (Top) Hit BLAST E Value	1.2E-02	1.2€-02	1.2E-02	1.2E-02	1.2E-02	1.2E-02[U91328.1	1.2E-02	1.2E-02	1.2E-02	1.2E-02	1.2E-02	1.2E-02	1.2E-02		200					1.2€-02								
Expression Signal	1.02	1.43	7.3	2.05		2.02	1.97	1.31	1.78	0.72		1.42	8.54	0.66		2.3					2.54	1.24	1.16	6.24	1.22	1.48		5.35
ORF SEQ ID NO:	28762	28762		29545		31139		31286		32765			34014			34/32					36461				27520		27987	
Exon SEQ ID NO:	15640	1	16346	16531		18163	1	1	ı	19417	1_		1_	1	1	27,209	2,403	L	L	1	1	L	L	L	14454	14892	14892	15236
Probe SEQ ID NO:	2514	2701	3170	3359	3362	7035	5154	5195	5871	6243	7147	7443	7465	77.29		8186	8321	8386	8386	9091	9839	9872	12757	12974	1298	1743	1743	2096

Page 174 of 550 Table 4 Single Exon Probes Expressed in Placenta

WO 01/57272

Probe         Exm         Oper SEQ         Exm         Top Hill Accession         Top Hill Accession         Top Hill Descriptor           SEQ         NO.         NO.         Signal         11,622 Nosesion         11,622 Nosesion         11,622 Nosesion         11,622 Nosesion         11,622 Nosesion         11,622 Nosesion         11,622 Nosesion         11,622 Nosesion         11,622 Nosesion         11,622 Nosesion         11,622 Nosesion         11,622 Nosesion         11,622 Nosesion         11,622 Nosesion         11,622 Nosesion         11,622 Nosesion         11,622 Nosesion         11,622 Nosesion         11,622 Nosesion         11,622 Nosesion         11,622 Nosesion         11,622 Nosesion         11,622 Nosesion         11,622 Nosesion         11,622 Nosesion         11,622 Nosesion         11,622 Nosesion         11,622 Nosesion         11,622 Nosesion         11,622 Nosesion         11,622 Nosesion         11,622 Nosesion         11,622 Nosesion         11,622 Nosesion         11,622 Nosesion         11,622 Nosesion         11,622 Nosesion         11,622 Nosesion         11,622 Nosesion         11,622 Nosesion         11,622 Nosesion         11,622 Nosesion         11,622 Nosesion         11,622 Nosesion         11,622 Nosesion         11,622 Nosesion         11,622 Nosesion         11,622 Nosesion         11,622 Nosesion         11,622 Nosesion         11,622 Nosesion         11,622 Nosesion         1	}						
16776         29782         3.59         1.1E-02         N99623.1         EST_HUMAN           17370         178081         3.59         1.1E-02         AIV813798.1         EST_HUMAN           17370         3.068         1.1E-02         AIV813798.1         EST_HUMAN           19461         32800         0.88         1.1E-02         AIV813798.1         EST_HUMAN           20830         34321         2.19         1.1E-02         BE34380.1         NT           21632         34551         1.25         1.1E-02         BE149611.1         EST_HUMAN           21639         34551         1.25         1.1E-02         BE31284         SWISSPROT           21630         34551         0.46         1.1E-02         BE31284         SWISSPROT           21630         35458         0.69         1.1E-02         AA082578.1         EST_HUMAN           22107         35641         0.7         1.1E-02         AA082578.1         EST_HUMAN           23334         36939         4.06         1.1E-02         AA3082578.1         EST_HUMAN           24283         35727         7.44         1.1E-02         AA3082578.1         EST_HUMAN           24283         35834         2.41 </td <td>ш W Z</td> <td></td> <td></td> <td>Most Similar (Top) Hit BLAST E Value</td> <td>Top Hit Acession No.</td> <td>Top Hit Database Source</td> <td>Top Hit Descriptor</td>	ш W Z			Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
16776         29792         3.59         1.1E-02 Ales3608.1         EST_HUMAN           17370         0.66         1.1E-02 ALO48383.2         EST_HUMAN           18081         32800         0.89         1.1E-02 BE14961.1         EST_HUMAN           21039         34221         2.19         1.1E-02 BE14961.1         EST_HUMAN           21039         34551         1.25         1.1E-02 BE14961.1         EST_HUMAN           21632         35661         0.46         1.1E-02 BE14961.1         EST_HUMAN           21632         35661         0.46         1.1E-02 BE14961.1         EST_HUMAN           21632         35661         0.46         1.1E-02 BE14961.1         EST_HUMAN           21632         35661         0.7         1.1E-02 BE14961.1         EST_HUMAN           22101         35641         0.7         1.1E-02 BE14961.0         SWISSPROT           23334         36689         4.06         1.1E-02 C04803.1         SWISSPROT           2345         2.02         1.1E-02 C04803.1         EST_HUMAN           2342         36247         7.44         1.1E-02 C04803.1         EST_HUMAN           2342         36247         2.41         1.1E-02 AW846120.1         EST_HUMAN	1	6119	5.31	1.1E-02	N99523.1	EST_HUMAN	za40e05.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:295040 5
17370         0.68         1.1E-02 AV813796.1         EST_HUMAN           18081         31657         1.27         1.1E-02 AL048363.2         EST_HUMAN           20830         34321         1.21         1.1E-02 BE149611.1         BST_HUMAN           21632         3562         0.46         1.1E-02 PB0394         SWISSPROT           21632         35621         0.46         1.1E-02 PB0394         SWISSPROT           21632         35645         0.69         1.1E-02 PB0394         SWISSPROT           21632         35641         0.7         1.1E-02 PB0394         SWISSPROT           22101         35641         0.7         1.1E-02 PB0394         SWISSPROT           22101         35641         0.7         1.1E-02 PB0394         SWISSPROT           22101         35641         0.7         1.1E-02 PW0394         SWISSPROT           23182         35627         7.44         1.1E-02 PW0394         SWISSPROT           23182         35641         0.7         1.1E-02 PW0394         SWISSPROT           23182         35641         0.7         1.1E-02 PW0394         SWISSPROT           23182         35727         7.44         1.1E-02 PW0394         SWISSPROT           <	1				AI653508.1	EST_HUMAN	tq955010.x1 NCI_CGAP_Ov23 Homo sapiens oDNA clone IMAGE:2216539 3' similar to SW:XPF_HUMAN Q92989 DNA-REPAIR PROTEIN COMPLEMENTING XP-F CELL;
19461         32800         0.89         1.1E-02         BE480.1         NT           20820         34321         2.19         1.1E-02         BE480.1         NT           21623         34551         1.25         1.1E-02         BE14961.1         EST_HUMAN           21623         35062         0.46         1.1E-02         P80394         SWISSPROT           21624         35621         0.46         1.1E-02         P80394         SWISSPROT           21625         35626         0.46         1.1E-02         P80394         SWISSPROT           21627         35458         0.69         1.1E-02         P80394         SWISSPROT           22101         35641         0.7         1.1E-02         PA0896180.1         EST_HUMAN           22101         35641         0.7         1.1E-02         AN9836180.1         EST_HUMAN           23171         36769         2.02         1.1E-02         AA082578.1         EST_HUMAN           24263         37934         2.41         1.1E-02         AA08258.1         EST_HUMAN           13245         26247         8.82         1.0E-02         AW946120.1         EST_HUMAN           16761         27785         0.97		L			AW813796.1	EST_HUMAN	RC3-ST0197-120200-015-g11 ST0197 Homo sapiens cDNA
19461         32800         0.89         1.1E-02         U6480.1         NT           20820         34321         2.19         1.1E-02         BE149611.1         EST_HUMAN           21039         34551         1.25         1.1E-02         P80394         SWISSPROT           21532         35061         0.46         1.1E-02         P80394         SWISSPROT           21532         35062         0.46         1.1E-02         P80394         SWISSPROT           21532         35662         0.46         1.1E-02         P80394         SWISSPROT           21620         35456         0.69         1.1E-02         P80394         SWISSPROT           22101         35641         0.7         1.1E-02         PA0896180.1         EST_HUMAN           22102         35727         7.44         1.1E-02         AA082578.1         EST_HUMAN           2334         36939         4.06         1.1E-02         AA082578.1         EST_HUMAN           13245         26247         8.82         1.0E-02         AA086389.1         EST_HUMAN           16761         27785         0.97         1.0E-02         AW0846120.1         EST_HUMAN           16761         27785         0.9	1				AL048383.2	EST_HUMAN	DKFZp586E0924_s1 586 (synonym: hute1) Homo saplens cDNA clone DKFZp586E0924
19401         32020         2.10         1.1E-02         BE149611.1         EST HUMAN           21039         34321         2.19         1.1E-02         BE31294         NT           21039         34551         1.25         1.1E-02         P80394         SWISSPROT           21532         35062         0.46         1.1E-02         P80394         SWISSPROT           21620         35643         0.69         1.1E-02         AW996160.1         EST HUMAN           22101         35641         0.7         1.1E-02         AW996160.1         EST HUMAN           22102         35642         0.69         1.1E-02         AW996160.1         EST HUMAN           22102         35641         0.7         1.1E-02         AA9082578.1         EST HUMAN           22102         36939         4.06         1.1E-02         AA314665.1         EST HUMAN           13245         28247         8.82         1.0E-02         AW946120.1         EST HUMAN           16761         27765         0.97         1.0E-02         AW946120.1         EST HUMAN           16762         288         1.0E-02         AW946120.1         EST HUMAN           16761         2743         1.0E-02	l				188480 1	ΙN	Bacillus subtilis SpoVK (spoVK), YnbA (ynbA), YnbB (ynbB), GlnR (glnR), glutamine synthetase (glnA), YnaA (ynaA), YnaB (ynaB), YnaC (ynaC), YnaD (ynaD), YnaE (ynaE), YnaF (ynaF), YnaG (ynaG), YnaH (ynaH), YnaI (ynaI), YnaJ (ynaJ), xyfan beta-1,4-xyfosl>
21030         34551         1.25         1.1E-02         9631294         NT           21532         35061         0.46         1.1E-02         P80394         SWISSPROT           21532         35062         0.46         1.1E-02         AW996160.1         EST_HUMAN           21620         35641         0.7         1.1E-02         AW996160.1         EST_HUMAN           22101         35641         0.7         1.1E-02         C04903.1         EST_HUMAN           22102         35637         7.44         1.1E-02         AA082578.1         EST_HUMAN           23334         36939         4.06         1.1E-02         AA34665.1         EST_HUMAN           24253         37934         2.41         1.1E-02         AA34665.1         EST_HUMAN           13245         28247         8.82         1.0E-02         AW946120.1         EST_HUMAN           16761         1.77         1.0E-02         AW946120.1         EST_HUMAN           16762         288         1.0E-02         AW946120.1         EST_HUMAN           16761         1.24         1.0E-02         AW946526.1         EST_HUMAN           16762         288         1.0E-02         AW946562.1         EST_HUMAN <td>1</td> <td></td> <td></td> <td></td> <td>BE149611.1</td> <td>EST HUMAN</td> <td>RC1-HT0266-100300-016-h07 HT0256 Homo saplens cDNA</td>	1				BE149611.1	EST HUMAN	RC1-HT0266-100300-016-h07 HT0256 Homo saplens cDNA
21532         35061         0.46         1.1E-02         P80394         SWISSPROT           21532         35082         0.46         1.1E-02         AW996160.1         EST_HUMAN           21920         35641         0.69         1.1E-02         AW996160.1         EST_HUMAN           22101         35641         0.7         1.1E-02         C04803.1         EST_HUMAN           22102         35631         0.7         1.1E-02         C04802.1         EST_HUMAN           23334         36939         4.06         1.1E-02         AA314665.1         EST_HUMAN           24263         37934         2.41         1.1E-02         AA314665.1         EST_HUMAN           13245         28247         8.82         1.0E-02         AW346120.1         EST_HUMAN           15761         1.71         1.0E-02         AW368128.1         EST_HUMAN           16703         27785         0.97         1.0E-02         AW368128.1         EST_HUMAN           16704         1.24         1.0E-02         AW368128.1         EST_HUMAN           16609         2.9525         1.24         1.0E-02         AW368251.1         EST_HUMAN           16704         2.6566         1.0E-02         AW					9631294	LN	Melanoplus sanguinipes entomopoxvirus, complete genome
21532         35062         0.46         1.1E-02         AW996160.1         EST_HUMAN           21920         35456         0.69         1.1E-02         AW996160.1         EST_HUMAN           22101         35641         0.7         1.1E-02         C04903.1         EST_HUMAN           22102         35632         7.44         1.1E-02         C04902.1         EST_HUMAN           23334         36939         4.06         1.1E-02         AA314665.1         EST_HUMAN           24253         37934         2.41         1.1E-02         AA314665.1         EST_HUMAN           13245         28247         8.82         1.0E-02         AW946120.1         EST_HUMAN           14705         27785         0.97         1.0E-02         AW946120.1         EST_HUMAN           16761         1.71         1.0E-02         AW946120.1         EST_HUMAN           16701         27785         0.97         1.0E-02         AW946120.1         EST_HUMAN           16702         1.24         1.0E-02         AW94656.1         EST_HUMAN           16703         2.7785         0.97         1.0E-02         AW94656.1         EST_HUMAN           16704         1.0E-02         AW946562.1	1	L			P80394	SWISSPROT	METALLOTHIONEIN (MT-1/MT-2)
21620         35458         0.69         1.1E-02 Aw996160.1         EST_HUMAN           22101         35641         0.7         1.1E-02 C04903.1         EST_HUMAN           22102         35727         7.44         1.1E-02 C04903.1         EST_HUMAN           23334         36939         2.02         1.1E-02 AA314665.1         EST_HUMAN           24253         37934         2.41         1.1E-02 AA314665.1         EST_HUMAN           13245         28247         8.82         1.0E-02 AW940120.1         EST_HUMAN           15761         1.71         1.0E-02 AW960120.1         EST_HUMAN           16763         2.7785         0.97         1.0E-02 AW940120.1         EST_HUMAN           16764         1.71         1.0E-02 AW960389.1         EST_HUMAN           16763         2.83         1.0E-02 AA968389.1         EST_HUMAN           16764         1.24         1.0E-02 AA968389.1         EST_HUMAN           16765         1.24         1.0E-02 AA968389.1         EST_HUMAN           16762         0.97         1.0E-02 AA806389.1         EST_HUMAN           16762         0.97         1.0E-02 AA806389.1         EST_HUMAN           16762         0.96         1.0E-02 AA806389.1         EST_HUM	L			_	P80394	SWISSPROT	METALLOTHIONEIN (MT-1MT-2)
22101         35641         0.7         1.1E-02 (64903.1         EST_HUMAN           22182         35727         7.44         1.1E-02 (64902.         SWISSPROT           23171         36769         2.02         1.1E-02 (64902.         SWISSPROT           23334         36939         4.06         1.1E-02 (AA314665.1         EST_HUMAN           24263         37934         2.41         1.1E-02 (AA946120.1         EST_HUMAN           13245         26247         8.82         1.0E-02 (AW846120.1         EST_HUMAN           16761         1.71         1.0E-02 (AW846120.1         EST_HUMAN           16762         27785         0.97         1.0E-02 (AW846120.1         EST_HUMAN           16761         1.71         1.0E-02 (AW846120.1         EST_HUMAN           16762         1.24         1.0E-02 (AW846120.1         EST_HUMAN           16763         288         1.0E-02 (AW846120.1         EST_HUMAN           16762         1.24         1.0E-02 (AW845621.1         EST_HUMAN           16762         0.77         1.0E-02 (AW845621.1         EST_HUMAN           16763         31015         6.10E-02 (AW845621.1         EST_HUMAN           16029         31017         4.14         1.0E-02 (AW84	Ļ				AW996160.1	EST_HUMAN	QV3-BN0045-220300-128-h02 BN0046 Homo capienc cDNA
23171         36769         2.02         1.1E-02         AA082578.1         EST_HUMAN           23334         36939         4.06         1.1E-02         AA314665.1         EST_HUMAN           24263         37934         2.41         1.1E-02         AA68228.1         EST_HUMAN           13245         26247         8.82         1.0E-02 AW344010.1         EST_HUMAN           15761         1.71         1.0E-02 AW368128.1         EST_HUMAN           16762         1.77         1.0E-02 AW368128.1         EST_HUMAN           16609         29525         1.24         1.0E-02 AW368128.1         EST_HUMAN           16762         1.71         1.0E-02 AW368128.1         EST_HUMAN           16763         288         1.0E-02 AW368128.1         EST_HUMAN           16764         1.24         1.0E-02 AW36858.1         EST_HUMAN           16765         0.77         1.0E-02 AW36858.1         EST_HUMAN           16763         30148         0.95         1.0E-02 AW345627.1         EST_HUMAN           1609         31074         4.14         1.0E-02 AL163302.2         NT           1609         31077         4.14         1.0E-02 AL163302.2         NT           18243         31322 </td <td>L</td> <td></td> <td></td> <td></td> <td>C04803.1</td> <td>EST_HUMAN</td> <td>CC4803 Human heart cDNA (YNakamura) Homo sapiens cDNA clone 3NHC4040</td>	L				C04803.1	EST_HUMAN	CC4803 Human heart cDNA (YNakamura) Homo sapiens cDNA clone 3NHC4040
23171         36769         2.02         1.1E-02         AA082578.1         EST_HUMAN           23334         36939         4.06         1.1E-02         AA314665.1         EST_HUMAN           24263         37934         2.41         1.1E-02         AA668239.1         EST_HUMAN           13245         26247         8.82         1.0E-02         AW846120.1         EST_HUMAN           15761         27785         0.97         1.0E-02         AW846120.1         EST_HUMAN           16761         1.77         1.0E-02         AW846120.1         EST_HUMAN           16762         27785         0.97         1.0E-02         AW846120.1         EST_HUMAN           16609         29525         1.24         1.0E-02         AW846580.1         EST_HUMAN           16762         29525         1.24         1.0E-02         AW845621.1         EST_HUMAN           17143         30148         0.85         1.0E-02         AW845621.1         EST_HUMAN           17143         30149         0.85         1.0E-02         AW845621.1         EST_HUMAN           18029         31077         4.14         1.0E-02         AL16308.2         NT           18024         31208         0.83	<u></u>				Q61982	SWISSPROT	NEUROGENIC LOCUS NOTCH 3 PROTEIN
23334         36939         4.06         1.1E-02         AA314665.1         EST_HUMAN           24263         37934         2.41         1.1E-02         AA668239.1         EST_HUMAN           13245         26247         8.82         1.0E-02         AW846120.1         EST_HUMAN           14705         27785         0.97         1.0E-02         AA808389.1         EST_HUMAN           16734         28344         2.88         1.0E-02         AA808389.1         EST_HUMAN           16609         29525         1.24         1.0E-02         BE968999.1         EST_HUMAN           1714         0.77         1.0E-02         BE968999.1         EST_HUMAN           1714         0.77         1.0E-02         BE968999.1         EST_HUMAN           1714         0.77         1.0E-02         BE968999.1         EST_HUMAN           1714         0.77         1.0E-02         BE968999.1         EST_HUMAN           1715         30148         0.69         1.0E-02         AR453302.2         NT           16029         31017         6         1.0E-02         AL163302.2         NT           16029         31208         0.83         1.0E-02         AL161530.2         NT	l			1	i	EST_HUMAN	zn24a01.r1 Stratagene neurœpithelium NT2RAMI 937234 Homo sapiens cDNA clone IMAGE:548328 5'
24263         37934         2.41         1.1E-02         AA668239.1         EST_HUMAN           13245         26247         8.82         1.0E-02         AW846120.1         EST_HUMAN           14705         27785         0.97         1.0E-02         AW868128.1         EST_HUMAN           16761         1.71         1.0E-02         AA808389.1         EST_HUMAN           16834         2.88         1.0E-02         BA808389.1         EST_HUMAN           16609         29525         1.24         1.0E-02         BE988989.1         EST_HUMAN           17140         0.7         1.0E-02         BE988989.1         EST_HUMAN           17160         29525         1.24         1.0E-02         BE988989.1         EST_HUMAN           17160         0.7         1.0E-02         BE988989.1         EST_HUMAN           17160         0.69         1.0E-02         AL163302.2         NT           18029         31017         6         1.0E-02         AL163302.2         NT           18029         31074         4.14         1.0E-02         AL163302.2         NT           18029         31074         4.14         1.0E-02         AL63302.2         NT           1						EST_HUMAN	EST186494 Colon carcinoma (HCC) cell line II Homo sapiens cDNA 5' end
25152         4.01         1.1E-02         AA668239.1         EST_HUMAN           13245         26247         8.82         1.0E-02         AW846120.1         EST_HUMAN           14705         27785         0.97         1.0E-02         AW868128.1         EST_HUMAN           16761         1.71         1.0E-02         AA808389.1         EST_HUMAN           16834         2.88         1.0E-02         BA808389.1         EST_HUMAN           16609         29525         1.24         1.0E-02         BE988999.1         EST_HUMAN           1743         30148         0.85         1.0E-02         AM845621.1         EST_HUMAN           17405         30165         0.59         1.0E-02         AL68302.2         NT           18029         31017         5         1.0E-02         AL68302.2         NT           18038         31074         4.14         1.0E-02         AL68302.2         NT           18243         31208         0.83         1.0E-02         AL68302.2         NT           18243         31322         0.83         1.0E-02         AL68567.1         EST_HUMAN           18729         31774         0.81         1.0E-02         AL761593.2         NT </td <td>L</td> <td></td> <td></td> <td></td> <td>11435505</td> <td>Į,</td> <td>Homo sapiens T-bαx 5 (TBX5), mRNA</td>	L				11435505	Į,	Homo sapiens T-bαx 5 (TBX5), mRNA
13245         26247         8.82         1.0E-02         AW849120.1         EST_HUMAN           14705         27785         0.97         1.0E-02         AW368128.1         EST_HUMAN           16734         29344         2.88         1.0E-02         AR806389.1         EST_HUMAN           1669         29525         1.24         1.0E-02         BE985566.1         EST_HUMAN           1672         1.24         1.0E-02         BE98898.1         EST_HUMAN           1674         0.05         1.0E-02         BE98898.1         EST_HUMAN           17143         30148         0.05         1.0E-02         AL163302.2         NT           18029         31074         4.14         1.0E-02         AL163302.2         NT           18039         31074         4.14         1.0E-02         AL163302.2         NT           18243         31208         0.63         1.0E-02         AL161593.2         NT           18364         31328         1.60         1.0E-02         PAL65089         SWISSPROT           18729         31745         0.81         1.0E-02         PAL65089         SWISSPROT	l				AA668239.1	EST HUMAN	eb77111.s1 Stratagene fetal retina 937202 Homo sapiens cDNA clone IMAGE:853005 3' similar to contains Alu repetitive element;
14705         27785         0.97         1.0E-02 AW368128.1         EST_HUMAN           16761         1.71         1.0E-02 AA606389.1         EST_HUMAN           16334         28344         2.88         1.0E-02 BE855565.1         EST_HUMAN           16609         29525         1.24         1.0E-02 BE96898.1         EST_HUMAN           16762         0.7         1.0E-02 AW845621.1         EST_HUMAN           1743         30148         0.85         1.0E-02 AW845621.1         EST_HUMAN           1743         30148         0.85         1.0E-02 AW845621.1         EST_HUMAN           18029         31017         6         1.0E-02 AL63302.2         NT           18039         31074         4.14         1.0E-02 AL63302.2         NT           18243         31208         0.83         1.0E-02 R96687.1         EST_HUMAN           18243         31332         1.96         1.0E-02 AL161583.2         NT           18754         31332         1.96         1.0E-02 P06599         SWISSPROT           18729         31745         0.81         1.0E-02 P05899         SWISSPROT				ľ	AW846120.1	EST_HUMAN	MR3-CT0176-111099-003-e10 CT0176 Homo sapiens cDNA
15761         1.71         1.0E-02 AA806389.1         EST_HUMAN           16334         2834         2.88         1.0E-02 BE835556.1         EST_HUMAN           16609         29525         1.24         1.0E-02 BE86899.1         EST_HUMAN           16762         0.7         1.0E-02 AW845621.1         EST_HUMAN           17143         30148         0.85         1.0E-02 AW845621.1         EST_HUMAN           17159         30165         0.85         1.0E-02 AL63302.2         NT           18029         31017         4.14         1.0E-02 AL63302.2         NT           18039         31074         4.14         1.0E-02 AL63302.2         NT           18243         31208         0.83         1.0E-02 AL163302.2         NT           18243         31332         1.96         1.0E-02 AL161593.2         NT           18729         31745         0.81         1.0E-02 AL161593.2         SWISSPROT	L	L			AW368128.1	EST_HUMAN	CM2-HT0177-041099-017-h12 HT0177 Homo sapiens cDNA
16334         2834         2.88         1.0E-02         BE835656-1         EST_HUMAN           16609         29525         1.24         1.0E-02         BE98999-1         EST_HUMAN           16762         0.7         1.0E-02         AW845621-1         EST_HUMAN           17143         30148         0.86         1.0E-02         AI065086-1         EST_HUMAN           18029         31017         6.99         1.0E-02         AL63302.2         NT           18039         31074         4.14         1.0E-02         R86567.1         EST_HUMAN           18243         31208         0.83         1.0E-02         AL161563.2         NT           18254         31332         1.96         1.0E-02         AL161563.2         NT           18729         31745         0.81         1.0E-02         AL161563.2         NT		15761	1.71	Ĺ	AA806389.1	EST_HUMAN	oc22h08.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1330495 3
16609         29525         1.24         1.0E-02 BE968999.1         EST_HUMAN           16702         0.7         1.0E-02 AW845621.1         EST_HUMAN           17143         30148         0.85         1.0E-02 AL05080.1         EST_HUMAN           18029         31017         5         1.0E-02 AL05302.2         INT           18029         31074         4.14         1.0E-02 R96567.1         EST_HUMAN           18243         31208         0.83         1.0E-02 AL161593.2         INT           18364         31332         1.96         1.0E-02 P06599         SWISSPROT           18729         31745         0.81         1.0E-02 P055891.1         EST_HUMAN					BE835556.1	EST_HUMAN	RC0-FN0025-250500-021-d02 FN0025 Homo sapiens cDNA
16762         0.7         1.0E-02 AW845621.1         EST_HUMAN           17143         30148         0.86         1.0E-02 A1065086.1         EST_HUMAN           17159         30165         0.59         1.0E-02 AL163302.2         NT           18029         31017         5         1.0E-02 AL163302.2         NT           18029         31074         4.14         1.0E-02 R96567.1         EST_HUMAN           18243         31208         0.83         1.0E-02 AL161593.2         NT           18364         31332         1.96         1.0E-02 P06599         SWISSPROT           18729         31745         0.81         1.0E-02 P052891.1         EST_HUMAN	1				BE968999.1	EST_HUMAN	601649967R1 NIH_MGC_74 Homo sepiens cDNA clone IMAGE:3833689 3
17143         30148         0.85         1.0E-02         Alo65086.1         EST_HUMAN           17169         30165         0.69         1.0E-02         AL163302.2         NT           18029         31077         5         1.0E-02         RF53521         NT           18039         31074         4.14         1.0E-02         R96567.1         EST_HUMAN           18243         31208         0.83         1.0E-02         AL161593.2         NT           18364         31332         1.96         1.0E-02         P06599         SWISSPROT           18729         31745         0.81         1.0E-02         H52681.1         EST_HUMAN	L				AW845621.1	EST_HUMAN	MR0-CT0060-081099-003-h10 CT0060 Homo sapiens cDNA
17169         30165         0.59         1.0E-02         AL163302.2         NT           18029         31017         6         1.0E-02         8753521         NT           18036         31074         4.14         1.0E-02         R96567.1         EST_HUMAN           18243         31208         0.83         1.0E-02         AL161593.2         NT           18364         31332         1.96         1.0E-02         P06599         SWISSPROT           18729         31745         0.81         1.0E-02         H52681.1         EST_HUMAN	L				A1065086.1	EST_HUMAN	HA0921 Human fetal liver cDNA library Homo sapiens cDNA
18029         31017         6         1.0E-02         8753521 NT           18036         31074         4.14         1.0E-02         R96567.1         EST_HUMAN           18243         31208         0.83         1.0E-02         AL161593.2         NT           18364         31332         1.96         1.0E-02         P06599         SWISSPROT           18729         31745         0.81         1.0E-02         H52681.1         EST_HUMAN	L				AL163302.2	TN	Homo saplens chromosame 21 segment HS21C102
18036         31074         4.14         1.0E-02 R96567.1         EST_HUMAN           18243         31208         0.83         1.0E-02 AL161593.2         NT           18364         31332         1.96         1.0E-02 P06599         SWISSPROT           18759         0.81         1.0E-02 H52681.1         EST_HUMAN	L					NT	Mus musculus caticotropin releasing hormone receptor 2 (Crirt2), mRNA
18243         31208         0.83         1.0E-02 AL161593.2         NT           18364         31332         1.96         1.0E-02 P06599         SWISSPROT           18729         31745         0.81         1.0E-02 H52881.1         EST_HUMAN					R96567.1	EST HUMAN	yq54h01.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:199633 5
18364         31332         1.96         1.0E-02 P06599         SWISSPROT           18729         31745         0.81         1.0E-02 H52881.1         EST_HUMAN	L				AL161593.2	NT	Arebidopsis thaliana DNA chromosome 4, contig fragment No. 89
18729 31745 0.81 1.0E-02 H52681.1   EST_HUMAN					P06599	SWISSPROT	EXTENSIN PRECURSOR
					H52681.1	EST_HUMAN	yu36h11.r1 Soares ovary tumor NbHOT Homo sapiens dDNA cione IMAGE:Z33941 3

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									for	3_cds1	ment MER5			SF3A66)					element											fernatively			
onigie Exori Fronce Expressed in Fracting	Top Hit Descriptor	Mus musculus transcription complex subunit NF-ATc4 (Nfatc4) gene, exons 1 and 2	Mus musculus synaptotagmin II (Syt2) gene, complete cds	MR4-BT0356-070100-201-h01 BT0356 Homo septens oDNA	WR4-BT0356-070100-201-h01 BT0356 Homo sapiens cDNA	Z.mays U3snRNA pseudogene	601459570F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3863177 5'	601459570F1 NIH_MGC_68 Forno sapiens cDNA clone IMAGE:3863177 5'	Crithidia fasciculata 27 kDa guide RNA-binding protein mRNA, complete cds; mitochondrial gene for mitochondrial product	tg55h07.x1 NCI_CGAP_Pr28 Homo sapiens cDNA clone IMAGE:2112733 3' similar to gb:X15183_cds1	HEAT SHOCK PROTEIN HSP 90-ALPHA (HUMAN); contains Alu repetitive element; contains element MER5	repetitive element;	AV760016 MDS Homo capiens cDNA clone MDSBDC10 5'	SPLICEOSOME ASSOCIATED PROTEIN 62 (SAP 62) (SPLICING FACTOR 3A SUBUNIT 2) (SF3A66)	RC2-DT0007-120200-016-h02 DT0007 Homo saplens cDNA	Homo sapiens renal dipeptidase (RDP) gene, complete cds	Mus musculus genomic fragment, 279 Kb, chromosome 7	H. saplens gene for Me491/CD63 antigen	wh42f09.x1 NCI_CGAP_Kid11 Homo sepiens cDNA clone IMAGE:2383433 3' similar to contains element	MENTAL INTENTAL INTENTION OF THE PROPERTY OF THE PROPERTY OF STATES OF THE PROPERTY OF STATES OF THE PROPERTY OF STATES OF THE PROPERTY OF STATES OF THE PROPERTY OF STATES OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE 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ANTIGEN)	COLLAGEN ALPHA 1(V) CHAIN PRECURSOR
C EAULI FIOD	Top Hit Database Source	TN	L'N	EST_HUMAN	EST_HUMAN	TN	EST_HUMAN	EST_HUMAN	LV			EST_HUMAN	EST HUMAN	SWISSPROT	EST_HUMAN	NT	ΙΝ	뒫	141111111111111111111111111111111111111	TOT HOMAN	ESI HUMAN	I LOU	EST HUMAN	FZ	EST HUMAN	EST_HUMAN	EST HUMAN	LN TN	EST HUMAN		NT	SWISSPROT	SWISSPROT
919	Top Hit Acession No.	1.0E-02 AF309388.1	1.0E-02 AF257303.1	1.0E-02 AW577113.1	1.0E-02 AW577113.1	229642.1	1.0E-02 BF036331.1	1.0E-02 BF036331.1	1.0F-02 AF157559.1		:	1.0E-02 AI417961.1	1.0E-02 AV760016.1	262203	1.0E-02 AW935521.1	570330.1	1.0E-02 AJ276505.1	X62654.1		9.0E-03 AI/96126.1	9.0E-03 BE781889.1	9.0E-03 ALT61559.2	9.0E-03 AI251 / 44.1		-	9.0E-03 BE745988.1	9.0E-03 AI242219.1	8922570 NT	9.0E-03 AL039991.1		9.0E-03 AF223391.1	P26011	P20908
	Most Similar (Top) Hit BLAST E Value	1.0E-02	1.0E-02	1.0E-02/	1.0E-02	1.0E-02 229642.1	1.0E-02	1.0E-02	1.05-02			1.0E-02/	1.0E-02	1.0E-02 Q62203	1.0E-02	1.0E-02 S70330.1	1.0E-02/	1.0E-02 X62654.1	200	9.0E-03	9.0E-03	9.05-03	9.0E-03/	9.0E-03 J05184.1	9.0E-03 /	9.0E-03	9.0E-03	9.0E-03	9.0E-03		9.0E-03/	9.0E-03 P26011	9.0E-03 P20908
	Expression Signal	99'0	1.29	2.78	2.78	1.69	6.34	6.34	212			1.7	1.95	1.76	3.58	4.31	1.4	2.91		9.69	1.56	12.04	280	99.0	1.19	4.01	0.61	0.91	0.8		0.54	0.54	1.47
	ORF SEQ ID NO:	32362	32764	32836		33646	36219	36220					38420		31762					27136		28721	29165				34169	34188			1	36690	
l	Exen SEQ ID NO:	19055	19416	19482	l	20216	22648	22648	24598	1		24628	24728	26206	25941	26002	25974	26060	i	-1	14449	15596	16147	1	ı		20693		21142	l			23104
	Probe SEQ ID NO:	5865	6242	6310	6310	690	9598	9593	11542			11573	11649	12278	12339	12355	12764	12949		916	1293	2469	702	3758	5931	6788	7623	7640	8059		8443	10050	10066

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Top Hit Descriptor	Homo sapiens NF2 gene	Homo sapiens preprogalanin (GAL1) gene, exons 1, 2, and 3	Homo sapiens preprogalarin (GAL1) gene, excns 1, 2, and 3	PM1-HT0452-291299-001-e09 HT0452 Homo saplens cDNA	hw/17b09.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3183161 3	Homo sapiens chromosome 21 segment HS21C067	PM1-HT0452-291299-001-e09 HT0452 Homo saplens cDNA	zh30e03.s1 Soares_pineal_gland_N3HPG Homo sapiens cDNA clone IMAGE:413590 3 similar to contains. Alu repetitive element;	Homo sapiens adenylosuccinate lyase gene, complete cds	Hamo sapiens chromosame 21 segment HS210083	RETROVIRUS-RELATED POL POLYPROTEIN (CONTAINS: REVERSE TRANSCRIPTASE; FINDONI ICLEASE)	AD CITY CONTROL OF THE	HOMO SAPIENS OLL BEITE IONES  INTERPRESSIONE  INTERPRESSIONE  INTERPRESSIONE  INTERPRESSIONE  INTERPRESSIONE  INTERPRESSIONE  INTERPRESSIONE  INTERPRESSIONE  INTERPRESSIONE  INTERPRESSIONE  INTERPRESSIONE  INTERPRESSIONE  INTERPRESSIONE  INTERPRESSIONE  INTERPRESSIONE  INTERPRESSIONE  INTERPRESSIONE  INTERPRESSIONE  INTERPRESSIONE  INTERPRESSIONE  INTERPRESSIONE  INTERPRESSIONE  INTERPRESSIONE  INTERPRESSIONE  INTERPRESSIONE  INTERPRESSIONE  INTERPRESSIONE  INTERPRESSIONE  INTERPRESSIONE  INTERPRESSIONE  INTERPRESSIONE  INTERPRESSIONE  INTERPRESSIONE  INTERPRESSIONE  INTERPRESSIONE  INTERPRESSIONE  INTERPRESSIONE  INTERPRESSIONE  INTERPRESSIONE  INTERPRESSIONE  INTERPRESSIONE  INTERPRESSIONE  INTERPRESSIONE  INTERPRESSIONE  INTERPRESSIONE  INTERPRESSIONE  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genome. (Closely related to SV40.)	A californica (marine gastropod mollusc) neuropeptide gene (bag ceil), exon 1, 5 end	Tursiops truncatus mRNA for p40-phox, complete cds	BASEMENT MEMBRANE-SPECIFIC HEPARAN SULFATE PROTEOGLYCAN CORE PROTEIN	PRECURSOR (HSPG) (PERLECAN) (PLC)	MR1-ST0111-111199-011-h06 ST0111 Homo sapiens CDNA	Mus musculus fusion 2 (human) (Fus2), mRNA	QV1-BT0677-040400-131-g03 BT0677 Hamo sapiens GUNA
Top Hit Database Source	H	ㅂ	H		EST HUMAN h		EST_HUMAN P	EST HUMAN	1		TOGGGGG	DAPAGI	Т		╗	7	П		SWISSPROT						SWISSPROT		LN	L <sub>N</sub>			EST_HUMAN		EST_HUMAN
Top Hit Acession No.					9.0E-03 BE348385.1	9.0E-03 AL183267.2	9.0E-03 BF351141.1	2 OE 03 4 4 7 23007 1				Ţ	16.1	32644	32644	8.0E-03 BE840049.1	8.0E-03 BF363327.1			261.1			8.0E-03 AF110520.1	8.0E-03 AP000002.1	P55577	8.0E-03 V01109.1	8.0E-03 M17197.1	8.0E-03 AB038267.1		P98160	8.0E-03 AW808692.1	9789956 NT	8.0E-03 BE086509.1
Most Similar (Top) Hit BLASTE Value	9.0E-03 Y18000.1	9.0E-03 L11144.1	9.0E-03 L11144.1	9.0E-03 B	9.0E-03 B	9.0E-03	9.0E-03	7 20 30 8	8.0E-03/	8 0F-03 /		8.05-03 P10200	8.0E-03 /	8.0E-03 P32644	8.0E-03 P32644	8.0E-03	8.0E-03	8.0E-03 P03181	8.0E-03 P03181	8.0E-03			8.0E-03	8.0E-03	8.0E-03 P55577	8.0E-03	8.0E-03	8.0E-03		8.0E-03 P98160	8.0E-03	8.0E-03	
Expression Signal	1.68	1.31	1.31	207	37.58	1.21	17.6	4	12.69	1 87		3.05	1.02	1.81	1.81	1.15	5.73	9.63	0.63	0.94			2.8	1.27	4.4	1.06	1.43	1.8		0.64			4.75
ORF SEQ ID NO:		38638	38639			32016			1	28480	601	28853	29628	29930	29931	30495		30961					31911	32857			33898			35707	L		
Exon SEQ ID NO:	24301	1	24937	L	1	1		i	ı	1	1	15741		16927	16927	17515	L	┖	1	1	1_		18834	25823	ı	L			1	22163	L	L	1
Probe SEQ ID NO:	11232	11951	11951	12494	12722	12838	13074		4014	2000	837	2617	3442	3766	3766	4372	4502	4839	4839	5271			5640	6328	6889	7059	7357	7744		9084	9111	9180	10154

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Top Hit Descriptor	601475619F1 NIH_MGC_68 Homo saplens cDNA clone IMAGE:3878405 5'	S.cerevisiae chromosome X reading trame OKF YUK I 52W	od80809.s1 NCI_CGAP_Ov2 Homo sapiens cDNA clone IMAGE:13/4232	od80aD9.s1 NCI_CGAP_Ov2 Homo saplens cDNA clone IMAGE:13/4232	Homo sapiens melanoma-associated antigen (MAGE-C1) gene, complete cas	Oryctolagus cuniculus elF-2a kinase mRNA, complete cds	Homo sapiens ABCG1 gene for ABC transporter (ATP-binding cassette, sub-family G (W HI I E), memoer 1), complete cds	qm55c09.x1 Soares_placenta_8tc8weeks_2NbHP8tc8W Homo sapiens cDNA clone IMAGE:1892752 3'	Cryptosportdium parwum HC-10 gene, complete cds	Cryptosporidium parvum HC-10 gene, complete cds	Glycine max glutathione S-transferase GST 21 mRNA, partial cds	AV731712 HTF Homo sapiens cDNA clone HTFAZF10 5	FORKHEAD BOX PROTEIN D3 (HNF3/FH TRANSCRIPTION FACTOR GENESIS) (HEFA I OCT I E NUCLEAR FACTOR 3 FORKHEAD HOMOLOG 2) (HFH-2)	ab79b09.s1 Stratagene fetal refina 937202 Homo sapiens cDNA clone IMAGE:853149 3	x/21b02.x1 Scares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2813739 3	HISTIDINE-RICH GLYCOPROTEIN PRECURSOR	rm37h07.x1 NCI_CGAP_Kid11 Homo sapiens cDNA done IMAGE:3032989 3' similar to contains Alu	repetitive element	473402.X1 Society Wasts, NHT Homo septems curve duri in the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contractio	ULH-Elia-akb-6-10-0-10.st NCI CGAP Supp name sapens cours managers.	Rattus norvegicus neuronal nicotinic acetylchollne receptor subunit (Alpha10) mRNA, complete cds	UI-H-Bi3-akb-o-10-0-UI.s1 NCI_CGAP_Sub5 Homo sapiens cUNA cione IMAGE:2733091 3	hh89a05.y1 NCI_CGAP_GU1 Homo sapiens cDNA clone IMAGE::2969936 5	Homo sapiens chromosome 21 segment HS21C078	y82g01.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:2118Z4 5 similar to gb:X14723 CLUSTERIN PRECURSOR (HUMAN);	RC1-CT0286-050400-018-c08 CT0286 Homo sepiens cDNA	2d33f10,r1 Soares_fetal_heart_NbHH19W Home sapiens GUNA clone iMAGE:342473.3	EST30674 Colon I Hamo sapiens CUINA 3 end
Top Hit Database Source	T HUMAN	╗		L HUMAN		NT	NT	EST_HUMAN	Ę	¥	NT	EST_HUMAN	SWISSPROT	EST HUMAN	П	SWISSPROT				EST_HUMAN	TN	EST_HUMAN	EST_HUMAN	N	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN
Top Hit Acession No.	8.0E-03 BE788441.1	8.0E-03 Z49652.1	8.0E-03 AA828817.1	8.0E-03 AA828817.1	8.0E-03 AF064589.1	8.0E-03 M69035.1	8.0E-03 AB038161.1	8.0E-03 AI277806.1	7.0E-03 AF097183.1	7.0E-03 AF097183.1	7.0E-03 AF243376.1	7.0E-03 AV731712.1	Q61060	7.0E-03 AA668298.1	7.0E-03 AW303599.1	7.0E-03 P04929		7.0E-03 AW,772132.1	7.0E-03 AI150273.1	7.0E-03 AW 444463.1	7.0E-03 AF196344.1	7.0E-03 AW 444463.1	7.0E-03 AW630888.1	7.0E-03 AL163278.2	7.0E-03 H71106.1	7.0E-03 AW861059.1	7.0E-03 W68251.1	7.0E-03 AA327129.1
Most Similar (Top) Hit BLAST E Value	8.0E-03	8.0E-03	8.0E-03	8.0E-03	8.0E-03	8.0E-03	8.0E-03	8.0E-03	7.0E-03			7.0E-03	7,0E-03 Q61060	7.0E-03	7.0E-03	7.0E-03		7.0E-03	7.0E-03	7.0E-03		7.0E-03						
Expression Signal	201	2.79	1.39	1.39	4.37	1.89	7.14	1.16	12.35	12.35	3.26	3.55	1.03	3.39	3.28	2		0.98	0.65	0.71	1.13	0.77	0.98	6.54	0.72	4.42		2.92
ORF SEQ ID NO:	37721		38433		Ĺ				26930		27231			27653					29824	30022	30071							33213
Exon SEQ ID NO:	24084	24300		L	l	1.		l	1			L	1	ı	1	1	<u> 1</u>	15815	16811	17023	17073	L		L	l	1		7 19826
Probe SEQ ID NO:	11005	11231	11683	11663	12015	12205	12252	13145	712	712	666	1140	1395	1426	1532	2332		2692	3648	3863	3914	4128	4721	6103	5940	6238	6444	6667

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	113387 ient ;									lar to contains										llar to contains											
Top Hit Descriptor	7g34b10.x1 NCI_CGAP_Bm23 Homo sapiens cDNA clone IMAGE:3308347 3' similar to TR:Q13387 Q13387 HYPOTHETICAL PROTEIN 384D8_2 ;contains TAR1.t2 TAR1 TAR1 repetitive element ;	CM2-CT0478-230800-347-b11 CT0478 Homo sapiens cDNA	S cerevisiae chromosome II reading frame ORF YBL077w	S.cerevisiae chromosome II reading frame ORF YBL077w	Homo capiens 959 kb contig between AML1 and CBR1 on chromosome 21q22, segment 3/3	Homo sapiens 959 kb contig between AML1 and CBR1 on chromosoms 21q22, segment 3/3	RC5-HT0582-160300-011-D02 HT0582 Homo sapiens cDNA	Homo sapiens neuropilin 2 (NRP2) gene, complete cds, alternatively spliced	Homo sapiens serine palmitoy/ transferase, subunit II gene, complete cds; and unknown genes	yy49c10.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:246066 3' similar to contains	Alu repetitive element;	BETA-GALACTOSIDASE PRECURSOR (LACTASE)	BETA-GALACTOSIDASE PRECURSOR (LACTASE)	AV687379 GKC Homo sapiens cDNA clone GKCAFC07 5'	wc37e09.x1 NCI_CGAP_Pr28 Homo sepiens cDNA clone IMAGE:2320840 3'	PM3-HT0344-181199-002-g06 HT0344 Homo sapiens cDNA	Bos taurus mRNA for NDP52, complete cds	Homo sapiens partial MUC5B gene, exon 1-29	Homo sapiens partial MUC5B gene, exon 1-29	w/5h01.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA cione IMAGE:242833 3' similar to contains	Alu repetitive element;	601145154F2 NIH MGC 19 Homo sapiens cDNA clone IMAGE:3160476 6	Homo sapiens LSFR2 gene, penultimate exon	Homo sapiens chromosome 21 segment HS21C100	hd22a05x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2910224 3' similar to swbyp Himan Orsaso ORPHAN NIICI FAR RECEPTOR PXR	STATE OF THE TOTAL OF THE TOTAL STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE	hd22a05.X1 Sogres_NFL_1_G50_S1 nom0 septems CUNA COTE MAGE.2910224 5 SILIMATE SW.PXR HUMAN 075469 ORPHAN NUCLEAR RECEPTOR PXR;	Danio rerio odorant receptor gene cluster	ah78e11.s1 Sogres, testis_NHT Homo sapiens cDNA clone 1321772 3'	ah78e11.s1 Soares_testis_NHT Homo sapiens cDNA clone 1321772 3'	yr7th04.r1 Scares fetal liver spleen 1NFLS Homo sepiens cDNA clone IMAGE:211351 5
Top Hit Database Source	EST_HUMAN	EST_HUMAN	NT	NT	NT	IN	EST_HUMAN	LN	ΙN		EST HUMAN	SWISSPROT	SWISSPROT	EST_HUMAN	EST_HUMAN	EST HUMAN	TN	LΝ	LN L		EST HUMAN	EST_HUMAN	NT	TN	, LONG	באורושוטוב וכש	EST HUMAN	N.	EST HUMAN	EST_HUMAN	EST HUMAN
Top Hit Acession No.	7.0E-03 BE857385.1	7.0E-03 BE928133.1	235838.1	235838.1	7.0E-03 AJ229043.1	7.0E-03 AJ229043.1	7.0E-03 BE175667.1	7.0E-03 AF281074.1	7.0E-03 AF111168.2		7.0E-03 N52378.1	P48982	P48982	7.0E-03 AV687379.1	7.0E-03 AI 799734.1	7.0E-03 BE154643.1	7.0E-03 AB008852.1	7.0E-03 AJ004862.1	7.0E-03 AJ004862.1		7.0E-03 H94065.1	7.0E-03 BE263253.1	7.0E-03 Y17455.1	7.0E-03 AL163300.2	A.M. C. A. A. A. A. A. A. A. A. A. A. A. A. A.	6.0E-U3 AW 311146.1	6.0F-03 AW511148.1	8.0E-03 AF112374.1	6.0E-03 AA759135.1	6.0E-03 AA759135.1	6.0E-03 H75690.1
Most Similar (Top) Hit BLAST E Value	7.0E-03	7.0E-03	7.0E-03 Z35838.1	7.0E-03 Z35838.1	7.0E-03	7.0E-03	7.0E-03	7.0E-03	7.0E-03		7.0E-03	7.0E-03 P48982	7.0E-03 P48982	7.0E-03	7.0E-03	7.0E-03	7.0E-03	7.0E-03	7.0E-03		7.0E-03	7.0E-03	7.0E-03	7.0E-03	L	6.0E-U3	6.0F-03	8.0E-03	6.0E-03	6.0E-03	6.0E-03
Expression Signal	1.05	1.93	4.78	4.78	0.59	69'0	2.48	0.58	0.64		0.68	2.72	2.72	1.34	0.82	0.47	2.41	1.55	1.55		1.95	1.46	1.76	1.68		α./ö	8 76	0.94	3 29	3.29	227
ORF SEQ ID NO:	33243	33550	34238	34239	34632		<u>.</u>						36549			37456		37838	L							2/494	27495		29147	L	Ш
Exen SEQ ID NO:	19853		20754	1	21114	21114	21384	21892	22652		22834	22961	22981		L		24141	L	24212			25534	1	<u> </u>		1442/	14427	1	1	1	I i
Probe SEQ ID NO:	9699	7228	7689	7689	8831	8031	8302	8813	9597		9794	9921	9921	10513	10704	10800	11065	11140	11140		12792	12800	12908	13058		1269	1260	2831	300	2956	3318

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	Top Hit Descriptor	Notoricus sp. cytochrome c oxidese subunit II gene, partial cds; mitochondrial gene for mitochondrial product	Fugu rubripes zinc finger protein, isotocin, fatty acid binding protein, sepiapterin reductase and vasotocin genes, complete cds	Fugu rubripes zinc finger protein, isotocin, fatty acid binding protein, seplapterin reductase and vasotocin	genes, complete eds	2513a11.r1 Soares_parathyroid_turnor_NbHPA Homo sapiens cDNA clone IMAGE:3221725	UI-H-BI4-apm-c-06-0-UI:s1 NCI_CGAP_Sub8 Homo saplens cDNA clone IMAGE:3087754 3	Mus musculus glucosamine-6-phosphate deaminase (Gnpi), mRNA	RC0-CT0204-240999-021-b10 CT0204 Homo sapiens cDNA	600942904F1 NIH_MGC_15 Homo saptens cDNA clone IMAGE:2959513 5	ov33c11.x1 Soares_testis_NHT Homo saplens cDNA clone IMAGE:1639124 3'	E3T27116 Cerebellum II Homo sapiens cDNA 5' end similar to EST containing Alu repeat	aj95g09.s1 Soares_parathyroid_tumor_NbHPA Homo sapiens cDNA clone IMAGE:1404256 31	Variola virus, complete genome	SYNAPSIN III	601112353F1 NIH_MGC_16 Homo saplens cDNA clone IMAGE:3353172 5'	EST11949 Uterus tumor I Homo sapiens cDNA 5' end	EST:11949 Uterus tumor i Homo sapiens cDNA 6 end	Homo saplens telomerase reverse transcriptase (TERT) gene, exons 7-16 and complete cds	ow13a04.x1 Soares_parathyrid_tumor_NbHPA Homo sapiens cDNA clone IMAGE:16466703' similar to	contains MERTIU. bit MERTIU repeatuve element ;	RCO-UMD051-210300-032-g0z Umd051 ngno saplens curo.	601454915F1 NIH_MGC_66 Homo sepiens cunA cione IMACE: 3006020 0	Subacute scienceing panencephalitis (SSPE) virus mRNA for fusion protein	igzzcoz.x1 NCI_CGAP_Kid11 Homo saplens cDNA clone IMAGE:2131202.3' similar to SW:K13A_HUMAN Bassas entrocomat procedural 1918 ·		Bacilius subtilis tenD gene	Home sapiens okadalc acid-inducible and cAMP-regulated phosphoprotein 19 (ARPP-19) mKNA, complete	cds	M thermoformicicum complete plasmid pFV1 DNA	Homo sapiens adlican mRNA, complete cds	EST374237 MAGE resequences, MAGG Homo sapiens cDNA	Homo seplens hypothetical zinc finger protein FLJ14011 (FLJ14011), mKNA
Top Hit	Database Source	ŢN	LN.		N	EST HUMAN	EST_HUMAN	NT	EST_HUMAN	EST HUMAN	EST HUMAN	EST_HUMAN	EST_HUMAN	LN	SWISSPROT	EST_HUMAN	EST_HUMAN	<b>EST_HUMAN</b>	NT		EST HOMAN	EST HUMAN	EST_HUMAN	N <sub>T</sub>	i i	EO HOMAN	N		NT	INT	TN	EST_HUMAN	¥
	l op hit Acession No.	5.0E-03 AF190338.1	3.0E-03 UD0880.1		3.0E-03 U90880.1	5.0E-03 W37985.1	6.0E-03 BF510986.1	6754029 NT	6.0E-03 AW 847284.1	6.0E-03 BE260108.1	5.0E-03 AI016833.1	5.0E-03 AA324242.1	6.0E-03 AA889972.1	9627521 NT	014994	6.0E-03 BE253748.1	6.0E-03 AA299442.1	6.0E-03 AA299442.1	6.0E-03 AF128894.1		6.0E-03 Al033980.1	_	6.0E-03 BF038198.1	6.0E-03 D10548.1			6.0E-03 AJ011849.1		6.0E-03 AF084555.1	6.0E-03 X68366.1	6.0E-03 AF245505.1	8.0E-03 AW962164.1	11545814 NT
	(10p) Hit BLAST E Vatue	6.0E-03	6.0E-03		6.0E-03	6.0E-03	6.0E-03	6.0E-03	6.0E-03	6.0E-03	6.0E-03	6.0E-03	6.0E-03	6.0E-03	6.0E-03 O14994	6.0E-03	6.0E-03	6.0E-03	ľ	ļ	6.0E-03	6.0E-03	6.0E-03	6.0E-03					6.0E-03	6.0E-03	6.0E-03		6.0E-03
	Signal	0.63	1.26		1.25	1.11	3.73	1.31	9.0	1.26	1.54	6.7	9.0	99.0	9.0	76.0	0.65	0.65	0.8			2.76	1.65	7.03		2.49	0.75		0.91	0.64	0.54	1,56	1.94
	ORF SEQ ID NO:		29655		29656			30034				30935	31392					33945	L			34763		36262			37011			37258		37697	
Exon	SEQ ID	16550	10636		16636	16800	16911	17036	17188	17223	17624	17950		L	L	L		20477	L_	ı			21318	22692	l		23400	L.	23538			24062	ı
Probe	SEQ ID NO:	3378	3460		3469	3836	3750	3877	4032	4067	4484	4817	5305	6281	6956	6994	7399	7399	7824		8042	8161	8236	9754		10249	10365		10603	10615	10861	10983	11049

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TOP HIS Delebase Source Not Muse musculus zho-finger protein mRNA, complete cds Not Muse musculus zho-finger protein mRNA, complete cds Not Muse musculus zho-finger protein mRNA, complete cds Not Muse musculus zho-finger protein mRNA, complete cds Not Morbanobacter una bernoaustar protein mRNA, done IMAGE:3889747 5  EST HUMAN MOSTORATE NIH_MOC_57 Harno sapiens cDNA done IMAGE:489271 27  Not Morbanobacter una bernoaustar popilicum from bases 429192 to 450296 (section 39 of 148) of the complete cds sympathy and complete cds sympathy and complete cds sympathy and complete complete cds sympathy and complete cds sympathy and complete cds sympathy and complete cds sympathy and complete cds sympathy and complete cds sympathy and complete cds sympathy and complete cds sympathy and complete cds sympathy and complete cds sympathy and complete cds sympathy and complete cds sympathy and complete cds sympathy and complete cds sympathy and complete cds sympathy and complete cds sympathy and complete cds sympathy and complete cds sympathy and complete cds sympathy and complete cds sympathy and complete cds sympathy and complete cds sympathy and complete cds sympathy and complete cds sympathy and complete cds sympathy and complete cds sympathy and complete cds sympathy and complete cds sympathy and complete cds sympathy and complete cds sympathy and complete cds sympathy and complete cds sympathy and complete cds sympathy and complete cds sympathy and complete cds sympathy and complete cds sympathy and complete cds sympathy and complete cds sympathy and complete cds sympathy and complete cds sympathy and complete cds sympathy and complete cds sympathy and complete cds sympathy and complete cds sympathy and complete cds sympathy and complete cds sympathy and complete cds sympathy and complete cds sympathy and complete cds sympathy and complete cds sympathy and complete cds sympathy and complete cds sympathy and complete cds sympathy and complete cds sympathy and complete cds sympathy and complete cds sympathy and complete cds s	TOP HIT PRESENCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE ST. 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Homo sapiens SCL gene locus	ž t	5.0E-03 038914.1 5.0E-03 A.1131016.1	_			-	4423
Citrus sinensis seed storage protein citrin mRNA, complete cds	IN	U38914.1		0.76		ı	442
VI/Y8010.11 Soares tetal liver spreen Tiving Saprens curva ciona invado.	EST_HUMAN	H78355.1					442
Natix domestica Zix typa gene	N.	AJ002125.1					454.
		AACSOOL O. I					4C.
EST12218 Uterus tumor I Homo sapiens cDNA 5' end		AA299875 1			L		,
Citrus sinensis seed storage protein citrin mRNA, complete ods	LZ LZ	U38914.1				1	3854
Pseudomonas aeruginosa strain PAO1 penicillin-binding protein 1B (ponts) gene, compirae cos	뇐	AF147449.2				١.	3790
Homo sapiens pertial LIMD1 gene for LIM domains containing protein i and N.K.A.Coo i gene	NT	AJ297357.1	L	0.84	-	1	335
1/86g02.61 Soares breast ZNbHbst Homo sapiens curvin trans invavor, robodoo	EST_HUMAN	R71794.1					3236
Arabidopsis thaliana DNA chromosome 4, contig tragment two. 3	Ŋ	AL161491.2		2.72		l	3223
yed/109.81 Soares infant Dienii Unio Truini Sapielis Curva crise infanticació	EST_HUMAN	T87623.1					3206
Agree C. 2008 Part Line Consistence (MACE 2020) 2	1	ADDOODOO.				- 1	2740
Home sapiens mRNA for KIAA1180 protein, partial cds	11	AD033008 4	L			1	
qd79d05.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1735689 3'	1.	Al138977.1					,
Arabidopsis theliane mRNA for DEAD box RNA helicase, KH3	۲	AJ010457.1	5.0E-03		L		1136
like protein, complete cds	NT	1.25105.1	ίĊ				687
Chlamydia trachomatis partial ORFB; aminoacyl-tRNA synthase, complete cds; complete OKFA, and grpE-						L	
like protein, complete cds	LNT	1.25105.1	5.0				687
Chlamydia trachomatis partial ORFB; aminoacyl-tRNA synthase, complete cds; complete ORFA, and grpE-					L	Ĺ	
like protein, complete cds	FZ	L25105.1	5.0	_			88
Chlamydia trachomatis partial ORFB; aminoacy/-tRNA synthase, complete ods; complete ORFA, and grpE-							
like protein, complete cds	N.	L25105.1	5.0				989
Chlamydia trachomatis partial ORFB; aminoacyf-tRNA synthase, complete cds; complete ORFA, and grpE-							
7n36b11.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3565664 3	<b>EST_HUMAN</b>	BF110298.1	9.0	1.19		<u> </u>	13147
R.norvegicus VEGP2 gene	LN	X74807.1	6.0E-03	1.61			13095
Brassica napus sig gene for S-locus glycoprotein, cultivar 1.2	NT	AJ245480.1	6.0E-03	2.41		ı	1294
SYNAPTONEMAL COMPLEX PROTEIN 1 (SCP-1 PROTEIN)	SWISSPROT	Q62209	6.0E-03	1.63		L	12590
Pneumocystis carinil f. sp. ratti guanine nucleotide binding protein alpha subunit (pcg1) gene, complete cds	NT	U30790.1		2.49			12532
						1	
genome	L	AE000833.1	6.0E-03	4.65			12451
1 COLUMN TO THE TANK OF THE TANK OF THE TANK OF THE TANK OF THE TANK OF THE COMPLETE	NICH TO INCIDIO	DF07 1 103.1	0.05-03	5.		-	12425
GOOMESONED MICH MCC 84 Homo content cONA done IMAGE-4292712 5	TO L		20.00	10.7		-	767
Rhodobacter capsulatus strain SB1003, partial genome	LZ		SOF-03		l	Ш.	133
601572746F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3839747 5	EST HUMAN	BE737895.1	6.0E-03			l.	11220
Mus musculus zinc-finger protein mRNA, complete ods	IN	U14556.1	6.0E-03	4.1			11228
	Source	ġ	Value	mußic	S S S S	ö	ö
Top Hit Descriptor	Top Hit Database	Top Hit Acession		Expression	ORF SEQ	Exon SEQ.ID	Probe SEQ ID
	Page I I I I I						

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	Top Hit Descriptor	on 16c02.x1 Normal Human Trabecular Bone Cells Homo sapiens cDNA clone NHTBC_cn15c02 random	Homo sapiens myosin-binding protein C, fast-type (MYBPC2) mKNA	SODIUM CHANNEL PROTEIN PARA (PARALYTIC PROTEIN)	PROBABLE UBIQUITIN CARBOXYL-TERMINAL HYDROLASE FAF-Y (UBIQUITIN THIOLESTERASE FAF-Y) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE FAF-Y) (DEUBIQUITIN-SPECIFIC BUZYME FAF- Y) (FAT FACETS PROTEIN RELATED, Y-LINKED) (UBIQUITIN-SPECIFIC PROTEASE 9, Y	CHROMOSOME)	Chlamydophila pneumonlae AR39, section 62 of 94 of the complete genome	600944564T1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:29608713	Mus musculus AMD1 gene for S-adenosylmethionine decarboxylase, complete cds	Tursiops truncatus mRNA for p40-phox, complete cds	Mus musculus dynein, axon, heavy chain 11 (Dnaho11), mRNA	EST03012 Fetal brain, Stratagene (cat#936206) Homo sapiens cDNA clone HFBCR93 similar to ESI	containing Alu repeat	RC3-CT0255-031099-011-f07 CT0255 Homo saplens cDNA	Homo sapiens MASL1 mRNA, complete cds	RCs-CT0281-081199-011-A05 CT0281 Homo saplens cDNA	RCs-CT0281-081199-011-A05 CT0281 Homo sapiens cDNA	BETA-GALACTOSIDASE PRECURSOR (LACTASE)	Mouse complement receptor (CR2) mKNA, 3 end	Escherichia coli genomic DNA. (19.1 - 19.4 min)	Rabbit utsroglobin (UGL) gene, exon 1	Piasmodium berghei 58 kDa phosphoprotein mKNA, partai cos	RC0-ST0379-210100-032-c02 ST0379 Homo sapiens cDNA	nj43h10.s1 NCI_CGAP_Prg Homo sapiens cDNA clone IMAGE:99558/	Homo sapiens PRO0471 protein (PRO0471), mKNA	ag49c10.s1 Gessler Wilms tumor Homo sapiens cDNA clone IMAGE:1120290 3	694F Heart Homo sepiens cDNA clone 694	xn59g05.x1 Soares_NHCeC_cervical_tumor Homo sapiens cDNA clone IMAGE:2698040 3' similar to	contains L1.t2 L1 repetitive element;	хл69g05,х1 Soares_NHCeC_cervical_tumor Homo sapiens cDNA clone IMAGE:zoso040 3 similar to contains L1.tz L1 repetitive element ;	Apple of Stratagene placenta (#937225) Homo sapiens cDNA clone IMAGE:70686 5	Doscott I Character Practice Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control
	Top Hit Database Source	7.1 EST_HUMAN G				SWISSPROT		EST_HUMAN 6	NT TN	TN	N LN	Г	EST HUMAN o	T HUMAN			EST_HUMAN R	SWISSPROT						EST_HUMAN n	IN	EST_HUMAN 8	EST_HUMAN 6	*	EST_HUMAN	EST HUMAN	Т	٦
,	Top Hit Acession No.	5.0E-03 AI752367.1				000507	5.0E-03 AE002234.2	5.0E-03 BE300091.1	5.0E-03 AB025024.1	5.0E-03 AB038267.1	6753651		5.0E-03 T05124.1	5.0E-03 AW854327.1	5.0E-03 AB016816.1	5.0E-03 AW855907.1	5.0E-03 AW855907.1	5.0E-03 P48982	5.0E-03 M61132.1	5.0E-03 D90723.1	5.0E-03 M25090.1	5.0E-03 L21710.1	5.0E-03 AW821888.1	5.0E-03 AA533143.1	7662557	5.0E-03 AA653261.1	5.0E-03 T19586.1		5.0E-03 AW170334.1	5 0F-03 AW170334.1	7,0450 4	5.0E-03 149153.1
	Most Similar (Top) Hit BLAST E Value	5.0E-03	5.0E-03	5.0E-03 P35500		5.0E-03 O00507	5.0E-03	5.0E-03	5.0E-03	5.0E-03	5.0E-03		5.0E-03	€.0E-03	5.0E-03	5.0E-03	5.0E-03	5.0E-03	5.0E-03	5.0E-03	5.0E-03	5.0E-03	5.0E-03	5.0E-03	5.0E-03	5.0E-03	5.0E-03		5.0E-03	5.05-03	10.5	5.0E-U3
-	Expression Signal	1.56	1.9	5.4		2.82	0.88	48.7	7.22	0.85	0.61		7.0	1.21	7.18			1.99			0.52		0.74				4.79		2.39	0.00		1.76
-	ORF SEQ ID NO:	30964		32417		32691			31520		33765	L	34198	L	34505			35045				_				١			37884			3 38004
	Exon SEQ ID NO:	17974	L	L.	l	19345	1	l	•	l			20722	L	1	i .	1	L	21890	L	1_	L	1	1	L	1_			24250	L		7 24363
	Probe SEQ ID NO:	4841	5286	5916		6169	6204	6726	9869	7185	7237		7654	7774	7944	8416	8415	8433	8811	9007	9140	10044	10176	10360	10539	10696	10050		11181	1 3	11181	11297

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Top Hit Descriptor	1248c04.yf NCI_CGAP_Bm52 Homo sapiens cDNA clone IMAGE:2291622 5	Mus musculus genomic fragment, 279 Kb, chromosome 7	Mus musculus genomic fragment, 279 Kb, chromosome 7	Galtus gallus glyceraldehyde-3-phosphate dehydrogenase mRNA, complete cds	Brugia malayi Y chromosome marker	Human pro-alpha1 type II collegen (COL2A1) gene exons 1-54, complete cds	zx75a03.s1 Soares overy tumor NbHOT Homo septens cDNA clone (MAGE:809548 3' similar to SW:DXA2_MOUSE P14685 PROBABLE DIPHENOL OXDASE A2 COMPONENT;	602077774F1 NIH_MGC_62 Homo sapiens cDNA clone IMAGE:4252002 5'	UI.H.BI3-akf-f-08-0-UI.s1 NCI_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2734215 3	UI-HF-BN0-akc-h-04-0-UI:1 NIH_MGC_50 Homb sapiens cDNA clone IMAGE:3076831 5'	yg51e04.s1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:35988 3'	PHOSPHATIDYLINOSITOL 3-KINASE 3 (PI3-KINASE) (PTDINS-3-KINASE) (PI3K)	on75g12.s1 Soares_NFL_T_GBC_S1 Homo sepiens cDNA clone IMAGE:1562566 3'	yg51e04.s1 Soares Infant brain 1NIB Homo sapiens cDNA clone IMAGE:35988 3'	RC3-BT0333-110100-012-f01 BT0333 Homo septens cDNA	z181a()8.r1 Stratagene colon (#937204) Homo sapiens cDNA clone IMAGE:510998 5	RC6-UM0014-170400-023-G01 UM0014 Hamo sepiens cDNA	zs59a01.r1 NCI_CGAP_GCB1 Homo saplens cDNA clone IMAGE:701/36 5	Rattus norvegicus type 1 astrocyle and offactory-limbic associated protein AT1-46 mRNA, complete cds	zl81a08.r1 Strategene colon (#937204) Homo sapiens cDNA clone IMAGE:510998 5	601304161F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3638510 5	RC6-UM0014-170400-023-G01 UM0014 Homo septens cDNA	Homo sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a), Ca2+/Calmodulin-dependent protein kinase I (CAMKI), creatine transporter (CRTR),	CDM protein (CDM), adrenoleukodystrophy protein >	Homo sepiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal	protein Lioa (NTLioa), Cazzycanicaemerachana in protein caracter (Crimic), coance caracter (Crimic), coance caracter (CDM) arterial adversation to rotein >	Hamo saciens polyalutamine-containing C140RF4 gene	Home canione milynithmine containing C140RF4 dene	Homo sepiens chromosome 21 segment HS21C084	PARA TEXASOR AND BOR MITORAL HAMA Services COMA	CALLA DI CALLA DE LA CALLA DE LA CALLA DE LA CALLA DE LA CALLA DE LA CALLA DE LA CALLA DE LA CALLA DE LA CALLA DE LA CALLA DE LA CALLA DE LA CALLA DE LA CALLA DE LA CALLA DE LA CALLA DE LA CALLA DE LA CALLA DE LA CALLA DE LA CALLA DE LA CALLA DE LA CALLA DE LA CALLA DE LA CALLA DE LA CALLA DE LA CALLA DE LA CALLA DE LA CALLA DE LA CALLA DE LA CALLA DE LA CALLA DE LA CALLA DE LA CALLA DE LA CALLA DE LA CALLA DE LA CALLA DE LA CALLA DE LA CALLA DE LA CALLA DE LA CALLA DE LA CALLA DE LA CALLA DE LA CALLA DE LA CALLA DE LA CALLA DE LA CALLA DE LA CALLA DE LA CALLA DE LA CALLA DE LA CALLA DE LA CALLA DE LA CALLA DE LA CALLA DEL CALLA DEL CALLA DE LA CALLA DE LA CALLA DE LA CALLA DEL CALLA DEL CALLA DEL CALLA DEL CALLA DEL CALLA DEL CALLA DEL CALLA DEL CALLA DEL CALLA DEL CALLA DEL CALLA DEL CALLA DEL CALLA DEL CALLA DEL CALLA DEL CALLA DEL CALLA DEL CALLA DEL CALLA DEL CALLA DEL CALLA DEL CALLA DEL CALLA DEL CALLA DEL CALLA DEL CALLA DEL CALLA DEL CALLA DEL CALLA DEL CALLA DEL CALLA DEL CALLA DEL CALLA DEL CALLA DEL CALLA DEL CALLA DEL CALLA DEL CALLA DEL CALLA DEL CALLA DEL CALLA DEL CALLA DEL CALLA DEL CALLA DEL CALLA DEL CALLA DEL CALLA DEL CALLA DEL CALLA DEL CALLA DEL CALLA DEL CALLA DEL CALLA DEL CALLA DEL CALLA DEL CALLA DEL CALLA DEL CALLA DEL CALLA DEL CALLA DEL CALLA DEL CALLA DEL CALLA DEL CALLA DEL CALLA DEL CALLA DEL CALLA DEL CALLA DEL CALLA DEL CALLA DEL CALLA DEL CALLA DEL CALLA DEL CALLA DEL CALLA DEL CALLA DEL CALLA DEL CALLA DEL CALLA DEL CALLA DEL CALLA DEL CALLA DEL CALLA DEL CALLA DEL CALLA DEL CALLA DEL CALLA DEL CALLA DEL CALLA DEL CALLA DEL CALLA DEL CALLA DEL CALLA DEL CALLA DEL CALLA DEL CALLA DEL CALLA DEL CALLA DEL CALLA DEL CALLA DEL CALLA DEL CALLA DEL CALLA DEL CALLA DEL CALLA DEL CALLA DEL CALLA DEL CALLA DEL CALLA DEL CALLA DEL CALLA DEL CALLA DEL CALLA DEL CALLA DEL CALLA DEL CALLA DEL CALLA DEL CALLA DEL CALLA DEL CALLA DEL CALLA DEL CALLA DEL CALLA DEL CALLA DEL CALLA DEL CALLA DEL CALLA DEL CALLA DEL CALLA DEL CALLA DEL CALLA DEL CALLA DEL CALLA DEL CALLA DEL CALLA DEL CALLA DEL
Top Hit Databese Source	EST_HUMAN	NT	NT	NT	NT	NT	EST_HUMAN	EST HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	SWISSPROT	EST_HUMAN	EST_HUMAN	EST HUMAN	EST HUMAN	EST_HUMAN	EST_HUMAN	INT	EST_HUMAN	EST_HUMAN	EST_HUMAN		<u>k</u>		H	į	1	Z Z	101	EST_HUMAN
Top Hit Acession No.	5.0E-03 BE048055.1	5.0E-03 AJ276505.1	5.0E-03 AJ276505.1	5.0E-03 AF047874.1	5.0E-03 AF067253.1	5.0E-03 L10347.1	5.0E-03 AA456597.1	5.0E-03 BF572332.1	5.0E-03 AW 449109.1	4.0E-03 AW 500196.1	4.0E-03 R45482.1	4.0E-03 P54675	4.0E-03 AAB39339.1	4.0E-03 R46482.1	4.0E-03 AW 749101.1	4.0E-03 AA099777.1	4.0E-03 AW 794740.1	4.0E-03 AA284374.1	4.0E-03 U33472.1	4.0E-03 AA099777.1	4.0E-03 BE410556.1	4.0E-03 AW794740.1		4.0E-03 U52111.2		4 05 00 150444 0	4.0E-03 0.02111.2	A 10-1000.	4.0E-03/AJZ///303.1	AL 103204.2	4.0E-03 BE154134.1
Most Similar (Top) Hit BLAST E Value	5.0E-03	5.0E-03	5.0E-03	5.0E-03	5.0E-03	5.0E-03	5.0E-03	5.0E-03	5.0E-03	4.0E-03	4.0E-03	4.0E-03	4.0E-03	4.0E-03	4.0E-03	4.0E-03	4.0E-03	4.0E-03	4.0E-03	4.0E-03	4.0E-03	4.0E-03		4.0E-03		200	20.4	3 2	4.0F-05	4.UE-02	4.0E-03
Expression Signal	3.41	1.4	4.1	11.86	21.79	2.03	1.94	5,99	2.66	1.54	1.75	1.36	4.37	1.65	2.85	34.06	1.83	1.48	2.68	17.33	2.08	1.53		1.95				2.97	2.97		1.09
ORF SEQ ID NO:			38760						31951							27393		27556	28026			28615		28875	L					28384	
Exen SEQ ID NO:	24666	1_	<u> </u>			25478	25504	L	L.	_	<u> </u>		$\mathbf{I}_{-}$	L	14109	14337	1	14488	14932	L	1	15483		15762	1			$\perp$			16471
Probe SEQ ID NO:	11615	12070	12070	12467	12616	12718	12760	12802	13002	242	334	456	919	86	934	1174	1196	1331	1783	2075	2321	2352	<u> </u> 	2639		_	6887 1	2/30	2755	2/61	3297

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Top Hit Descriptor	PM1-HT0340-151299-003-h08 HT0340 Homo saplens cDNA	xj98f04.x1 NCI_CGAP_Co18 Homo sapiens cDNA clone IMAGE:2665279 3'	xj98f04.x1 NCI_CGAP_Co18 Homo sapiens cDNA clone IMAGE:2665279 3'	OI. FACTORY RECEPTOR 511 (OLFACTORY RECEPTOR-LIKE PROTEIN OLF1)	OLFACTORY RECEPTOR 511 (OLFACTORY RECEPTOR-LIKE PROTEIN OLF1)	Mus musculus fumor susceptibility protein 101 (tag101) gene, complete cas	Homo sapiens TNNT1 gene, exons 1-11 (and joined CDS)	UI-HF-BNO-akj-e-10-0-UI.r1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3077466 5	Drosophila melanogaster anon2D7 (anon2D7) mRNA, complete cds	Rattus norvegicus beta-catenin binding protein mRNA, complete cds	(HPRG)	MAJOR SURFACE-LABELED TROPHOZOITE ANTIGEN PRECURSOR	DKFZp78111014_r1 761 (syncnym: hamy2) Homo sapiens cDNA clone DKFZp76111014 6	Rattus norvegicus opsin gene, complete cds	hg46c07.x1 NCI_CGAP_GC6 Homo saplens cDNA done IMAGE:2948652 31	601076015F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3461954 5'	ej32f11.s1 Soares_testis_NHT Homo sapiens cDNA clone 1392045 3'	Lycopersicon esculentum knotted 3 protein (TKn3) mRNA, complete cds	Homo sapiens chromosame 21 segment HS210078	Homo saplens chromosame 21 segment HS21C078	MUGIN 2 PRECURSOR (INTESTINAL MUCIN 2)	%37g12.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2271814 3	7e31b02.x1 NCI_CGAP_Lu24 Homo sepiens cDNA clone IMAGE:3284043 3'	H.saplens hcglX gene	ADAM-TS 5 (A DISINTEGRIN AND METALLOPROTEINASE WITH THROMBOSPONDIN MOTIFS 5)	Piete antelium dinamidalm AXA dandonment medela DE4127 (DE4127) mene martial cids	Activase in the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of th	Homo sapiens KIAAU345 gene product (KIAAU345), mr.v.A	Plasmodium falciparum replication factor C cubunit 1 (ric1) gene, complete cds	Homo sapiens P2X7 gene, exon 12 and 13	te49511.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2090013 3' similar to contains Alu	repetitive element;	Homo sapiens chromosome 21 segment HS21C009	Homo saplens chromosome 21 segment HS21C078
Top Hit Database Source	П				ISSPROT			EST_HUMAN					EST_HUMAN		EST_HUMAN		EST_HUMAN	NT	NT ·	TN			r HUMAN	NT	TOGGSSWIS	ion less				N		LHOMAN	N	
Top Hit Acession No.	4.0E-03 BE154134.1	4.0E-03 AW 188426.1	4.0E-03 AW 188426.1	Q13606	4.0E-03 Q13606	4.0E-03 AF060868.1				4.0E-03 AF169825.1	P04196		4.0E-03 AL133871.1		4.0E-03 AW 590572.1	4.0E-03 BE548453.1	4.0E-03 AA813222.1	4.0E-03 U76408.1	4.0E-03 AL163278,2	4.0E-03 AL163278.2	4.0E-03 Q02817	4.0E-03 AI681483.1	4.0E-03 BE670170.1	4.0E-03 X92109.1	100 00 107	781 187	AF11194	7662067 NT	4.0E-03 AF139827.1	4.0E-03 Y12855.1		4.0E-03 AI553983.1	4.0E-03 AL163209.2	4.0E-03 AL163278.2
Most Similar (Top) Hit BLAST E Value	4.0E-03	4.0E-03	4.0E-03	4.0E-03 Q13606	4.0E-03	4.0E-03	4.0E-03	4.0E-03	4.0E-03	4.0E-03	4.0E-03 P04196	4.0E-03 P21849	4.0E-03	4.0E-03	4.0E-03	4.0E-03	4.0E-03	4.0E-03	4.0E-03	4.0E-03	4.0E-03	4.0E-03	4.0E-03	4.0E-03	00 10 4	4.00-03	4.0E-U3	4.0E-03	4.0E-03	4.0E-03		1		
Expression Signal	1.09	0.83	0,83	0.64	0.05	0.72	2.18	96.0	1.58	27.24	3.1	1.8	8.0	4.18	76.0	1.78	1.07	1.41	1.12	1.12	3.73	0.96	0.62	0.85		70.0	4.51	2	29'0	0.51		7.06	3.24	
ORF SEQ ID NO:	29492	29798	29799	29880		30207			31564	31726	32416	32418			32892	32969			l											L		35529		35723
Exan SEQ ID NO:	16471	16783	16783	16875	16875	17196		18452		18713	19102		_	19384	19533	1_	L	_		L		L	乚	20758		- 1	1	21479	21745	21840	Ļ		22169	
Probe SEQ ID NO:	3297	3619	3619	3714	4021	4040	4102	6339	5390	5515	5914	5918	6003	6203	6363	6439	689	6914	7217	7217	7348	7589	7591	7693		8128	8238	8398	8865	8761		8911	0606	9100

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	. Top Hit Desariplar
4858	17991	30978	0.69		3.0E-03 AL119067.1	EST HUMAN	DKFZp761B0712_r1 761 (synonym: hamy2) Homo sapiens cDNA clone DKFZp761B0712.5
	1.						ab18a08.x5 Stratagene lung (#837210) Homo sapiens cDNA clone IMAGE:841142.3' similar to contains Alu
4955	18085	31061	2.05			EST_HUMAN	repetitive element;
4978	18107	31083	5:53		3.0E-03 BE787946.1	EST_HUMAN	601482715F1 NIH_MGC_68 Homo saplens cDINA cione IMAGE:3839463 3
5255		L	6.0	3.0E-03	4506414 NT	NT	Homo sapiens RAP1, GTPase activating protein 1 (RAP1GA1) mRNA
5255	ı		0.9	3.0E-03	4506414 NT	N	Homo sapiens RAP1, GTPase activating protein 1 (RAP1GA1) mRNA
							qe80bf0.xt Soares_fetal_lung_NbHL19W Homo saplens cDNA clone IMAGE:1745275 3' similar to
5262	18381	31347	1.75		3.0E-03 AI193860.1	EST_HUMAN	SW:APT/_MOUSE QUOSEO CLATTRIN COAT ASSEMBLE PROTEIN ALL COMMENS MICH.
5380	1				8922499 NT	FZ	Homo sapiens hypothetical protein FLJ10539 (FLJ10539), mRNA
5673	L	32153			3.0E-03 AJ249981.1	Ϋ́	Mus musculus mRNA for hypothetical protein (ORF2 ortholog)
	1				100000	ŢŅ	Mus musculus H2-M alpha chain (H2-Ma) gene, H2-M beta 2 chain (H2-Mb2) gene, H2-M beta 1 chain (H2- Mh3) nene Iow molecular weight protein 2 Lmp2 (Lmp2) gene, complete cds
5744	ı			Ì	1033323.1	TOT LOUGH	2913410 rt Sories NhHMPt, St Home saniens cDNA clone IMAGE:813163 5
9683	- [	33231	9.72	$\perp$	3.0E-03 AA456/01.1	NA POINTS	Fugu rubripes mRNA for sodium channel alpha subunit, partial cds
8	-1				, ,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,	H	Kluvermunes mandanus nord3 dene for purine-cytosine permease
7354	- [				3.0E-03 AJ011419.1	z ł	Own setting cane for hZIP protein complete cds
7691	_1		"		3.0E-03 AB021 /38.1	Į.	LIVER BUTTO BUTTO STORE OF THE TOTAL OF THE STORE OF THE STORE OF THE STORE OF THE STORE OF THE STORE OF THE STORE OF THE STORE OF THE STORE OF THE STORE OF THE STORE OF THE STORE OF THE STORE OF THE STORE OF THE STORE OF THE STORE OF THE STORE OF THE STORE OF THE STORE OF THE STORE OF THE STORE OF THE STORE OF THE STORE OF THE STORE OF THE STORE OF THE STORE OF THE STORE OF THE STORE OF THE STORE OF THE STORE OF THE STORE OF THE STORE OF THE STORE OF THE STORE OF THE STORE OF THE STORE OF THE STORE OF THE STORE OF THE STORE OF THE STORE OF THE STORE OF THE STORE OF THE STORE OF THE STORE OF THE STORE OF THE STORE OF THE STORE OF THE STORE OF THE STORE OF THE STORE OF THE STORE OF THE STORE OF THE STORE OF THE STORE OF THE STORE OF THE STORE OF THE STORE OF THE STORE OF THE STORE OF THE STORE OF THE STORE OF THE STORE OF THE STORE OF THE STORE OF THE STORE OF THE STORE OF THE STORE OF THE STORE OF THE STORE OF THE STORE OF THE STORE OF THE STORE OF THE STORE OF THE STORE OF THE STORE OF THE STORE OF THE STORE OF THE STORE OF THE STORE OF THE STORE OF THE STORE OF THE STORE OF THE STORE OF THE STORE OF THE STORE OF THE STORE OF THE STORE OF THE STORE OF THE STORE OF THE STORE OF THE STORE OF THE STORE OF THE STORE OF THE STORE OF THE STORE OF THE STORE OF THE STORE OF THE STORE OF THE STORE OF THE STORE OF THE STORE OF THE STORE OF THE STORE OF THE STORE OF THE STORE OF THE STORE OF THE STORE OF THE STORE OF THE STORE OF THE STORE OF THE STORE OF THE STORE OF THE STORE OF THE STORE OF THE STORE OF THE STORE OF THE STORE OF THE STORE OF THE STORE OF THE STORE OF THE STORE OF THE STORE OF THE STORE OF THE STORE OF THE STORE OF THE STORE OF THE STORE OF THE STORE OF THE STORE OF THE STORE OF THE STORE OF THE STORE OF THE STORE OF THE STORE OF THE STORE OF THE STORE OF THE STORE OF THE STORE OF THE STORE OF THE STORE OF THE STORE OF THE STORE OF THE STORE OF THE STORE OF THE STORE OF THE STORE OF THE STORE OF THE STORE OF THE STORE OF THE STORE OF THE STORE OF THE STORE OF THE STORE OF THE STORE OF THE STORE OF THE
8124		34726			3.0E-03 BF333058.1	EST_HUMAN	KCU-BIUGIZ-COUSUC-USZ-SVI BIUGIZ HUMB SAPISIS CLI CO
8124			0.9		3.0E-03 BF333058.1	EST_HUMAN	RC0-B10812-250900-052-e0/ B10612 nome sapiens colors
8350	L.	34955	1.4		3.0E-03 N92580.1	EST_HUMAN	2b27b04.s1 Soarces parathyroid tumor Northy Horno saprement of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the
8490		35108	0.47		3.0E-03 AI866028.1	EST_HUMAN	w/2409.x1 NCI_CGAP_U11 Hamo sapiens cUNA date IMMCE. 2423041 3
8510	21591	L	0.63		3.0E-03 M63498.1	NT	S.cerevidae UGA35 gene, complete cds
8655	1		1.34		3.0E-03 P51989	SWISSPROT	HETEROGENEOUS NUCLEAR RIBONUCLEOPRO JEIN AZ HOMOLOG I (HINRIN AZ A)
8679	ĺ	35295	1.5	_	3.0E-03 AL163268.2	NT	Home sapiens chromosome 21 segment HSZ1CUDS
8786	ĺ		1.45		3.0E-03 Q9QM81	SWISSPROT	NONSTRUCTURAL PROTEIN V
	1						hh80f10.x1 NCI_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2969131 3' similar to contains L1.t1 L1
9182	22270		10.8		3.0E-03 AW613774.1	EST_HUMAN	repetitive element;
9245	1	35866				Ā	Arebidopsis theliana DNA chromosome 4, contig fragment No. 85
	1				l		ov03d12.x1 NCI_CGAP_Ktd3 Homo sapiens cDNA done IMAGE:1636247 3' similar to gb:X57138_ma1
6926			96.6		3.0E-03 AI016731.1	EST_HUMAN	HISTONE H2B.2 (HUMAN);
9280	22358	35906			3.0E-03 BF338078.1	EST_HUMAN	G02035980F1 NCI_CGAP_Bm64 Homo sapiens cDNA clone IMAGE:4183938 5
OBO	1_	1	0.78		3.0E-03 D90901.1	ΙN	Synechocystis sp. PCC6803 complete genome, 3/27, 271600-402289
3009	1	34804		1	3 0E-03 BE154670.1	EST HUMAN	PM3-HT0344-071299-003-407 HT0344 Homo sapiens cDNA
£ 8	80017 C	١	2 2	1	3 0F 03 P03355	SWISSPROT	POL POLYPROTEIN [CONTAINS: PROTEASE; REVERSE TRANSCRIPTASE; RIBONUCLEASE H]
3854	- 1		2.2	١	ol Fusion	2000	

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	Top Hit Descriptor	CIRCUMSPOROZOITE PROTEIN PRECURSOR (CS)	RETROVIRUS-RELATED POL POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE; ENDONUCLEASE]	HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN A2 HOMOLOG 1 (HNRNP A2(A))	Homo sapiens chromosome 21 segment HS21C103	Homo sapiens ATP/GTP-blnding protein (HEAB), mRNA	Oryza sativa gene for bZIP protein, complete cds	SMALL PROLINE RICH PROTEIN II (SPR-II) (CLONE 930)	Homo sapiens golgin-like protein (GLP) gene, complete cds	Homo sapiens trinucleotide repeat DNA binding protein p20-060bP (CGCBP) gene, complete cus	Homo sapiens trinucleotide repeat DNA binding protein p20-C3GBP (CGGBP) gene, complete cas	RETROVIRUS-RELATED POL POLYPROTEIN (CONTAINS: REVERSE TRANSCRIP I ASE ; [ENDONUCLEASE]	UI-H-BI2-ahi-d-06-0-UI.s1 NCI_CGAP_Sub4 Homo sapiens cDNA clone IMAGE:2726842 3'	promma-5.E07.r bivumor Homo sapiens cDNA 5'	077b10.s1 Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:1622779 3' similar to	contains L1.t3 MER26 repetitive element;	Homo sapiens gene for CMP-N-acety/neuraminic acid hydroxy/ase, partial cds	Rettus norvegicus mRNA for connexin36 (cx36 gene)	RING CANAL PROTEIN (KELCH PROTEIN)	RING CANAL PROTEIN (KELCH PROTEIN)	yd15h03.r1 Soares fetal liver spleen 1NFLS Homo sapiens cUNA cione IMACE: 106341 5	Human alpha-2-plasmin inhibitor gene, exons 6 and 7	Inu86f01.s1 NCI_CGAP_Alv1 Homo sepiens cDNA clone IMAGE:1217393	Homo sapiens tumor-related protein URC2 (URC2) gene, complete cas	PLATELET-ENDOTHELIAL TETRASPAN ANTIGEN 3 (PETA:3) (GP27) (MEMBKANE GLYCOPROTEN  SFA-1) (QD151 ANTIGEN)	Homo sapiens procollagen-lysine, 2-exeglutarate 5-dioxygenase (lysine hydroxylase, Ehlers-Danlos syndrome	type VI) (PLOD) mRNA	Homo sapiens procollagen-lysine, 2-oxoglutarate 5-dioxygenase (lysine hydroxylase, Ehlers-Danlos syndrome	type VI) (PLOD) mRNA	COLLAGEN ALPHA 5(IV) CHAIN PRECURSOR	zx4za10.r1 Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:789114 5	CM2-HT0183-061099-018-d03 HT0183 Homo sapiens cDNA
	Top Hit Database Source	SWISSPROT	SWISSPROT	SWISSPROT	N	TN	NT	SWISSPROT	NT	N	NT.	SWISSPROT	EST HUMAN	EST HUMAN		EST HUMAN	NT	INT	SWISSPROT	SWISSPROT	EST_HUMAN	ΝΤ	EST_HUMAN	NT	TORISSIMS	200	LN S		NT	SWISSPROT	EST_HUMAN	EST HUMAN
	Top Hit Acession No.	208672	911369	51989	3.0E-03 AL 163303.2	5803028 NT	3.0E-03 AB021736.1	P22531	3.0E-03 AF266285.1	3.0E-03 AF094481.1	3.0E-03 AF094481.1	P11369	3.0F-03 AW 294812.1	3.0E-03 AI525056.1		3.0E-03 AA993154.1	3.0E-03 AB009668.1	3.0E-03 AJ296282.1	Q04652	Q04652	2.0E-03 T70874.1	2.0E-03 M20783.1	2.0E-03 AA661605.1	2.0E-03 AF284446.1	סעאמעם	encot 1	4557836 NT		4557836 NT	P29400	2.0E-03 AA450138.1	2.0E-03 BE144908.1
-	Most Similar (Top) Hit BLAST E Value	3.0E-03 P08672	3.0E-03 P11369	3.0E-03 P51989	3.0E-03/	3.0E-03	3.0E-03	3.0E-03 P22531	3.0E-03	3.0E-03	3.0E-03	3 0F-03 P11369	3.0F-03	3.0E-03		3.0E-03	3.0E-03	3.0E-03	2.0E-03 Q04652	2.0E-03 Q04652	2.0E-03	2.0E-03	20E-03	2.0E-03	00540 EV 30 C		2.0E-03	1				
	Expression Signal	6.51	2.31	1.44	3.89	2.67	1.45	1.47	1.9	2.52	2.52	1.36	1 46	1.62		1.24	1.76	1.23			11.88	2.08		20.85			2.20		2.26	6.17		
	ORF SEQ ID NO:		36738				34241		ŀ	38457	_		1			38346		32057		L			27626			7 7 7 7	27778		77777		28053	
	Exon SEQ ID NO:	22948		_	L		L	l	23918	24762	L	<u> </u>				25179	1_	$\mathbf{L}_{-}$	1_	1	ı	١.	<u> </u>	14560	1	146/2	14698	Ι.	14698	1	1.	1
	Probe SEQ ID NO:	8066	40,000	10200	10344	11085	11458	11722	11732	11770	11770	1040	13077	12189	200	12235	12296	12481	528	528	808	1394	1397	1406		1519	1546		1546	162	1811	1928

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Probe SEQ ID NO:	SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
2051	15192	28305		2.0E-03	2.0E-03 AF302691.1	NT	Mus musculus myelin expression factor-3-like protein gene, partial cds
2324		l	26.0	2.0E-03	2.0E-03 AL163302.2	IN	Homo sapiens chromosome 21 segment HS21C102
2647	15770	   		2.0E-03	2.0E-03 AW137782.1	EST_HUMAN	UI-H-BI1-adi-9-10-0-UI.s1 NCI_OGAP_Sub3 Homo sapiens oDNA clone IMAGE:2717010 3'
3503	L	29680		2.0E-03	AA450138.1	EST_HUMAN	zx42a10.r1 Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:789114 5'
3510				2.0E-03	2.0E-03 BF568955.1	EST_HUMAN	602183960T1 NIH_MGC_42 Homo sapiens cDNA clone IMAGE:4300070 3'
	l			300		Ŀ	H.sapiens DMA, DMB, HLA-Z1, IPP2, LMP2, TAP1, LMP7, TAP2, DOB, DQB2 and RING8, 9, 13 and 14
3756	- [			2.0E-03	2.0E-03 X87344.1	z	genies
4062	J			2.0E-03	2.0E-03 AB040802.1	Z	Katus novegicus intiva io streb i, complete con stress occurs no stress stress stress stress stress stress stress stress stress stress stress stress stress stress stress stress stress stress stress stress stress stress stress stress stress stress stress stress stress stress stress stress stress stress stress stress stress stress stress stress stress stress stress stress stress stress stress stress stress stress stress stress stress stress stress stress stress stress stress stress stress stress stress stress stress stress stress stress stress stress stress stress stress stress stress stress stress stress stress stress stress stress stress stress stress stress stress stress stress stress stress stress stress stress stress stress stress stress stress stress stress stress stress stress stress stress stress stress stress stress stress stress stress stress stress stress stress stress stress stress stress stress stress stress stress stress stress stress stress stress stress stress stress stress stress stress stress stress stress stress stress stress stress stress stress stress stress stress stress stress stress stress stress stress stress stress stress stress stress stress stress stress stress stress stress stress stress stress stress stress stress stress stress stress stress stress stress stress stress stress stress stress stress stress stress stress stress stress stress stress stress stress stress stress stress stress stress stress stress stress stress stress stress stress stress stress stress stress stress stress stress stress stress stress stress stress stress stress stress stress stress stress stress stress stress stress stress stress stress stress stress stress stress stress stress stress stress stress stress stress stress stress stress stress stress stress stress stress stress stress stress stress stress stress stress stress stress stress stress stress stress stress stress stress stress stress stress stress stress stress stress stress stress stress stress stress stress stress stress stress stress stress stress
4229	17376		2.39	2.0E-03 P03374	P03374	SWISSPROT	ENV POLYPROTEIN CONTAINS: COAT PROTEIN GPSZ; COAT PROTEIN GPSS]
4290	17435	30423	1.02	2.0E-03	2.0E-03 AA179693.1	EST_HUMAN	zp13h01.r1 Stratagene fetal retina 937202 Homo saptens cDNA cone IMACE:009361 5
4336			13.93	2.0E-03	2.0E-03 U68491.1	NT	Rattus norvegicus 5-hydroxydryptamine7 receptor gene, partial cds
4632			1.99	2.0E-03	2.0E-03 L35079.1	NT	Porcine rotavirus major outer capsid protein (VPT) mRNA, complete cds
4547			1.22	2.0E-03	2.0E-03 AW297380.1	EST_HUMAN	UI-H-BW 0-air-g-03-0-UI.s1 NCI_CGAP_Sub6 Homo sapiens cDNA clone IMAGE:2730413 3'
4551	Ļ	30670		2.0E-03	2.0E-03 AI064746.1	EST_HUMAN	HA0507 Human fetal liver cDNA library Homo saplens cDNA
4668	L	L		2.0E-03	2.0E-03 L42512.1	N	Drosophila melanogaster shortsighted class 2 (shs) mRNA, complete cds
4668	L	30791		2.0E-03	2.0E-03 L42512.1	N	Drosophila melanogaster shortsighted class 2 (shs) mRNA, complete cds
	L						Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively
4828	17961	30949	1.02		2.0E-03 AF223391.1	ΝΤ	paliced
4832	L.		1.57	2.0E-03	2.0E-03 R87773.1	EST_HUMAN	yo45e02.s1 Soares adult brain N2b4HB55Y Homo sapiens cDNA clone IMAGE:180890 3'
4962	18091	31067	1.07	2.0E-03 P11000	P11000	SWISSPROT	WALL-ASSOCIATED PROTEIN PRECURSOR
	1_						Homo sapieno X-linked anhidroitic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat
5132	18257	31223	0.84	2.0E-03	2.0E-03 AF003528.1	N⊤	regions
5604		31849		2.0E-03	2.0E-03 BF241410.1	<b>EST_HUMAN</b>	601876385F1 NIH_MGC_55 Homo saplens cDNA done IMAGE:4104692 5
5745	L.	ļ	1,88	2.0E-03	2.0E-03 AB014593.1	TN	Homo sapiens mRNA for KIAA0693 protein, partial ods
5828	L		2.08		2.0E-03 U63711.1	LN	Xenopus laevis xefiitin mRNA, complete cds
6236	L_				P23477	SWISSPROT	ATP-DEPENDENT NUCLEASE SUBUNIT B
6236	L		3.93		P23477	SWISSPROT	ATP-DEPENDENT NUCLEASE SUBUNIT B
6476	19643	L			2.0E-03 Q95203	SWISSPROT	CARBONIC ANHYDRASE-RELATED PROTEIN 2 PRECURSOR (CARP 2) (CA-RP II) (CA-XI)
6476	1				2.0E-03 Q95203	SWISSPROT	CARBONIC ANHYDRASE-RELATED PROTEIN 2 PRECURSOR (CARP 2) (CA-RP II) (CA-XI)
6478					2.0E-03 BF308187.1	EST_HUMAN	601887434F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4121408 5
							ADAM-TS 7 PRECURSOR (A DISINTEGRIN AND METALLOPROTEINASE WITH THROMBOSPONDIN
6514			. 2.16		2.0E-03 Q9UKP4	SWISSPROT	MOTIFS 7) (ADAMTS-7) (ADAM-TS7)
6515	1				2.0E-03 AV709075.1	EST HUMAN	AV709075 ADC Homo saplens cDNA clone ADCAEF09 6
6544	١.		1.45		2.0E-03 X94451.1	NT	L.esculentum mRNA for lysyl-tRNA synthetase (LysRS)

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	Top Hit Descriptor	wu36h09.x1 Soares_Dieckgraefe_colon_NHCD Homo sapiens cDNA clone IMAGE:2522177 3' similar to SW:RL29_HUMAN P47914 60S RIBOSOMAL PROTEIN L29 ;contains element MSR1 repetitive element ;	213a11.s1 Scares fetal liver splean_1NFLS_S1 Homo sepiens cDNA clone IMAGE:4306523	Connorhabditis elegans mRNA for galectin LEC-11, complete cds	CM4-BT0366-061299-054-d01 BT0366 Homo sepiens cDNA	qm99d11.x1 NCI_CGAP_Lu5 Homo seplens cDNA clone IMAGE:1896885 3	yd77g10.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:114306 5	PROTEOGLYCAN LINK PROTEIN PRECURSOR (CARTILAGE LINK PROTEIN) (LP)	h37b06x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE::2934035 3 similar to 1 K:Q90976 Q60976 JERKY: ;	yx42g06.s1 Soares melanocyte 2NbHM Homo capiens cDNA clone IMAGE:2644423' similar to contains	L1.b2 L1 repetitive element;	yx42g06.s1 Scares melanocyte 2NbHM Homo sapiens cDNA clone IMAGE:2644423' similar to contains	L1.b2.L1 repetitive element;	HYPOTHETICAL 32.8 KD PROTEIN C6G9.05 IN CHROMOSOME I	LAMININ ALPHA-1 CHAIN PRECURSOR (LAMININ A CHAIN)	Homo sapiens Retina-derived POU-domain factor-1 (RPF-1), mRNA	Homo sapiens Retina-derived POU-domain factor-1 (RPF-1), mKNA	AU136879 PLACE1 Homo sapiens cDNA clone PLACE1004839 5	Homo sapiens ASCL3 gene, CEGP1 gene, C11 arf14 gene, C11 arf15 gene, C11 arf16 gene and C11 arf17	gens	MR2-UM0025-300300-102-102 UM0020 Homo taptens curva	MR2-UM0025-300300-102-102 UM0025 Homo sapiens cUNA	Homo sapiens mannosidase, beta A, lysosomai (MANBA) gene, and ubiquiun-corijugaling elizyrine EZD o (1185/2031) cenes complete cits	2. Sources (et al liver scheen 1NFLS Homo sapiens cDNA clone IMAGE:194296 3.	Judgendo et Sonnes fedel litrer enleen 1NFI S Home saniens cDNA clone IMAGE:194296 3'	OCANOS I COMES I COMES I COMES I COMES I COMES I COMES I COMES I COMES I COMES I COMES I COMES I COMES I COMES I COMES I COMES I COMES I COMES I COMES I COMES I COMES I COMES I COMES I COMES I COMES I COMES I COMES I COMES I COMES I COMES I COMES I COMES I COMES I COMES I COMES I COMES I COMES I COMES I COMES I COMES I COMES I COMES I COMES I COMES I COMES I COMES I COMES I COMES I COMES I COMES I COMES I COMES I COMES I COMES I COMES I COMES I COMES I COMES I COMES I COMES I COMES I COMES I COMES I COMES I COMES I COMES I COMES I COMES I COMES I COMES I COMES I COMES I COMES I COMES I COMES I COMES I COMES I COMES I COMES I COMES I COMES I COMES I COMES I COMES I COMES I COMES I COMES I COMES I COMES I COMES I COMES I COMES I COMES I COMES I COMES I COMES I COMES I COMES I COMES I COMES I COMES I COMES I COMES I COMES I COMES I COMES I COMES I COMES I COMES I COMES I COMES I COMES I COMES I COMES I COMES I COMES I COMES I COMES I COMES I COMES I COMES I COMES I COMES I COMES I COMES I COMES I COMES I COMES I COMES I COMES I COMES I COMES I COMES I COMES I COMES I COMES I COMES I COMES I COMES I COMES I COMES I COMES I COMES I COMES I COMES I COMES I COMES I COMES I COMES I COMES I COMES I COMES I COMES I COMES I COMES I COMES I COMES I COMES I COMES I COMES I COMES I COMES I COMES I COMES I COMES I COMES I COMES I COMES I COMES I COMES I COMES I COMES I COMES I COMES I COMES I COMES I COMES I COMES I COMES I COMES I COMES I COMES I COMES I COMES I COMES I COMES I COMES I COMES I COMES I COMES I COMES I COMES I COMES I COMES I COMES I COMES I COMES I COMES I COMES I COMES I COMES I COMES I COMES I COMES I COMES I COMES I COMES I COMES I COMES I COMES I COMES I COMES I COMES I COMES I COMES I COMES I COMES I COMES I COMES I COMES I COMES I COMES I COMES I COMES I COMES I COMES I COMES I COMES I COMES I COMES I COMES I COMES I COMES I COMES I COMES I COMES I COMES I COMES I COMES I COMES I COMES I COMES I COMES I COMES I COMES I COMES I COMES I COMES I COMES I COMES I COMES I COMES I COMES I COMES I COMES I COMES	TENASCIN PRECURSOR (TN) (HEXABRACHION) (CYLOLACTIN) (NEURONECLIN) (GWEW) (47) (MIOTENDINOUS ANTIGEN) (GLIOMA-ASSOCIATED-EXTRACELLULAR MATRIX ANTIGEN) (GP 150-	225) (TENASCIN-C) (TN-C)	BETA-GALACTOSIDASE PRECURSOR (LACTASE)	BETA-GALACTOSIDASE PRECURSOR (LACTASE)	Homo saplens caspase recruitment domain-containing protein (BCL10) gene, complete cus
Single Lability See	. Top Hit Database Source		T_HUMAN	П		EST_HUMAN qn		SWISSPROT PF	EST HUMAN Q	Т	EST_HUMAN L1		٦		ISSPROT			T_HUMAN		٦	П	EST_HUMAN M	Ī	TUIMAN	Т	ES HOMAIN	<u> </u>	SWISSPROT 2	SWISSPROT B	ISSPROT	H H
Signio.	Top Hit Acession No.	2.0E-03 AI991089.1	2.0E-03 AA677831.1			2.0E-03 AI298883.1	1		2 0F-03 AW 592004.1	Γ	-					6005856 NT	W 55855 NT	2.0E-03 AU136679.1		7	٦	2.0E-03 AW 796111.1		2.0E-03 AF224003.1	1,2000,1	2.0E-03 H50832.1		P24821	P48982	P48982	2.0E-03 AF097732.1
	Most Similar (Top) Hit BLAST E Value	2.0E-03	2.0E-03	2.0E-03 /	2.0E-03	2.0E-03 /	2.0E-03	2.0E-03 P07354	2 0F-03		2.0E-03 N20287.1		2.0E-03 N20287.1	2.0E-03 Q92350	2.0E-03 P19137	2.0E-03	2.0E-03	2.0E-03		2.0E-03	2.0E-03	2.0E-03	L	2.00	2.05-03	2.0E-03		2.0E-03 P24821	2.0E-03 P48982	2.0E-03 P48982	2.0E-03
	Expression Signal	1.36	0.7	1.35	3.3	0.65	8.0	1.41	26.0		5.49		5.49	0.64	1,09	1.04	49.	1,03		6:0	0.79	62'0			0.7.1	0.71		3.33		١.	9.0
	ORF SEQ ID NO:		33326	31517	33554	33833	33994	34342	34840		35023		35024	35069	35097	35153	35164	35181	Ì.,							36363		38264	L.		36552
	Exon SEQ ID NO:	19892	19930	18525	20136	20376	20521	20850	21323		21493	١	21493	21540	21562	1	21617	1	L.	21694	19018	19018			┙	22791		22896		1	22964
	Probe SEQ ID NO:	6738	6775	2098	7231	7294	7444	7794	8241		8412		8412	8459	8481	8536	8536	8561		8614	9336	9396		9441	9726	9726		9758	9868	888	9924

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					)		
Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
3260	16434	29452	2.81	1.0E-03	.0E-03 P18915	SWISSPROT	CARBONIC ANHYDRASE VI PRECURSOR (CARBONATE DEHYDRATASE VI) (CA-VI) (SECRETED CARBONIC ANHYDRASE) (SALIVARY CARBONIC ANHYDRASE)
3374	İ		0.75		0E-03 P08547	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
3632	16796	20813	0.94	1.0E-03	.0E-03 U68061.1	ΤN	Human MUC2 gene, promoter reglan
3632	16796	29814	0.94	1.0E-03	1.0E-03/U68061.1	NT	Human MUC2 gene, promoter region
3755	ı		1.43	Ì	1.0E-03 AB044400.1	NT	Homo sapiens SVMT gene for synaptic vesicle monoamine transporter, exons 14, 15
4034		30200	0.98		.0E-03 AW170552.1	EST HUMAN	xn63d07.x1 Sogres_NHCeC_cervical_tumor Homo sapiens cDNA clone IMAGE:2698381 3' sImilar to contains TAR1.t1 TAR1 repetitive element;
4044	L				I.0E-03 Z49649.1	ΝŢ	S.cerevisiae chromosome X reading frame ORF YJR149w
4556		30673	2.34		.0E-03 BE939162.1	EST_HUMAN	RC1-TN0128-160800-021-901 TN0128 Homo saplens cDNA
4598	17735		; • •		.0E-03 BE246536.1	EST HUMAN	TCBAP1D4909 Pediatric pra-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA Homo sapiens cDNA clone TCBAP4909
4785	ì	30908			.0E-03 U29449.1	NT	Caenorhabditis elegans spiloed leader RNA (SL3 alpha), (SL4), and (SL5) genes
4945	18075				.0E-03 AI073485.1	EST_HUMAN	ov45c04.x1 Soares_testis_NHT Homo saplens cDNA clone IMAGE:1640262 3'
4945	18075	31051	2.54	,	1.0E-03 AI073485.1	EST_HUMAN	ov45c04.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1640262 3*
4946	18076		9	-	.0E-03 BE154067.1	EST_HUMAN	PM0-HT0339-200400-010-D02 HT0339 Homo sapiens aDNA
5188	18310		15.5	-	.0E-03   O46409	SWISSPROT	APOLIPOPROTEIN A-IV PRECURSOR (APO-AIV)
5324	18437		4.73	ļ	.0E-03 BE219340.1	EST_HUMAN	hv81f02.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3176955 31
5423	18624		2	1.0E-03	1.0E-03 AA290951.1	EST_HUMAN	284401.71 NCI_CGAP_GCB1 Homo capiens cDNA clone IMAGE:700345 5
5518	18716	31730	3.57	1.0E-03	1.0E-03 AJ006345.1	NT	Homo sapiens KVLQT1 gene
5572	18768			,	1.0E-03 K03332.1	LN L	Epstein-Barr virus (AG876 isolate) U2-R2 domain encoding nuclear protein EBNA2, complete cds
5572	18768			•	.0E-03 K03332.1	ΙN	Epstein-Barr virus (AG876 isolate) U2-IR2 domain encoding nuclear protein EBNA2, complete cds
5690	18884		0.95	l	.0E-03 BE796491.1	EST_HUMAN	601589841F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3943954 5
9699	18890	32181	1.77		.0E-03 Q02388	SWISSPROT	COLLAGEN ALPHA 1(VII) CHAIN PRECURSOR (LONG-CHAIN COLLAGEN) (LC COLLAGEN)
	L						yyo7h06.r1 Sogres melanocyte 2NbHM Homo saplens cDNA clone IMAGE:270587 5' similar to contains
5751	18943	32244	0.8		1.0E-03 N41974.1	EST_HUMAN	element wicko repetutve etement
5751	18943	32245	0.8		1.0E-03 N41974.1	EST HUMAN	yyO7n06.r1 Soares melanocyte 2NbHM Homo saplens cDNA clone IMAGE;270587 5' similar to contains element MER6 repetitive element ;
6033	L		0.59		1.0E-03 BF541639.1	EST HUMAN	602068042F1 NIH_MGC_58 Homo saplens cDNA clone IMAGE:4068907 5'
6144	L		2.75	Ĺ	1.0E-03 X07699.1	FN	Mouse nucleolin gene
6184	19360	32708			1.0E-03 BE963939.2	EST HUMAN	601657519R1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3875693 3'
6321	19493		8.77		11526176 NT	TN S	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1), mRNA
6464		32992			1.0E-03 T87761.1	EST_HUMAN	yd93a11.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:115772.5
6239	19702		1.68		1.0E-03 AW902585.1	EST HUMAN	QV3-NN1024-260400-171-g05 NN1024 Homo sapiens cDNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
6895	20046	١	1.41	1.0E-03	I.0E-03 L77570.1	NT	Homo sapiens DiGeorge syndrome critical region, centromeric end
7302	<u> </u>	33843	2.81	1.0E-03	1.0E-03 D16826.1	NT	Human gene for fourth somatostatin receptor subtype
7656			1.12	1.0E-03	1.0E-03 AJ229042.1	NT	Homo saplens 959 kb contig between AML1 and CBR1 on chromosome 21q22, segment 2/3
7		34370	1 08	,	0F-03 U52111 2	TN	Homo capieno X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a), Ce2+/Celmodulin-dependent protein kinase I (CAMKI), creatine transporter (CRTR). CDM protein (CDM), adrendeukodystrophy protein >
7885	1				1.0E-03 M63376.1	NT	Human TRPM-2 protein gene, exons 1,2 and 3
7934	L				1.0E-03 BE880044.1	EST_HUMAN	601491081F1 NIH_MGC_69 Hamo sapiens cDNA clone IMAGE:3893276 5
8073	1	L		]_	1.0E-03 AF274581.1	LN	Homo sapiens prolactin-releasing peptide receptor gene, 5' flanking region
8136	١.		5.02		1.0E-03 AJ251973.1	NT	Homo sapiens partial steerin-1 gene
				_	4 OF 09 AA122230 1	NAMIL	zk97c09.s1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:480768 3' similar to contains L1.tt L1 renetitive element :
8337	- 1	35048	235		1.0E-03 AF153980.1	LS	Homo sapiens exastoses-like protein 1 (EXTL1) gene, exons 2 through 11, and complete cds
8625	21705				1.0E-03 U29397.1	LN	Rattus norvegicus plasma membrane Ca2+ ATPase Isoform 3 (PMCA3) gene, 5' flanking region
914	1			İ	1.0E-03 Y11204.1	LN	V.cartert gene encoding valvaxopsin
9170	1	35791			1.0E-03 AW840353.1	EST_HUMAN	GM3-LT0079-170200-092-e07 LT0079 Homo sapiens cDNA
				<u> </u>			Homo sapiens X28 region near ALD locus containing dual specificity phosphalase 9 (DUSP9), ribosomal protein L188 (RPL18a), Ca2+/Calmodulin-dependent protein kinase I (CAMKI), creatine transporter (CRTR),
9281	22357		0.65		1.0E-03 U52111.2	LN	CDM protein (CDM), adrenoleukodystropny protein >
9319	3 22395	35947			1.0E-03 M30471.1	LN	Human class III alcohol dehydrogenase (ADH5) chi subunit mRNA, complete cos
9315	3 22395	35948	3.89		1.0E-03 M30471.1	NT	Human class III alcohol dehydrogenase (ADH5) chi subuhit mKnA, complete cos
9796	L		0.47		1.0E-03 AI247482.1	EST_HUMAN	dr.56d01.x1 Soares_feta_liver_sploen_1NFLS_S1 Homo sepiens cDNA clone IMAGE: 1848673.3 similer to gb:M97388 TATA-BINDING PROTEIN-ASSOCIATED PHOSPHOPROTEIN (HUMAN);
9807	L	36424	2.06		1.0E-03 AF011400.1	NT	Thermotoga neapolitana alpha-1,6-galactosidase (agIA) gene, complete cds
9807	<b>!</b>				1.0E-03 AF011400.1	IN	Thermotoga neapolitana alpha-1,6-galactosidase (aglA) gene, complete cds
10025	1	<u> </u>	88.0		1.0E-03 Q0112B	SWISSPROT	BONE PROTEOGLYCAN II PRECURSOR (PG-S2) (DECORIN) (PG40) (DERMATAN SULFATE PROTEOGLYCAN-II) (DSPG)
10366	Ł	L			1.0E-03 AF003529.1	LΝ	Homo sapiens glypican 3 (GPC3) gene, partial cds and flanking repeat regions
10372	ł				1.0E-03 AF097485.1	LΝ	Homo sapiens transducin beta-like 2 (TBL2) gene, complete cds
	1					100	OV78/08.x1 Soares_testis_NHT Homo sepiens cDNA clane IMAGE:1643175 3' cimilar to contains MER39.b1
10522	- 1	١			1.0E-03 AI024350.1	ESI HUMAN	Micros Micros repound element,  Decidenate perintings DAM certifier 323 of 529 of the complete genome
1082	3 23856	ļ		1	1.0E-03 AE004/62.1	Z	F Settlement as an experience of the settlement of the settlement of the settlement of the settlement of the settlement of the settlement of the settlement of the settlement of the settlement of the settlement of the settlement of the settlement of the settlement of the settlement of the settlement of the settlement of the settlement of the settlement of the settlement of the settlement of the settlement of the settlement of the settlement of the settlement of the settlement of the settlement of the settlement of the settlement of the settlement of the settlement of the settlement of the settlement of the settlement of the settlement of the settlement of the settlement of the settlement of the settlement of the settlement of the settlement of the settlement of the settlement of the settlement of the settlement of the settlement of the settlement of the settlement of the settlement of the settlement of the settlement of the settlement of the settlement of the settlement of the settlement of the settlement of the settlement of the settlement of the settlement of the settlement of the settlement of the settlement of the settlement of the settlement of the settlement of the settlement of the settlement of the settlement of the settlement of the settlement of the settlement of the settlement of the settlement of the settlement of the settlement of the settlement of the settlement of the settlement of the settlement of the settlement of the settlement of the settlement of the settlement of the settlement of the settlement of the settlement of the settlement of the settlement of the settlement of the settlement of the settlement of the settlement of the settlement of the settlement of the settlement of the settlement of the settlement of the settlement of the settlement of the settlement of the settlement of the settlement of the settlement of the settlement of the settlement of the settlement of the settlement of the settlement of the settlement of the settlement of the settlement of the settlement of the settlement
1082		37479	0.5		1.0E-03 AE004762.1	LN	Pseudomonas aeruginosa PAU1, section 323 of 329 of the curiplicite genunia

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				Т	7	т			7	Т	コ	П	Т	$\neg$	T	T	Т	T	Т		Г	П	T	0	Т	Т	T	Т	Т			١
	Top Hit Descriptor	ng55g12.s1 NCI_CGAP_LIp2 Homo saplens cDNA clone IMAGE:939718 similar to contains L1.b3 L1 L1 repetitive element;	wg36i09.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo septens cDNA clone IMAGE:2367209 31	Homo sapiens mRNA for FLJ00035 proteth, partial cds	BONE MORPHOGENETIC PROTEIN 1 PRECURSOR (BMP-1)	BONE MORPHOGENETIC PROTEIN 1 PRECURSOR (BMP-1)	Homo sapiens Bruton's tyrosine kinase (BTK), alpha-D-galactosidase A (GLA), L44-like ribosomal protein (L44L) and FTP3 (FTP3) genes, complete cds	HSC28A072 normalized infant brain cDNA Homo sapiens cDNA clone c-28a07 3'	CM1-BT0614-110300-142-b12 BT0614 Homo sapiens cDNA	yg13c06.r1 Soares Infant brain 1NIB Homo sapiens cDNA clone IMAGE:32298 5'	Homo sepiens Retina-dorived POU-domain factor-1 (RPF-1), mRNA	602013339F1 NCI_CGAP_Brn64 Homo saplens cDNA clone IMAGE:4149297 6	wj15a11.x1 NCI_CGAP_Kld12 Homo saptens cDNA clone IMAGE:2402876 3'	Homo sepiens epsilon-1 pseudogene (IGHEP1) gene, 5 flanking region	Homo sapiens epsilon-1 pseudogene (IGHEP1) gene, 6' flanking region	Homo sapiens CCR8 chemokine receptor (CMKBR8) gene, complete cds	RC2-HT0560-190200-011-f09 HT0560 Homo sapiens cDNA	RC2-HT0560-190200-011-f09 HT0560 Homo saplens cDNA	GLUCOSE TRANSPORTER TYPE 5, SMALL INTESTINE (FRUCTOSE TRANSPORTER)	y894c11.c1 Scares_pineal_gland_N3HPG Homo sapiens cDNA clone IMAGE:231956.3' similar to contains I OR1 reportitive element:	DKFZp586M2024_r1 586 (synanym: hute1) Homo sapiens cDNA clone DKFZp586M2024	wi35g02.x1 NCI_CGAP_Ut1 Homo saplens cDNA clone IMAGE:2426930 3'	RC2-BN0120-250400-012-h11 BN0120 Homo sapiens cDNA	Lytechinus variegatus embryonic blastocoelar extracellular matrix protein precursor (ECM3) mRNA, complete	cds	Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22, segment 2/3	UFH-BI0-aab-e-09-0-UI.s1 NCI_CGAP_Sub1 Homo saplens cDNA clone IMAGE:2708825 3	NUCLEOSIDE DIPHOSPHATE KINASE B (NDK B) (NDP KINASE B) (NM23-M2) (P18)	RC1-HT0269-261199-012-d08 HT0269 Homo sapiens cDNA	wi78g11.x1 NCI_CGAP_Lu19 Homo sapiens cDNA clone IMAGE:2408804 3' similar to contains element L1 repetitive element;	HYPOTHETICAL 29.3 KD PROTEIN (ORF92)	
	Top Hit Database Source	EST_HUMAN	EST_HUMAN	NT	SWISSPROT	SWISSPROT	N.	EST HUMAN	EST_HUMAN	EST_HUMAN	٦	EST_HUMAN	EST_HUMAN	NT	NT	NT	EST_HUMAN	EST_HUMAN	SWISSPROT	EST HIMAN	EST HUMAN	EST HUMAN	EST_HUMAN		LΝ	NT	EST_HUMAN	SWISSPROT	EST_HUMAN	EST HUMAN	SWISSPROT	
B	Top Hit Acession No.	7.0E-04   AA516212.1	7.0E-04 AI769331.1	7.0E-04 AK024446.1	P13497	P13497	7.0E-04 U78027.1	240561.1	7.0E-04 BE077941.1	7.0E-04/R17336.1	6005855 NT	6.0E-04 BF341380.1		6.0E-04 K01315.1	6.0E-04 K01315.1	6.0E-04 U45983.1	6.0E-04 BE173435.1	6.0E-04 BE173435.1	P46408	8 0E.04 H02047 4	6 0E-04 Al 048507 2	6.0E-04 AI858286.1	6.0E-04 BE005850.1		6.0E-04 AF287478.1	6.0E-04 AJ229042.1	6.0E-04 AW013847.1	6.0E-04 Q01768	6.0E-04 AW380519.1	6.0E-04 AI817088.1	5 0F-04 0 10341	210071
	Most Similar (Top) Hit BLAST E Vatue	7.0E-04	7.0E-04	7.0E-04	7.0E-04 P13497	7.0E-04 P13497	7.0E-04	7.0E-04 Z40561.1	7.0E-04	7.0E-04	7.0E-04	6.0E-04	6.0E-04	6.0E-04	6.0E-04	6.0E-04	6.0E-04	6.0E-04	6.0E-04 P46408	8 00 04	6.0E-04	6.0E-04	6.0E-04		6.0E-04	6.0E-04	6.0E-04	ı				Į
	Expression Signal	0.93	2.33	0.72	0.65	0.65	1.7	3.76	9.28	2.66	5.43	76.0	1.64	0.65	0.65	3.91	0.89	0.89	4.58		88.8	0.53	2.29		0.84	2.07	2.47		3.31	14.14		
	ORF SEQ ID NO:	32745			36639			38578					30232	30341	30342	30430	1	30684					36922			38462					26882	
	SEQ ID NO:	19396	19801	20455	,	l	24853	24881	25481	25650	ı	ı	Ι.	17350	17350	17444	ł	17703	21133	į .	22222	١.	L	<u> </u>	23582		24864	L	L	1	ı	- 1
	Probe SEQ ID NO:	1229	6642	7378	10008	10008	11865	11893	12723	13001	13038	2760	4069	4201	4201	4301	4565	4565	8050	2000	10185	10215	10285		10547	11774	11866	11937	12363	13226	888	3

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Top Hit Descriptor  Toy Hit Descriptor  Toy Hit Descriptor  Toy Hit Descriptor  Toy Hit Descriptor  MAGE-11-st NGI_GGAP_Cot1 Homo sapiens cDNA  Toy Hit Descriptor  MOTIFISTY (ADAM-TS-7) (ADAM-TS7)  Bos taurus micromolar calcium activated neutral protease 1 (CAPN1) gene, exone 11-20, and partial cds  ANDIAGE-13-14-15-15 (ADAM-TS-7) (ADAM-TS7)  Bos taurus micromolar calcium activated neutral protease 1 (CAPN1) gene, exone 11-20, and partial cds  ANDIAGE-13-15 (ADAM-TS-7) (ADAM-TS7)  Bos taurus micromolar calcium activated neutral protease 1 (CAPN1) gene, exone 11-20, and partial cds  ANDIAGE-13-15-15 (ADAM-TS-7) (ADAM-TS7)  Bos taurus micromolar calcium activated neutral protease 1 (CAPN1) gene, exone 11-20, and partial cds  Add 370-6x1 Strategene colon (48-37-204) Homo sapiens cDNA clone IMAGE-1399-238 3' similar to contains element  MER22 repetitive cleared. Btooweeks_2NbH-P8tc9W Homo sapiens cDNA clone IMAGE-1399-238 3' similar to contains element  AMER22 repetitive cleared. A VASCULAR ENDOTHELIAL GROWTH FACTOR RECEPTOR 1  GOSAP_GOSAP_GOSA 1 VASCULAR ENDOTHELIAL GROWTH FACTOR RECEPTOR 1  GROWTH FACTOR RECEPTOR 1  GROWTH FACTOR RECEPTOR 1  GROWTH FACTOR RECEPTOR 1  GROWTH FACTOR RECEPTOR 1  GROWTH FACTOR RECEPTOR 1  GROWTH FACTOR RECEPTOR 1  GROWTH FACTOR RECEPTOR 1  GROWTH FACTOR RECEPTOR 1  GROWTH FACTOR RECEPTOR 1  GROWTH FACTOR RECEPTOR 1  GROWTH FACTOR RECEPTOR 1  GROWTH FACTOR RECEPTOR 1  GROWTH FACTOR RECEPTOR 1  GROWTH FACTOR FACTOR RECEPTOR 1  GROWTH FACTOR FACTOR FACTOR FACTOR FACTOR FACTOR FACTOR FACTOR FACTOR FACTOR FACTOR FACTOR FACTOR FACTOR FACTOR FACTOR FACTOR FACTOR FACTOR FACTOR FACTOR FACTOR FACTOR FACTOR FACTOR FACTOR FACTOR FACTOR FACTOR FACTOR FACTOR FACTOR FACTOR FACTOR FACTOR FACTOR FACTOR FACTOR FACTOR FACTOR FACTOR FACTOR FACTOR FACTOR FACTOR FACTOR FACTOR FACTOR FACTOR FACTOR FACTOR FACTOR FACTOR FACTOR FACTOR FACTOR FACTOR FACTOR FACTOR FACTOR FACTOR FACTOR FACTOR FACTOR FACTOR FACTOR FACTOR FACTOR FACTOR FACTOR FACTOR FACTOR FACTOR FACTOR FACTOR FACTOR FACTOR FACTOR FACTOR FACTOR FA		Top Hit Acession No.   AW861844.1   AA548931.1   AA548931.1   AA756080.1   AA756080.1   AA756080.1   AA756080.1   AA756080.1   AA756080.1   AA814519.1   AA814519.1   AA814519.1   AA814519.1   AA814519.1   AA814519.1   AA568513.1   AU52871.1   AU52871.1   AU52871.1   AU52871.1   AU52871.1   AU52871.1   AA750263.1   AA750263.1	A STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STA	Signal	유		SEQ ID NO: NO: 1531 1531 1531 15301 12012 12012 12012 12012 12012 12012 12012 12012 12012 12012 12012 12012 12012 12012 12012 12012 12012 12012 12012 12012 12012 12012 12012 12012 12012 12012 12012 12012 12012 12012 12012 12012 12012 12012 12012 12012 12012 12012 12012 12012 12012 12012
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Homo sapiens chromosome 21 segment HS21C078	<u>F</u>	4.0E-04 AL163278.2		1.87			2148
Homo sapiens chromosome 21 segment HS21C078	<u>FN</u>	4 AL163278.2					214B
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	NEWDE	4 AASBS313.1	-	2.39			33
#15h02 s.1 NCI CGAP Pri Homo septens cDNA clone IMAGE:913875	T LI INANI	A A ARROGA O 4	Ĺ	ľ	l	ı	
3os taurus micromolar calcium activated neutral protease 1 (CAPN1) gene, exons 11-20, and partial cds	¥	4 AF248054.1					212
DKFZp588MZ024_T1 388 (synonym: nu(e)) Hamo sapiens curva cione un zpocomzuz+		4 AL048507.2		1.9			1220
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HUMAN); contains Alu repetitive element;	EST HUMAN	4 AI188382.1					3143
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p33b08.r1 Stratagene colon (#937204) Homo sapions cDNA clone IMAGE:588663 5					33317	l	3765
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MOTIFO () (ALDAIVI 15-1) (ALDAIVI 151)	Т	4 Q9UKI-4	5.0E-0				889
INDAMES OF TRACES OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTR							
SPORTE ERITORIA.	Т	4 AA548931.1					8
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k27e11.s1 NCI_CGAP_Co11 Homo sapiens cDNA clone IMAGE:1014764 3' similar to contains Alu							
27 - C. 10223-00-307 C. 1022-00-307	٦		9.0E-0	2.03			1531
NVC CT0225-030-030-007 CT0225 Home seniers cDNA	Т	T	10.4	000		┙	1
	Source		BLAST E Vatue	Signal	ö N Q		Ö
Top Hit Descriptor	Top Hit Database		Most Simila (Top) Hit	Expression	ORF SEQ		ag C
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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
289	15811			4.0E-04	4.0E-04 O96615	SWISSPROT	SERICIN-2 (SILK GUM PROTEIN 2)
3233	16407		2.78	4.0E-04	4.0E-04 AF281074.1	TN	Homo sapiens neuropilin 2 (NRP2) gene, complete cds, alternatively spliced
3397	16567		0.69	4.0E-04	4.0E-04 AI720263.1	EST_HUMAN	as70b08.x1 Barstead colon HPLRB7 Homo sapiens cDNA clone IMAGE:2334039 3' pimilar to TR:Q13825 Q13825 ALL-BINDING PROTEIN/ENOYL-COA HYDRATASE. ;
3443	16611		9.0	4.0E-04	4.0E-04 AV696624.1	EST_HUMAN	AV696624 GKC Homo sapiens cDNA clone GKCFFH07 5
44	17583		3.24	4.0E-04	4.0E-04/AA576331.1	EST_HUMAN	rh10a10.s1 NCI_CGAP_Co1 Homo saplens cDNA clone IMAGE:951930 3' similar to gb:M21121 T-CELL SPECIFIC RANTES PROTEIN PRECURSOR (HUMAN);
4443	17583		3.24	4.0E-04	4.0E-04 AA576331.1	EST_HUMAN	rh10a10.s1 NCI_CGAP_Co1 Homo sapiens cDNA clone IMAGE:951930 3' similar to gb.M21121 T-CELL SPECIFIC RANTES PROTEIN PRECURSOR (HUMAN);
4659	17795	30781		4.0E-04	4.0E-04 AA086324.1	EST_HUMAN	zn61c08.s1 Stratagene muscle 937209 Homo sapiens cDNA clone IMAGE:562670 3/
5199	18320			4.0E-04	4.0E-04 BE560660.1	EST_HUMAN	601345895F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3678910 5
7418	20496	33965	1.55	4.0E-04	4.0E-04 P48442	SWISSPROT	EXTRACELLULAR CALCIUM-SENSING RECEPTOR PRECURSOR (CASR) (PARATHYROID CELL CALCIUM-SENSING RECEPTOR)
7705	20770		0.85	4.0E-04	4.0E-04 AL161566.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 66
7896	20948	34456	9.0	4.0E-04	4.0E-04 AU122079.1	EST_HUMAN	AU122079 MAMMA1 Homo sapiens cDNA clone MAMMA1001620 5'
8733	21813			4.0E-04	4.0E-04 BF240712.1	EST HUMAN	601875985F1 NIH_MGC_55 Hamo sapiens cDNA clone IMAGE:4099700 5
8741	21820	35354	1.68	4.0E-04	4.0E-04 N25507.1	EST_HUMAN	yx39e12.r1 Soares melanocyte 2NbHM Homo sapiens cDNA clone IMAGE;264142 5'
9892	22932	36515	3.37	4.0E-04		EST_HUMAN	ov87h03.s1 Soares_testis_NHT Hamo sapiens cDNA clone IMAGE:1644341 3'
10045	23083		1.12	4.0E-04		NT	Mus musculus neuropilin-2(a17) mRNA, alternatively spliced, complete cds
12691	25908		1.56	4.0E-04	4.0E-04 AF254822.1	N⊤	Homo sapiens SMARCA4 isoform (SMARCA4) gene, complete cds, alternatively spliced
160	13385	26415	3.21	3.0E-04	3.0E-04 AL119426.1	EST_HUMAN	DKFZp761J221_r1 761 (synonym: hamy2) Homo sapiens cDNA clone DKFZp761JZZ1 5
200	13423	26454	1.7	3.0E-04	3.0E-04 P49259	SWISSPROT	180 KD SECRETORY PHOSPHOLIPASE A2 RECEPTOR PRECURSOR (PLA2-R)
803	14078		1.63	3.0E-04	3.0E-04 U83991.1	NT	Human short chain ecyl CoA dehydrogenase gene, exons 1 and 2
1886	15030	28137		3.0E-04	3.0E-04 AI262100.1	EST_HUMAN	qz28d03.y1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE::2028197 b
1901	15044		76.0	3.0E-04	3.0E-04 AI399674.1	EST_HUMAN	th23a02.x1 NCI_CGAP_Pr28 Homo sapiens cDNA clone IMAGE:2119082 3'
3383	16554	29568	4.35		3.0E-04 P25147	SWISSPROT	INTERNALIN B PRECURSOR
4071	17227	L	4.94	3.0E-04	3.0E-04 P49448	SWISSPROT	GLUTAMATE DEHYDROGENASE 2 PRECURSOR (GDH)
4167	17317		1.36		3.0E-04 AJZ71735.1	NT	Homo sapiens Xq pseudoautosomal region; segment 1/2
4205	17354		1.06		3.0E-04 BE140609.1	EST_HUMAN	RC0-HT0014-310599-028 HT0014 Homo sapiens cDNA
4635	17771		1.16		3.0E-04 BE148546.1	EST_HUMAN	MR0-HT0241-030200-008-c01 HT0241 Homo capiens cDNA
4937	18067		5.2		3.0E-04 BE153778.1	EST_HUMAN	PMp-HT0339-190200-007-g12 HT0339 Homo sepiens cDNA
5004	18133	31107	0.65		3.0E-04 AW937723.1	EST HUMAN	QV3-DT0045-221299-046-d09 DT0045 Hamo sapiens cDNA
6271	19445		5.58	١.	3.0E-04 AL163281.2	본	Homo sapiens chromosome 21 segment HS21C081
6969	20187	33611	1.54	_	3.0E-04 AL163278.2	N	Homo sapiens chromosome 21 segment HS21C078

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Probe SEQ ID NO:	SEQ 1D NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
7130	18556		0.67	3.0E-04	Г	EST HUMAN	RC4-NN0027-080400-011-b08 NN0027 Homo saplens cDNA
7765	1	34316		3.0E-04		SWISSPROT	PROTEIN-TYROSINE PHOSPHATASE DELTA PRECURSOR (R-PTP-DELTA)
8454	1	L		3.0E-04	3.0E-04 P22607	SWISSPROT	FIBROBLAST GROWTH FACTOR RECEPTOR 3 PRECURSOR (FGFR-3)
10124	1			3.05-04	0E-04 AA454055.1	EST HUMAN	248408.r1 Scares_testis_NHT Homo sapiens cDNA clone IMAGE:795471 5' similar to gb:M62762 VACUOLAR ATP SYNTHASE 16 KD PROTECLIPID SUBUNIT (HUMAN);
10381	23416			3.0E-04	.0E-04 A1992139.1	EST HUMAN	wt75a11.x1 Soares_thymus_NHFTh Homo sapiens cDNA clone IMAGE:2513276 3'
10676	1			9	0E-04/AA781201.1	EST HUMAN	ajz4g05.s1 Soares_testis_NHT Homo sapiens cDNA clone 1391288 3' similar to gb:M36072 60S RIBOSOMAL PROTEIN L74 (HUMAN);
	1						nc38e04.r1 NCI_CGAP_Pr2 Homo saplens cDNA clone IMAGE:1010430 similar to contains L1.t2 L1
12249	26164		2.39		3.0E-04 AA228301.1	EST_HUMAN	repetitive element;
12646	l			3.0E-04	AB018292.1	NT .	Homo sapiens mRNA for KIAA0749 protein, partial cds
13114	ı		4.81	3.0E-04	AL134483.1	EST_HUMAN	DKFZp547L185_r1 547 (syronym: hfbr1) Homo sapiens cDNA clone DKFZp547L185 5
180	13403	26432	1 33		AF217796.1	IN	Homo sapiens SCG10 like-protein, helicase-like protein NHL, M68, and ADP-ribosylation factor related protein 1 (ARFRP1) genes, complete cds
491				L	2.0E-04 AU146707.1	EST HUMAN	AU146707 HEMBB1 Homo sapiens cDNA clone HEMBB1001253 3'
930	1_	١.			1	닏	Human dystrophin gene
930	Ĺ	27169			M86524.1	Ę	Human dystrophin gene
1206	1				2.0E-04 Al286021.1	EST_HUMAN	qh98e11.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1855052 3' similar to contains MER3.b2 MER3 repetitive element ;
1213	1		2.6		AL163203.2	Ā	Homo sapiens chromosome 21 segment HS21C003
1879	ı		1.71		2.0E-04 AF224268.1	NT	Mus musculus 5' flanking region of Pitx3 gene
100	1		5		2000 A A A Z B C B C A	ENT HIMAN	zu39b05.s1 Soares ovary tumor NbHOT Homo sapiens cDNA clone IMAGE:740337 3' similar to contains Alui repetitive element:
/077	200		2		74410000. I	ACMOI - CO	
		·- <u>-</u>			·	•••	Human germline T-cell receptor beta chain TCRBV17S1A1T, TCRBV2S1, TCRBV10S1P, TCRBV19S1P, TCRBV15S1, TCRBV14S1, TCRBV14S1,
2641	15764	28878			2.0E-04 U66061.1	LZ.	TCRBV3S1, TCRBV4S1A1T, TRY4, TRY5, TRY6, TRY7, TRY8, TCRBD1, TCRBJ1S1, TCRBJ1S2,>
3052		L			2.0E-04 AI124529.1	EST_HUMAN	am58c09.x1 Johnston frontal cortex Homo saplens cDNA done IMAGE:1539760 3'
3415	16584	1 29600	0.82	2.0E-04	5174736 NT	NT	Homo sapiens tubulin, beta, 4 (TUBB4) mRNA
3622	1				2.0E-04 BE082317.1	EST_HUMAN	QV2-BT0636-070500-194-b07 BT0636 Homo sapiens cDNA
4022	ł	30187			2.0E-04 AW978441.1	EST_HUMAN	EST390550 MAGE resequences, MAGP Homo saplens cDNA
4261	17406	2	5.5		2.0E-04 U01029.1	NT	Phaseolus vulgaris nitrate reductase (PVNR2) gene, complete cds
4791	17926			2	.0E-04 H96265.1	EST_HUMAN	yu01e11.r1 Soares_pineal_gland_N3HPG Homo sapiens cDNA clone IMAGE::232556 5
4791		30915	1.75	. '	2.0E-04 H96265.1	EST_HUMAN	vu01e11.r1 Soares_pineal_gland_N3HPG Homo sapiens cDNA clone IMAGE::232555 5

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Top Hit Descriptor	Gallus gallus proteasome 28 kDa subunit homdog mRNA, complete cds	Danio rerio hagoromo gene, exons 1 to 6, partial cds	Dictyostelium discoldeum interaptin (abpD) gene, complete cds	AV654352 GLC Homo sapiens cDNA clone GLCDUH10 3	tqc3b11.x1 NCI_CGAP_Ut3 Homo sapiens cDNA clone IMAGE:2207709 3	EST11191 Uterus Homo sapiens cDNA 5' end similar to EST containing O family repeat	Homo sapiens cell cycle progression 3 protein (DNJ3) mRNA	Mus musculus G protein coupled receptor gene, complete cds; and unknown gene	AU121712 MAMMA1 Homo sapiens cDNA clone MAMMA1000798 5	QV0-CT0387-180300-167-e10 CT0387 Homo sapiens cDNA	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG	MYOMESIN 2 (M-PROTEIN) (165 KD TITIN-ASSOCIATED PROTEIN) (165 KD CONNECTIN- ASSOCIATED PROTEIN)	Scianum lycopersicum phytochrome F (PHYF) gene, partial cds	Solanum lycopersicum phytochrome F (PHYF) gene, partial cds	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORC1L4 genes,	complete cds)	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, commete cds)		Home sapiens FRA3B common fragile region, diadenosine triphosphate hydrolase (FHIT) gene, exon 5	Human immunoglobulin C(mu) and C(delta) neavy criain genes (consider regions)	al22a12.s1 Soares_testis_NHT Homo sapiens cUNA cione 1343516 3	GASTRULA ZINC FINGER PROTEIN ALCGRAST	RC3-HT0254-161099-011-505 H10254 Home saplens culvA	Zu68c11.1 Soares testis NHI Homo sapiens cuna cione invade: 142804 3	AV730373 HTF Homo saplens cDNA clone HTFAAAUT 3	401f11,x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE::2140269 3 similar to contains Aiu repenuve	element	U-H-BIT-adm-0-04-0-U-ST NCI_CGAPT_Gubs nome septicits convocation in the convocation in the convocation in the convocation in the convocation in the convocation in the convocation in the convocation in the convocation in the convocation in the convocation in the convocation in the convocation in the convocation in the convocation in the convocation in the convocation in the convocation in the convocation in the convocation in the convocation in the convocation in the convocation in the convocation in the convocation in the convocation in the convocation in the convocation in the convocation in the convocation in the convocation in the convocation in the convocation in the convocation in the convocation in the convocation in the convocation in the convocation in the convocation in the convocation in the convocation in the convocation in the convocation in the convocation in the convocation in the convocation in the convocation in the convocation in the convocation in the convocation in the convocation in the convocation in the convocation in the convocation in the convocation in the convocation in the convocation in the convocation in the convocation in the convocation in the convocation in the convocation in the convocation in the convocation in the convocation in the convocation in the convocation in the convocation in the convocation in the convocation in the convocation in the convocation in the convocation in the convocation in the convocation in the convocation in the convocation in the convocation in the convocation in the convocation in the convocation in the convocation in the convocation in the convocation in the convocation in the convocation in the convocation in the convocation in the convocation in the convocation in the convocation in the convocation in the convocation in the convocation in the convocation in the convocation in the convocation in the convocation in the convocation in the convocation in the convocation in the convocation in the convocation in the convocation in the convocation in t	RC2-BT0317-150200-011-N04-B1031/ Home Sapiens culvA	HYPOTHE ICAL 29.1 KD PROTEIN IN CRIBI SINEGLON (ON 2)	Caenorhabdias elegans nomeodomain protein (intess) mixtys, complete cue	Homo sapiens DINA for amylota predutsor protein, complete dus
Top Hit. Database Source	N	NT.	TN	EST_HUMAN	EST HUMAN	EST_HUMAN	IN	NT	EST_HUMAN	EST HUMAN	SWISSPROT	SWISSPROT	LZ.	LN		LN	₽N		FZ	LN.	EST_HUMAN	SWISSPROT	EST_HUMAN	EST_HUMAN	EST_HUMAN		EST_HUMAN	EST_HUMAN	EST_HUMAN	SWISSPROT	z	<u>F</u>
Top Hit Acession No.	.0E-04 U09226.1	2.0E-04 AB037997.1	2.0E-04 AF057019.1	2.0E-04 AV654352.1	2.0E-04 AI690862.1	2.0E-04 AA296652.1	4758179 NT	2.0E-04 AF140708.1	2.0E-04 AU121712.1	2.0E-04 AW860963.1	P08548	P54296	2.0E-04 U32444.2	2.0E-04 U32444.2		2.0E-04 AB026898.1	2 OF 04 AB026808 1	חבסקסקט.	2.0E-04 AF020503.1	2.0E-04 X57331.1	2.0E-04 AA725700.1	2.0E-04 P18715	2.0E-04 BE148303.1	2.0E-04 AA405777.1	2.0E-04 AV730373.1		2.0E-04 AI440282.1	2.0E-04 AW 136740.1	2.0E-04 BE066781.1	2.0E-04 P21733	2.0E-04 L19248.1	2.0E-04 D87675.1
Most Similar (Top) Hit BLAST E Value	2.0E-04	2.0E-04 /	2.0E-04	2.0E-04	2.0E-04	2.0E-04	2.0E-04	2.0E-04	2.0E-04	2.0E-04	2.0E-04 P08548	2.0E-04 P54296	2.0E-04	2.0E-04		2.0E-04	20.00	£.0L-04	2.0E-04	2.0E-04	2.0E-04	2.0E-04	2.0E-04					2.0E-04	2.0E-04			
Expression Signal	1.22	1.47	0.92	1.11	1.83	0.93	0.92	1.01	2.57	0.84	13.66	1,45	1.02	1.02		1.24	7	17.	2.14	0.67	0.58	0.47	1.16	2.06				2.39	2.71	32.04		1.29
ORF SEQ ID NO:		31256				32365						34357			l	35094		CROCS		35561	36173				37798	L		38443				
Exan SEQ ID NO:	18046	١.	ı	L	ı	1			1	١.	ı	20863	ı	21224	1	21560		21500	21842	l	22800	L	L	l_		1	24638	l_	L.	3 25086		Li
Probe SEQ ID NO:	4918	5171	5216	5661	5674	5868	8999	6368	7378	7478	7798	7808	8142	8142		8479		84/3	8763	8941	9535	9619	19180	10223	11088		11585	11710	11859	12106	12121	13191

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	SEQ ID NO: 13867 14285 144285 144303 144303 144303 144303 144303 145828 155889 155889 16589 16589 16589 16589 16589 16589 16589 16589 16589 16589 16589 16589 16589 16589 16589 16589 16589 16589 16589 16589 16589 16589 16589 16589 16589 16589 16589 16589 16589 16589 16589 16589 16589 16589 16589 16589 16589 16589 16589 16589 16589 16589 16589 16589 16589 16589 16589 16589 16589 16589 16589 16589 16589 16589 16589 16589 16589 16589 16589 16589 16589 16589 16589 16589 16589 16589 16589 16589 16589 16589 16589 16589 16589 16589 16589 16589 16589 16589 16589 16589 16589 16589 16589 16589 16589 16589 16589 16589 16589 16589 16589 16589 16589 16589 16589 16589 16589 16589 16589 16589 16589 16589 16589 16589 16589 16589 16589 16589 16589 16589 16589 16589 16589 16589 16589 16589 16589 16589 16589 16589 16589 16589 16589 16589 16589 16589 16589 16589 16589 16589 16589 16589 16589 16589 16589 16589 16589 16589 16589 16589 16589 16589 16589 16589 16589 16589 16589 16589 16589 16589 16589 16589 16589 16589 16589 16589 16589 16589 16589 16589 16589 16589 16589 16589 16589 16589 16589 16589 16589 16589 16589 16589 16589 16589 16589 16589 16589 16589 16589 16589 16589 16589 16589 16589 16589 16589 16589 16589 16589 16589 16589 16589 16589 16589 16589 16589 16589 16589 16589 16589 16589 16589 16589 16589 16589 16589 16589 16589 16589 16589 16589 16589 16589 16589 16589 16589 16589 16589 16589 16589 16589 16589 16589 16589 16589 16589 16589 16589 16589 16589 16589 16589 16589 16589 16589 16589 16589 16589 16589 16589 16589 16589 16589 16589 16589 16589 16589 16589 16589 16589 16589 16589 16589 16589 16589 16589 16589 16589 16589 16589 16589 16589 16589 16589 16589 16589 16589 16589 16589 16589 16589 16589 16589 16589 16589 16589 16589 16589 16589 16589 16589 16589 16589 16589 16589 16589 16589 16589 16589 16589 16589 16589 16589 16589 16589 16589 16589 16589 16589 16589 16589 16589 16589 16589 16589 16589 16589 16589 16589 16589 16589 16589 16589 16589 16589 16589 16589 16589 16589 16589 16589 16589 16589 16589 16589 16589 1658	R E	Sign		ssi	Top Hit Source Source Source Source Source THUMAN THUMAN THUMAN THUMAN TSSPROT THUMAN THUMAN THUMAN THUMAN THUMAN THUMAN THUMAN THUMAN THUMAN THUMAN THUMAN THUMAN THUMAN THUMAN	Top Hit Descriptor  Top Hit Descriptor  Top Hit Descriptor  I I. II. Li Trepelitive element;  ENETROVINUS-RELATED POL POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE;  ENDONUCLE ASE]  UI-H-BIO-aab-e-09-0-UI st NG_CGAP_Subt Homo sapiens cDNA clone IMAGE:2708825 3*  UI-H-BIO-aab-e-09-0-UI st NG_CGAP_Subt Homo sapiens cDNA clone IMAGE:2708825 3*  Mapulla anguilla dopamine DATA receptor (41A1) gene, complete cds  Kaposi's sarcome-associated herpesvirus ORF 69 gene, partial cds; and ORF 69, kaposin, v-FLIP, v-cyclin, latent nuclear antigen, ORF K14, v-GPCR, putstive phosphoriosylformylglycinamidine synthase, and LAMP  (LAMP) genes, complete cds  Kaposi's sarcome-associated herpesvirus ORF 68 gene, partial cds; and ORF 69, kaposin, v-FLIP, v-cyclin, latent nuclear antigen, ORF K14, v-GPCR, putstive phosphoriosylformylglycinamidine synthase, and LAMP  (LAMP) genes, complete cds  Kaposi's sarcome-associated herpesvirus ORF 68 gene, partial cds; and ORF 69, kaposin, v-FLIP, v-cyclin, latent nuclear antigen, ORF K14, v-GPCR, putstive phosphoriosylformylglycinamidine synthase, and LAMP  (LAMP) genes, complete cds  Kaposi's sarcome-associated herpesvirus ORF 69 gene, partial cds; and ORF 69, kaposin, v-FLIP, v-cyclin, latent nuclear antigen, ORF (44, v-GPCR, putstive phosphoriosylformylglycinamidine synthase, and LAMP  (LAMP) genes, complete cds  Fequis caballus DNA, chronosome 24q14, microsatellite TKY38  Fequis caballus DNA, chronosome 24q14, microsatellite TKY38  Fequis caballus DNA, chronosome 24q14, microsatellite TKY38  Fequis caballus DNA, chronosome 24q14, microsatellite TKY38  MoLosa elpha 1 type-N/ Collagen mRNA  NoLosa elpha 1 type-N/ Collagen mRNA  NoLosa elpha 1 type-N/ Collagen mRNA  NoLosa elpha 1 type-N/ Collagen mRNA  NoLosa elpha 1 type-N/ Collagen mRNA  NoLosa elpha 1 type-N/ Collagen mRNA  NoLosa elpha 1 type-N/ Collagen mRNA  NoLosa elpha 1 type-N/ Collagen mRNA  NoLosa elpha 1 type-N/ Collagen mRNA  NoLosa elpha 1 type-N/ Collagen mRNA  NoLosa elpha 1 type-N/ Collagen mRNA  NoLosa elpha 1 type-N/ Collage
7744	20417	33879	13.49	1.0E-04	1.0E-04 AI251980.1 1.0E-04 AAB30453.1	EST_HUMAN	qv67410.x1 NCI_CGAP_Ov32 Homo sapiens cDNA clone IMACE:1985683 3: ab54q08.s1 Stratagene lung (#937210) Homo sapiens cDNA clone IMAGE:854664 3'
9538 9538 9525 9625	21266 22603 22613 22680	1111			1.0E-04 AMOSOMS.1 1.0E-04 ANSOMS.0 1.0E-04 T77153.1 1.0E-04 T77153.1	20.1 EST HUMAN SWISSPROT SWISSPROT EST HUMAN 10883876 NT	wickedbr. Statesgale Tig (2005) 1 Homo sapiens cDNA clone IMAGE:2356742 3' wickedbr. X Soares, NFL_TGBC_31 Homo sapiens cDNA clone IMAGE:2356742 3' CYSTATIN.RELATED EPIDIDYMAL SPERMATOGENIC PROTEIN PRECURSOR (CYSTATIN 8) sq72c08.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:113774 5' Homo sapiens phospholipid scramblase 1 (PLSCR1), mRNA
384D	77000			]			

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Top Hit Descriptor	INE-1 REVERSE TRANSCRIPTASE HOMOLOG	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG	ZINC FINGER PROTEIN 157	Mouse alpha leukocyte Interferon gene, complete cds	Homo sapiens mRNA for KIAA1142 protein, partial cds:	xv49g12.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2816518 3'	NEURONAL-GLIAL CELL ADHESION MOLECULE PRECURSOR (NG-CAM)	NEURONAL-GLIAL CELL ADHESION MOLECULE PRECURSOR (NG-CAM)	ah45c11.s1 Soares_testis_NHT Homo saptens cDNA done 1292468.3'	wi54c11.x1 NCI_CGAP_Co16 Home sapiens cDNA clone IMAGE:2394068 3' similar to contains MER6.t1	MERO fepaluve denne, or in a selbitarit nora inson	KOLYL 4-HYDROXYLASE ALPHA-Z SUBUNI PRECURSUR	UI H-BI1-eer-d-05-0-UI:s1 NC_CGAP_Sub3 Homo capiens cDNA clone IMAGE:2720289 3	UI-H-Bi1-aer-d-05-0-UI.s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2720289 3'	Homo sapiens gene for cholecystokinin type-A receptor, complete cds	Homo sapiens methyl-CpG binding protein 1 (MBD1) gene, exon 15b	xa34g05.x1 NCI_CGAP_Br18 Homo sapiens cDNA clone IMAGE:2568728 3' similar to contains L1.t2 L1	repetitive element ;	qv23f06.x1 NCI_CGAP_Lym6 Homo sapiens cDNA clone IMAGE:1982435 3' similar to contains element	MIR repetitive element ;	PROLYL 4-HYDROXYLASE ALPHA-2 SUBUNIT PRECURSOR	Homo sapiens MSH55 gene, partial cds; and CLIC1, DDAH, G6b, G6c, G5b, G6d, G6e, G6f, BAT5, G5b, CSK2B, BAT4, G4, Apo M, BAT3, BAT2, AIF-1, 1C7, LST-1, LTB, TNF, and LTA genes, complete cds	Pisum sativum mRNA for beta-1,3 glucanase (gns2 gene)	Pisum sativum mRNA for beta-1,3 glucanase (gns2 gene)	Human platelet-derived growth factor A chain (PDGFA) gene, exons only	wy78a04.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo saplens cDNA clone IMAGE:2554638 3'	Mus musculus gene for hexakinase II, exon 1 (and joined CDS)	Human haptoglobin and haptoglobin-related protein (HP and HPR) genes, complete cds	ZSBBh01.s1 NCI_CGAP_GCB1 Homo sepiens cDNA clone IMAGE:704593 3' similar to contains Alu	Percurve etement, company etement, mont i repetative etement ; RC3_CT0208_2200000011_FD4_CT0208_Home seriens cDNA	AND CLOSE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF	KC3-CIUZUS-ZZUSGG-U11-EU4 CIUZUS Hamo sapiens alina
Top Hit Database Source	SWISSPROT	SWISSPROT	SWISSPROT		±N	EST HUMAN		SWISSPROT	EST_HUMAN		_	ヿ	П	EST_HUMAN	INT	NT		EST_HUMAN			SWISSPROT	NT	¥	LV.		EST_HUMAN	Г	Ā		EST HUMAN	Т	EST_HUMAN
Top Hit Acession No.	P08547	P08548	P51786	1.0E-04 M28587.1	1.0E-04 AB032968.1	1.0E-04 AW 269061.1	Q03696	003696	9.0E-05 AA718933.1	A 000000514	9.0E-05 AI /62209.1	060716	9.0E-05 AW 204958.1	9.0E-05 AW 204958.1	9.0E-05 D85606.1	9.0E-05 AF120982.1		9.0E-05 AW073078.1		9.0E-05 AI287878.1	Q60716	9.0E-05 AF129756.1	8.0E-05 AJ251646.1	8.0E-05 AJ251646.1	8.0E-05 M83575.1	8.0E-05 AW044605.1	8.0E-05 Y11666.1	8.0E-05 M69197.1		8.0E-05/A/2/9333.1	AVV 041 440. I	7.0E-05 AW 847445.1
Most Similar (Top) Hit BLAST E Value	1.0E-04 P08547	1.0E-04 P08548	1.0E-04 P51786	1.0E-04	1.0E-04	1.0E-04	1.0E-04 Q03696	1.0E-04 Q03696	9.0E-05	20.00	9.05-05	9.0E-05/060716	9.0E-05	9.0E-05	9.0E-05	9.0E-05		9.0E-05		9.0E-05	9.0E-05 Q60716	9.0E-05	8.0E-05	8.0E-05	8.0E-05	8.0E-05	8.0E-05	8.0E-05		١	Į	7.0E-US
Expression Signal	3.59	1.12	0.46	2.3	1.81	1.94	1.57	1.57	2.44	,	1.13	1.37	2.44	2.44	3.03	3.3		2.31		1.61	3.41	3.37	1.22	3.11	1.01	0.78	0.51	2.58		1.78	9.10	3.16
ORF SEQ ID NO:		37060	37431		38637	38680		38710	26936		1	32595	34301	34302		36211		38127			32595		27080			30719	35568				١	26597
Exan SEQ ID NO:	23417	23455		L	24936	24976	25008	25008	13898	ŀ		- 1	20811	20811	22639	22641		24463				26016	L.	14063	ı	17741	22027	24480		Z60C1		13568
Probe SEQ ID NO:	10382	10420	10775	11622	11950	11891	12024	12024	716	3	4196	88	7751	1751	2677	6/96		11402		11518	11916	12469	44	88	3015	4604	8948	11419		13159	/00	357

Page 200 of 550 Table 4 Single Exon Probes Expressed in Placenta

					,		
Probe SEQ ID NO:	Exen SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
581	13773	26793	1.14	7.0E-05	7.0E-05 L49075.1	EST_HUMAN	HUM072014F Human fovea cDNA Homo sapiens cDNA clone EST HFD072014
581	13773			7.0E-05	0E-05 L49075.1	EST_HUMAN	HUM072014F Human fovea cDNA Homo sapiens cDNA clone EST HFD072014
1080	14246	Ì		7.0E-05	0E-05 Q22949	SWISSPROT	PROBABLE GLYCEROL-3-PHOSPHATE ACYLTRANSFERASE, MITOCHONDRIAL PRECURSOR (GPAT)
2783	15899	_		7.0E-05	78.2	Ν	Homo sapiens chromosome 21 segment HS21C078
3227	16401	29413		7.0E-05		۲N	Dictyostellum discoldeum gene for TRFA, complete cds
4168	1		0.85	7.0E-05	0E-05 AF111167.2	LN	Homo sapiens jun dimerization protein gene, partial cds; cfos gene, complete cds; and unknown gene
4492	17632	30614		7.0E-05	.0E-05 AL163201.2	TN	Homo sapiens chromosome 21 segment HS210001
5041	l.		99.0	7.0E-05	9845300 NT	l. 1	Rat cytomegalovirus Maastricht, complete genome
88	1	35033		7.0E-05	.0E-05 AA505582.1	EST_HUMAN	hh93g01.s1 NCI_CGAP_Br2 Homo sapiens cDNA clone IMAGE:966096 3
9753	ı	36261	3.6	7.0E-05	.0E-05 T07095.1	EST HUMAN	EST04984 Fetal brain, Stratagene (cat#936206) Homo sapiens cDNA clone HFBED60
11430	24491		5.87	7.0E-05	1	LN	Homo sapiens sarcoglycan, epsilon (SGCE), mRNA
2083	<u>L</u>		1.59	6.0E-05		NT	Homo seplens chromosome X open reading frame 6 (CXORF6) mRNA
2083		28345		6.0E-05	4885170 NT	N L	Homo sapiens chromosome X open reading frame 6 (CXORF6) mRNA
300					6 0F_05 A 655241 1	FST HUMAN	wb54h06.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2309531 3' similar to gb:J03250 UNA TOPOISOMERASE I (HUMAN);
2875	1				AF053630.1	N-	Homo sapiens monocyte/neutrophil elastase inhibitor gene, complete cds
6034	1	32538	3.26			SWISSPROT	CONTACTIN PRECURSOR (GLYCOPROTEIN GP135)
9034	1	L			Ì '	SWISSPROT	CONTACTIN PRECURSOR (GLYCOPROTEIN GP135)
6533	1	33070	1.5			EST_HUMAN	yv50g11.r1 Soares fetal liver spieen 1NFLS Homo sapiens cDNA clone IMAGE::246Z12.5
7073	1	L		_	AA897680.1	EST_HUMAN	oj80a03.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:15045883
8276	ı	34876			6.0E-05 BE064410.1	EST HUMAN	RC4-BT0311-141199-011-h06 BT0311 Homo sapiens cDNA
8276	ı	ĺ	1.03		BE064410.1	EST HUMAN	RC4-BT0311-141199-011-h06 BT0311 Homo sapiens cDNA
	l						208c08.s1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:491726 3' similar to
8638					6.0E-05 AA150482.1	EST HUMAN	COMBINS EIGHER WIETCA REPORTED IN
8643	21723	35260			6.0E-05 AW896629.1	EST_HUMAN	PM4-NN0050-310300-001-110 NN0050 Homo sapiens outne
8780					6.0E-05 Q60401	SWISSPROT	COMPLEMENT DECAY-ACCELERATING FACTOR PRECURSOR
9452	L	L			6.0E-05 P08607	SWISSPROT	C4B-BINDING PROTEIN PRECURSOR (C4BP)
9462					6.0E-05 P08607	SWISSPROT	C4B-BINDING PROTEIN PRECURSOR (C4BP)
9721	22786				6.0E-05 T94149.1	EST_HUMAN	ye28c12.r1 Stratagene lung (#937210) Homo sapiens cDNA clone IMAGE:119052 5
9922	1		0.69		6.0E-05 AW627985.1	EST HUMAN	hi37a03.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE.29/4444 3
10087	1				.0E-05 R75639.1	EST HUMAN	yi§9d08.s1 Soares placenta Nb2HP Homo sepiens cDNA clone IMAGE:143535 3' simitar to contains Alu repetitive element, contains LTR7 repetitive element;
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					,		
Probe SEQ ID	Exon SEQ ID	ORF SEQ	Expression	Most Similar (Top) Hit BLAST E	Top Hit Acession	Top Hit Database	Top Hit Descriptor
Ö	Ö		j 5	Value			IS SOCION TO THE
11807	24797	38495		6.0E-05	6.0E-05 AA044015.1	П	zk68f02.r1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:48/USS 3
12699		31773	9.37	6.0E-05	6.0E-05 AW890110.1	EST_HUMAN	MR0-NT0038-250400-001-409 N I 0038 Homo sapiens culty
1435	١_	27661	20.87	5.0E-05	AW39200	EST_HUMAN	QV4-ST0234-241199-040-h11 ST0234 Flomo sapiens culvA
1912	L	L	1.07	5.0E-05	N 16853891 NT	L	Homo capiens 22kDa peroxisoma membrane protein-like (LOCOCCO), mixika
2924			0.64	5.0E-05	5.0E-05 AJ251058.1	NT	Homo sapiens MEP1A gane, promoter region and exon 1
4088	L	30250	3.16	5.0E-05	5.0E-05 AJ251884.1	NT	Homo sapiens partial SLC22A3 gene for extraneuronal monoamine (ransporter (Elivi I), excit I
5642	1		11.81	5.0E-05	5.0E-05 X58855.1	NT	Human MLC1emb gene for embryonic myosin alkaline light chain, 301 K
6115	1			5.0E-05	5.0E-05 AV653544.1	EST_HUMAN	AV653544 GLC Homo sapiens cDNA clone GLCDMA06 3
6297	1	١		5.0E-05	5.0E-05 AF260225.1	NT	Homo sapiens TESTIN 2 and TESTIN 3 genes, complete cds, auernatively spiliced
7485					5.0E-05 AB037964.1	NT	Mus musculus gene for calretinin, exon 1
12486	L		5.28	5.0E-05 P49193	P49193	SWISSPROT	RETINAL-BINDING PROTEIN (RALBP)
12750			6.9	5.0E-05 P49193		SWISSPROT	RETINAL-BINDING PROTEIN (RALBP)
2868			2.73	İ_	<u>-</u> -	LN	Human renin (REN) gene, 5' flanking region
AROR	1				4.0E-05 P49193	SWISSPROT	RETINAL-BINDING PROTEIN (RALBP)
4605	1	30724		L	4.0E-05 P49193	SWISSPROT	RETINAL-BINDING PROTEIN (RALBP)
	1	l			4 OF OF AF184488 1	LN	Chotosporidium parvum Isolate Zetre 15 kDa glycoprotein go15 gene, partial cds
4997				ļ	AF242040	114	Organnila melanodaster senseless protein (sens) gene, complete cds
5131		31222			4.0E-05 AFZ12313.1	<u> </u>	11-0-cylination DBNA complete refs
9723					4.0E-05 AF202635.1	Į.	HOND SERVERY FOLIOUS MINING AND AND METALCAL ACTORIDASE)
10617		37260	0.54		4.0E-05 P23780	SWISSPROT	BEIA-GALACIOSIDASE FRECUNSON (LACINOS) (NOIS CENTRO) (SINGLE IS CONTINUED TO CONTINUE TO CONTINUE TO CONTINUE TO CONTINUE TO CONTINUE TO CONTINUE TO CONTINUE TO CONTINUE TO CONTINUE TO CONTINUE TO CONTINUE TO CONTINUE TO CONTINUE TO CONTINUE TO CONTINUE TO CONTINUE TO CONTINUE TO CONTINUE TO CONTINUE TO CONTINUE TO CONTINUE TO CONTINUE TO CONTINUE TO CONTINUE TO CONTINUE TO CONTINUE TO CONTINUE TO CONTINUE TO CONTINUE TO CONTINUE TO CONTINUE TO CONTINUE TO CONTINUE TO CONTINUE TO CONTINUE TO CONTINUE TO CONTINUE TO CONTINUE TO CONTINUE TO CONTINUE TO CONTINUE TO CONTINUE TO CONTINUE TO CONTINUE TO CONTINUE TO CONTINUE TO CONTINUE TO CONTINUE TO CONTINUE TO CONTINUE TO CONTINUE TO CONTINUE TO CONTINUE TO CONTINUE TO CONTINUE TO CONTINUE TO CONTINUE TO CONTINUE TO CONTINUE TO CONTINUE TO CONTINUE TO CONTINUE TO CONTINUE TO CONTINUE TO CONTINUE TO CONTINUE TO CONTINUE TO CONTINUE TO CONTINUE TO CONTINUE TO CONTINUE TO CONTINUE TO CONTINUE TO CONTINUE TO CONTINUE TO CONTINUE TO CONTINUE TO CONTINUE TO CONTINUE TO CONTINUE TO CONTINUE TO CONTINUE TO CONTINUE TO CONTINUE TO CONTINUE TO CONTINUE TO CONTINUE TO CONTINUE TO CONTINUE TO CONTINUE TO CONTINUE TO CONTINUE TO CONTINUE TO CONTINUE TO CONTINUE TO CONTINUE TO CONTINUE TO CONTINUE TO CONTINUE TO CONTINUE TO CONTINUE TO CONTINUE TO CONTINUE TO CONTINUE TO CONTINUE TO CONTINUE TO CONTINUE TO CONTINUE TO CONTINUE TO CONTINUE TO CONTINUE TO CONTINUE TO CONTINUE TO CONTINUE TO CONTINUE TO CONTINUE TO CONTINUE TO CONTINUE TO CONTINUE TO CONTINUE TO CONTINUE TO CONTINUE TO CONTINUE TO CONTINUE TO CONTINUE TO CONTINUE TO CONTINUE TO CONTINUE TO CONTINUE TO CONTINUE TO CONTINUE TO CONTINUE TO CONTINUE TO CONTINUE TO CONTINUE TO CONTINUE TO CONTINUE TO CONTINUE TO CONTINUE TO CONTINUE TO CONTINUE TO CONTINUE TO CONTINUE TO CONTINUE TO CONTINUE TO CONTINUE TO CONTINUE TO CONTINUE TO CONTINUE TO CONTINUE TO CONTINUE TO CONTINUE TO CONTINUE TO CONTINUE TO CONTINUE TO CONTINUE TO CONTINUE TO CONTINUE TO CONTINUE TO CONTINUE TO CONTINUE TO CONTINUE TO CONTINUE TO CONTINUE TO C
	L.						hi86c07.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA done IMAGE:29/4380 3 similar to contains
11007	24086	37723			4.0E-05 AW627946.1	EST_HUMAN	element with repeatuve cannon.
12343	ł		3.27		4.0E-05 AL163252.2	ΝŢ	Homo saptens chromosome 21 segment 1321 July 2
12426	25302		1.47		4.0E-05 AW117580.1	EST_HUMAN	xdg3e09.x1 Soares_NFL_T GBC_S1 Home sapiens culve cione invececo.5 15.5
13180	L		1.16		4.0E-05 AA417756.1	EST_HUMAN	zv01e11.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:/46232 3
	1_						qh64c10.x1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone iMAGE:1049456 5 similar to
809	13881	26914	0.8		3.0E-05 AI248061.1	EST HUMAN	contains Alu repetitive element; contains element KER repetitive element;
100	1	L	ľ		3.0E-05 AW273851.1	EST_HUMAN	xx24g03.x1 Soares_NFL_T_GBC_S1 Home saplens cDNA clone IMAGE:2814100.3
1850	П	\  _			3.0E-05 BE169211.1	EST HUMAN	PM1-HT0521-120200-001-e10 HT0521 Homo sapiens cDNA
300	1				3 0E-05 BE169211.1	EST HUMAN	PM1-HT0521-120200-001-e10 HT0521 Homo saplens cDNA
8	┸	-					alora 1.x1 Sogres NhHMPu S1 Homo sapiens cDNA clone IMAGE: 1879748 3' similar to TR: 008632
2366	16537		0.7		3.0E-05 AI288919.1	EST HUMAN	008632 GLYCINE TYROSINE-RICH HAIR PROTEIN.;
3	1	30625		L	3 0F-05 BE169211.1	EST HUMAN	PM1-HT0521-120200-001-610 HT0521 Homo sapiens cDNA
2 2	1				3 0E-05 BE169211.1	EST HUMAN	PM1-HT0521-120200-001-e10 HT0521 Homo sapiens cDNA
25	- [	30020			2 OF 05 A A 3 6 8 7 0 4	EST HUMAN	EST79996 Piacenta I Homo sepiens cDNA similar to similar to p53-associated protein
4588	3 17725	۱	1.11		AAAAAAA		

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Top Hit Descriptor	EST79996 Placenta I Homo saplens cDNA similar to similar to p53-associated protein	Homo sapiens NOD1 protein (NOD1) gene, exons 1, 2, and 3	qn64c10.x1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1849458 3' similar to	Contains Ail repenitive element contains element NETA repenitive element;	Mus musculus myosin light chain z, predursor lymphocyte-specific (Mytozpi), mrtvA	Homo saplens SYBL1 gene, exons 6-8	Homo sapiens SYBL1 gene, exons 6-8	601567451F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3842292 5'	zs60b05.s1 Stratagene schizo brain S11 Homo sapiens cDNA clone IMAGE:701841 3'	hi94e08.x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3009638 3'	Homo sapiens interleukin-1 receptor antagonist homolog 1 (IL1HY1), mRNA	MELANOMA-ASSOCIATED ANTIGEN 8 (MAGE-8 ANTIGEN)	Human Alu-family cluster 5' of alpha(1)-acid glycoprotein gene	EST84475 Colon adenocarchoma IV Homo sapiens cDNA 5' end	wg36f09.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2367209 3'	PROTEIN KINASE C-BINDING PROTEIN NELL2 PRECURSOR (NEL-LIKE PROTEIN 2)	PROTEIN KINASE C-BINDING PROTEIN NELL2 PRECURSOR (NEL-LIKE PROTEIN 2)	Homo sapiens DiGeorge syndrome critical region, centromeric end	Homo sapiens Xq pseudoautosomal region; segment 1/2	xs89d06.x1 NCI_CGAP_Ut2 Homo sapiens cDNA clone IMAGE:2776811 3'	qhg8e11:x1 Soares_NFL_T_GBC_S1 Homo saplens cDNA clone IMAGE:1855052 3' similar to contains MER3.b2 MER3 repetitive element';	Human adenosine deaminase (ADA) gene, complete cds	zq48a12.r1 Stratagene hNT neuron (#937233) Homo sapiens cDNA clone IMAGE:632734 5' similar to	contains Alu repetitive element; contains element L1 repetitive element;	RC3-BT0319-120200-014-h08 BT0319 Homo sapiens oDNA	Homo saplens p47-phαx (NCF1) gene, complete cds	H.sapiens DNA for endogenous retroviral like element	S.cerevisiae 12.8 Kbp fragment of the left arm of chromosome XV	DKFZp5661064_r1 566 (synonym: hfkd2) Homo sapiens cDNA clone DKFZp5661064 5'	Homo sapiens SCL gene locus	Homo sapiens TNNT1 gene, exons 1-11 (and joined CDS)	Homo sepiens chromosome 9 duplication of the T cell receptor beta locus and trypsinogen gene families
Top Hit Database Source	EST_HUMAN	IN	1000	ESI HUMAN	LN	ĽΝ	NT	EST_HUMAN	EST_HUMAN	EST HUMAN	LN	SWISSPROT	TN	EST_HUMAN	EST_HUMAN	SWISSPROT	SWISSPROT	IN	LN	EST_HUMAN	EST HUMAN	L		EST_HUMAN	EST_HUMAN	뒫	Z	FZ	EST_HUMAN	Ę	F	TA
Top Hit Acession No.	3.0E-05 AA368679.1	3.0E-05 AF149773.1	7 7000	3.0E-05 AIZ48061.1	11072102 NT	3.0E-05 AJ225782.1	3.0E-05 AJ225782.1	3.0E-05 BE733157.1	3.0E-05 AA284049.1	3.0E-05 AW770982.1	6912431 NT	P43361	X03273.1	3.0E-05 AA372562.1	3.0E-05 AI769331.1				3.0E-05 AJZ71735.1	3.0E-05 AW518689.1	2 0E-05 AI286021.1	M13792.1		2.0E-05 AA160562.1	2.0E-05 BE066036.1	2.0E-05 AF184614.1	2.0E-05 X89211.1	2.0E-05 X95465.1	2.0E-05 AL039107.1	2.0E-05 AJ131016.1	2.0E-05 AJ011712.1	2.0E-05 AF029308.1
Most Similar (Top) Hit BLAST E Value	3.0E-05	3.0E-05	10	3.0E-05	3.0E-05	3.0E-05	3.0E-05	3.0E-05	3.0E-05	3.0E-05	3.0E-05	3.0E-05 P43361	3.0E-05 X03273.1	3.0E-05	3.0E-05	3.0E-05 Q62918	3.0E-05 Q62918	3.0E-05 L77570.1	3.0E-05	3.0E-05	2.05-05	2.0E-05 M13792.1		2.0E-05	2.0E-05	2.0E-05	2.0E-05	2.0E-05	2.0E-05	2.0E-05	2.0E-05	2.0E-05
Expression Signal	1.11	0.93		0.7	1.72	1.21	1.21	2.26	1.55	1.56	1.63	0.59	. 0.51	1.1	3.62	0.92	0.92	1.61	1.37	1.20	149	14.63		6.90	52.1	1.04	1.12	0.87	0.81	9.0	1.84	0.87
ORF SEQ ID NO:	30708	65808			١	33456	33457			35718	35721	35726		36154		37403	37404					28886					29643			31106		
Exan SEQ ID NO:	17725	17876		13881	18869	20047	20047	21164	21628	22173	22177	22181	22407	22586	22903	23788	23788	25255	25374	26196	15531	15773		15893	16382	16597	16622	16748	17068	18132	19068	ı
Probe SEQ ID NO:	4588	4741	1	4959	5675	6897	6897	8082	8547	9094	8608	9102	9331	9521	9863	10755	10765	12353	12651	12913	2400	2650		7772	3207	3429	3455	3583	3909	5003	5878	6609

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Top Hit Descriptor	RENAL SODIUMIDICARBOXYLATE COTRANSPORTER (NA(+)/DICARBOXYLATE COTRANSPORTER)	RENAL SODIUM/DICARBOXYLATE COTRANSPORTER (NA(+)/DICARBOXYLATE COTRANSPORTER)	qc72a02.x1 Soares_placenta_8tb6weeks_2NbHP8to9W Homo sapiens cDNA clone IMAGE:1715114 3' similar to contains L1.t3 L1 repetitive element;	nw06d12.s1 NCI_CGAP_SS1 Hamo sapiens cDNA clone IMAGE:12385193'	P.faiciparum mRNA for AARP1 protein, partial	qz47b06.x1 NCi_CGAP_Kld11 Homo sapiens cDNA clone IMAGE:2030003 3' similar to 1R:002711 002711 PRO-POL-DUTPASE POLYPROTEIN ;	wu35h07.x1 Scares_Dieckgraefe_colon_NHCD Homo sapiens cDNA clone IMAGE:2522077 31	Heterodontus francisci HoxA10 (HoxA10), HoxA9 (HoxA9), HoxA7 (HoxA7), HoxA6 (HoxA6), HoxA5 (HoxA5), HoxA4 (HoxA4), HoxA3 (HoxA2), HoxA2 (HoxA2), and HoxA1 (HoxA1) genes, complete cds	Heterodontus francisci Hoxa10 (Hoxa10), Hoxa9 (Hoxa9), Hoxa7 (Hoxa7), Hoxa6 (Hoxa6), Hoxa5 (Hoxa5), Hoxa4 (Hoxa4), Hoxa4 (Hoxa2), Hoxa41 (Hoxa2), and Hoxa1 (Hoxa4), genes, complete cds	Homo saplens Indolethylamine N-methyltransferase (INMT) mRNA, INMT-2 allele, complete cds	tg2bh05.x1 NCI_CGAP_CLL1 Homo sapiens cDNA clone IMAGE::2109369 3'	COMPLEMENT DECAY-ACCELERATING FACTOR (CD55)	COMPLEMENT DECAY-ACCELERATING FACTOR (CD55)	Homo sapiens chromosome 21 segment HS21C007	7175g09.yr NCI_CGAP_Brn20 Homo sapiens cDNA clone IMAGE:3340576 5	w91a06.r1 Scares_placenta_8tc9weeks_2NbHP8tc9W Homo sapiens cDNA clone IMAGE:259570 5'	yw91a06.r1 Soares_placenta_8tc9weeks_2NbHP8tc9W Homo sapiens cDNA clone IMAGE:259570 5	wu35h07.x1 Soares_Dieckgraefe_colon_NHCD Homo sapiens cDNA clone IMAGE:2522077 3'	RC5-HT0582-280300-012-E12 HT0582 Homo sapiens cDNA	we12h05.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2340921 3'	hw21a03.x1 NCI_CGAP_Xid11 Homo sapiens cDNA clore IMAGE:3183532 3' similar to TR:Q12832 Q12832 GLYCOPHORIN HEP2;	xe89a03.xf NCI_CGAP_Co17 Homo sapiens cDNA clone IMAGE:2573832.3' similar to contains L1.b3 L1 repetitive element;
Top Hit Database Source	SWISSPROT	SWISSPROT	EST_HUMAN 8	Г	П	EST_HUMAN (	EST_HUMAN V	+ Z			EST HUMAN	П	/ISSPROT	NT	EST_HUMAN	EST_HUMAN	EST_HUMAN			EST_HUMAN		EST_HUMAN
Top Hit Acession No.	Q13183	Q13183	2.0E-05 AI149272.1	20E-05 AA714330.1	2.0E-05 Y08926.1	2.0E-05 A1492860.1	2.0E-05 AI991025.1	2 0E-05 AF224262 1	O DE DE AEODADEO 4	2.0E-05 AF128847.1	2.0E-05 AI381040.1	2.0E-05 P49457	P49457	2.0E-05 AL163207.2	2.0E-05 BF055939.1	2.0E-05 N41751.1	2.0E-06 N41751.1	2.0E-05 AI991025.1	2.0E-05 BE175801.1	2.0E-05 AI912713.1	2.0E-05 BE348229.1	2.0E-05 AW074604.1.
Most Similar (Top) Hit BLAST E Value	2.0E-05 Q13183	2.0E-05 Q13183	2.0E-05	20E-05	2.0E-05	2.0E-05	2.0E-05	2.0E-05	20.00	2.0E-05	2.0E-05	2.0E-05	2.0E-05 P49457	2.0E-05	2.0E-05	2.0E-05	2.0E-05	2.0E-05	2.0E-05	2.0E-05	2.0E-05	
Expression Signal	0.91	0.91	0.79	2.11	1.69	-	7.24	6		0	1.58	0.56		9.0	0.94	3.53	3.53		1.55			8.13
ORF SEQ ID NO:	32601		_			33523		33844			34671			36764	36984	37472	37473		37549			
Exon SEQ ID NO:	19273	1	1	Г		20107	ı	20385		1	1_	1.	上	l		23850	Ι.					1
Probe SEQ ID NO:	8092	6092	6288	9760	7042	7054	7062	7303		7524	BORO	9467	9467	10127	10339	10817	10817	10881	11738	11981	12477	12592

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Original Laborate Labrata Contraction	Top Hit Descriptor	Homo sapiens ABCA1 (ABCA1) gene, complete cds	AU131513 NT2RP3 Homo sapiens cDNA clone NT2RP3002707 5'	qf68g11.x1 Soares_testis_NHT Hamo sapiens cDNA clone IMAGE:1755236 3'	Hamo sapiens chromosame 21 segment HS210082	Drosophila melanogaster strain Lamto 120 Suppressor of Hairless (Su(H)) gene, partial cds	Homo sepiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively	spliced	MOSAIC PROTEIN LON	Homo sapiens chromosome 21 segment HS21C003	zw69g04.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:781494 5'	xy49g11.x1 NCI_CGAP_Lu34.1 Homo sapiens cDNA clone IMAGE:2856548 3'	Homo sapiens chromosome 21 segment HS21C046	H.sapiens repeat region	Homo sapiens Spast gene for spastin protein	Ins19g02.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:11841143' similar to contains L1.11 L1	L1 ropetitive element;	Homo sapiens phospholipase A2, group X (PLA2G10) mRNA, and translated products	7p57401.x1 NC_CGAP_Pr28 Homo sepiens cDNA clone IMAGE:3649945 3' similar to contains MER10.b3	REDICTOR DESCRIPTION OF THE TYPE A ANTIDEN (SCAN) (BO(SCAN)	Library Comment Head Comment Comment Comment Comment Comment Comment Comment Comment Comment Comment Comment Comment Comment Comment Comment Comment Comment Comment Comment Comment Comment Comment Comment Comment Comment Comment Comment Comment Comment Comment Comment Comment Comment Comment Comment Comment Comment Comment Comment Comment Comment Comment Comment Comment Comment Comment Comment Comment Comment Comment Comment Comment Comment Comment Comment Comment Comment Comment Comment Comment Comment Comment Comment Comment Comment Comment Comment Comment Comment Comment Comment Comment Comment Comment Comment Comment Comment Comment Comment Comment Comment Comment Comment Comment Comment Comment Comment Comment Comment Comment Comment Comment Comment Comment Comment Comment Comment Comment Comment Comment Comment Comment Comment Comment Comment Comment Comment Comment Comment Comment Comment Comment Comment Comment Comment Comment Comment Comment Comment Comment Comment Comment Comment Comment Comment Comment Comment Comment Comment Comment Comment Comment Comment Comment Comment Comment Comment Comment Comment Comment Comment Comment Comment Comment Comment Comment Comment Comment Comment Comment Comment Comment Comment Comment Comment Comment Comment Comment Comment Comment Comment Comment Comment Comment Comment Comment Comment Comment Comment Comment Comment Comment Comment Comment Comment Comment Comment Comment Comment Comment Comment Comment Comment Comment Comment Comment Comment Comment Comment Comment Comment Comment Comment Comment Comment Comment Comment Comment Comment Comment Comment Comment Comment Comment Comment Comment Comment Comment Comment Comment Comment Comment Comment Comment Comment Comment Comment Comment Comment Comment Comment Comment Comment Comment Comment Comment Comment Comment Comment Comment Comment Comment Comment Comment Comment Comment Comment Comment Comment Comment Comment Comment Comment Comment Comment Comment Comment Comment Comment Comment Comment Comment Comment C	Homo sapiens chromosome 21 segment HSZTCUZ/	zx36h12.s1 Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:788519 3' similar to gb:L02932 PEROXISOME PROLIFERATOR ACTIVATED RECEPTOR ALPHA (HUMAN);	2s05e11.r1 NCI_CGAP_GCB1 Hamo saplens cDNA clone IMAGE:684332 5' similar to contains Alu	repetitive element; contains element TAR1 repetitive element;	AV732190 HTF Hono sapiens cDNA clone HTFBIH01 5'	hd41b02.x1 Scares_NFL_T_GBC_S1 Homo saplens cDNA clone IMAGE:2912043 3' similar to contains	OFR.t1 OFR repetitive element	hd41b02x1 Scares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2912043 3' similar to contains	OFR.t1 OFR repetitive element;	UI-H-BIZ-egk-e-08-0-UI.s1 NCI_CGAP_Sub4 Homo sepiens cDNA clone IMAGE:2724398 3'	UI-H-BI2-egk-a-08-0-UI.s1 NOI_CGAP_Sub4 Homo septens cDNA clone IMAGE:2724398 3'	he07c10.x1 NOI_CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2873010 3' similar to contains L1.t2 L1 repetitive element;
	Top Hit Database Source	LZ.	EST_HUMAN	EST_HUMAN	L'N	ΙΝ		NT	SWISSPROT	NT	EST_HUMAN	EST_HUMAN	N	Ν	N-		EST_HUMAN	NT	1445	EST HUMAN	SWISSTAC	INT	EST_HUMAN		EST_HUMAN	EST_HUMAN		EST_HUMAN		EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN
5	Top Hit Acessian Na	2.0E-05 AF275948.1	2.0E-05 AU131513.1	2.0E-05 AI200970.1	1.0E-05 AL163282.2	1.0E-05 AF088273.1		1.0E-05 AF223391.1	P81274	1.0E-05 AL163203.2	1.0E-05 AA431119.1	1.0E-05 AW419134.1	1.0E-05 AL163246.2	1.0E-05 Z18943.1	1.0E-05 AJ246003.1		1.0E-05 AA641846.1	4505844 NT	1 0000010	1.0E-05 BF2ZZ640.1	1 10474	1.0E-05 AL163227.2	1.0E-05 AA452578.1		1.0E-05 AA236110.1	1.0E-05 AV732190.1		1.0E-05 AW 610902.1		1.0E-05 AW 510902.1	1.0E-05 AW291521.1	1.0E-05 AW 291521.1	1.0E-05 AW466995.1
	Most Similar (Top) Hit BLAST E Value	2.0E-05	2.0E-05	20E-05	1.0E-05	1.0E-05		1.0E-05	1.0E-05 P81274	1.0E-05	1.0E-05	1.0E-05	1.0E-05	1.0E-05	1.0E-05		1.0E-05	1.0E-05	T 0	1.0E-05	1.0E-031 18474	1.0E-05	1.0E-05		1.0E-05	1.0E-05		1.0E-05		1.0E-05	1.0E-05	1.0E-05	1.0E-05
	Expression Signal	3.24	2.01	1.64	1.86	1.71		0.97	11.86	1.45	2.14	2.24	0.86	0.64	1.13		4.24	5.19		0.73	2.03	2.39	2.59		12.29	180		0.79		0.79	1.18	1.18	2.04
	ORF SEQ ID NO:		32014		28983	29905				30420			31179	l				33759	Ì_	4554			35887		36107	36275	L	36682		36683			
	Exan SEQ ID NO:	25905	25551	25787	16071	16901		17074	17230	17433	17535	18104	18207	18212	20043		20135	20316	0000	78877	21000	22195	22337		22544	22708		23081		23081	23158	23158	23422
	Probe SEQ ID NO:	12650	12825	13206	2759	3740		3915	4074	4288	4392	4975	5079	5084	889		7230	7232	- 50	× (2)	OCA/	9116	9260		9487	9996		10043		10043	10120	10120	10387

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	Top Hit Descriptor	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RoRet gene, end sodium phosphate transporter (NPT3) gene, complete ods	Hüman hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HIA-H) gene, RoRet gene, and sodium phosphate transporter (NPT3) gene, complete cds	Hano sapiens chromosome 21 segment HS21C103	#73a08.x1 NCI_CGAP_HSC3 Hamo sepiens cDNA clone IMAGE:2246386 3	qg11b08.x1 Soares_placenta_8tx9weeks_2NbHP8tx9W Homo sapiens cDNA clone IMAGE:1759191 3'	Human alanhe:giyoxylate aminotransferase (AGXT) gene, exons 1 and 2	Homo capiens differentiation antigen CD20 gene, exons 5, 6	RC1-BT0313-110500-017-a07 BT0313 Homo sopieno cDNA	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG	ox20g01.x1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA done IMAGE:1656912 3' similar to	contains Alu repetitive element;	Homo sapiens chromosome 21 segment HS21C009	SUSHI REPEAT-CONTAINING PROTEIN SRPX PRECURSOR (DRS PROTEIN) (DOWN-REGULATED BY V-SRC)	ALCONOMINATION PROTEIN SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF TH	SUSHI REPEA I-CONTAINING PROTEIN SRPA PRECURSOR (DAS PROTEIN) (DOMINING PROTEIN) (BOTTON DE BY V-SRC)	Human apolipoprotein E (APOE) gene, hepatic control region HCR-2	PUTATIVE SERINE/THREONINE-PROTEIN KINASE C22E12.14C	RC3-CT0283-201199-011-h11 CT0283 Homo sapiens cDNA	zt22d05.s1 Soares ovary turnor NDHOT Homo saplens cDNA clone IMAGE:713865 3' similar to contains	MER9.t1 MER9 repetitive element ;	FASCICLIN II, PHOSPHATIDYLINOSITOL-LINKED ISOFORM PRECURSOR (FAS II)	FASCICLIN II, PHOSPHATIDYLINOSITOL-LINKED ISOFORM PRECURSOR (FAS II)	abg0f10.s1 Stratagene lung (#937210) Homo sapiens cDNA clone IMAGE:854251 3' similar to contains	MER20.t1 MER20 repetitive element;	Homo sapiens KIAA0555 gene product (KIAA0555), mRNA	qw16g09.x1 NCI_CGAP_Ut3 Homo sapiens cDNA done IMAGE:1991296 3' similar to contains Alu repetitive	element	EST99205 Thyroid Homo sapiens cDNA 5' end similar to ES' containing L1 repeat
	Top Hit Database Source	· ½	LΝ	LΝ	EST_HUMAN	EST_HUMAN	IN	TN	EST HUMAN	SWISSPROT		EST_HUMAN	ĮN.	TOGGSSIMIS	OWIGGENO	SWISSPROT	LN LN	SWISSPROT	EST HUMAN		EST_HUMAN	SWISSPROT	SWISSPROT		EST_HUMAN	LN	) 	EST_HUMAN	EST HUMAN
	Top Hit Acesslan No.	1.0E-05 U91328.1	.0E-05 U91328.1	1.0E-05 AL163303.2	9.0E-06 AI583811.1	9.0E-06 AI218983.1	9.0E-06 M61755.1	1,23416.1	9.0E-06 BE065042.1	P08547		9.0E-06 Al034370.1	9.0E-06 AL163209.2	OBSTRO	000/00	Q63769	9.0E-06 U35114.1	Q10364	8.0E-06 AW362539.1		8.0E-06 AA284847.1	P34083	P34083		7.0E-06 AA669729.1	7662177 NT		7.0E-06 Al368252.1	7.0E-06 AA385542.1
	Most Similar (Top) Hit BLAST E Value	1.0E-05	1.05-05	1.0E-05	9.0E-06	9.0E-06	90-30'6	9.0E-06 L23416.1	90E-06	9.0E-06 P08547			90-30'6		l	9.0E-06 Q63769	Ì	9.0E-06 Q10364				8.0E-06 P34083	8.0E-06 P34083			7.0E-06			
	Expression Signal	2.22	2.22	1.4	5.83	6.11	2.58	2.48	0.82	2.82		12.35	1.17	0	5.0	3.3	4.43	3,61			2.75				1.73	3.12		10.58	0.85
	ORF SEQ ID NO:	37860	37861			29348		32528				34515	35280		33803	35804					33276	L				27708	L		
	Exen SEQ ID NO:	24230	24230	$l_{\perp}$	15854	16340	L	1	i	1		21003			L9777	22261	ı	<u> </u>	1_		19884	ı	}	L		L		16113	ı
	Probe SEQ ID NO:	11159	11159	13023	2737	3165	3698	6025	7003	7598		7953	8659	3	9183	9183	9473	11180	2596		6728	10751	10751		1002	1470		2936	3654

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Probe SEQ ID NO:	Exen SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acessian No.	Top Hit Database Source	Top Hit Descriptor
5813	19003		5.49	7.0E-06	.0E-06 AW883141.1	7	QV2-OT0062-250400-173-h01 OT0062 Homo saplens cDNA
5925	19112	32424	0.93	7.0E-06	7.0E-06 N98645.1	EST_HUMAN	176507.71 Soares, multiple, scierosis, Zhorinish Homo sapiens cunh cione invade, 2104.12.3
8989		35608	0.83	7.0E-08	11420709 NT	TN	Hamo sapiens DNA segment, numerous copies, expressed probes (GS1 gene) (DXF68S1E), mRNA
10104	23142			7.0E-06	7.0E-06 Q61147	SWISSPROT	CERULOPLASMIN PRECURSOR (FERROXIDASE)
12202	1	31547	1.68	7.0E-06	7.0E-06 BF215972.1	EST_HUMAN	601881522F1 NIH_MGC_67 Homo sapiens CDNA clone IMAGE: 409397.2 3
2984	1	29177	1.17	6.0E-06	3.0E-06 BE069189.1	EST_HUMAN	QV3-BT0379-010300-105-411 B10379 Homo sapiens culvA
3784	16945	29952		6.0E-06	3.0E-06 BE069189.1	EST HUMAN	QV3-BT0379-010300-105-d11 BT0379 Homo sapiens curve
4876			2.13	6.0E-06	8.0E-06 Q01456	SWISSPROT	OVARIAN ABUNDAN I MESSAGE PROTEIN (DAM PROTEIN)
488	18013		2.19		8.0E-06 A(040099.1	EST_HUMAN	ox08e02.x1 Scares_fetal_liver_spieen_1NFLS_S1 Homo saplens curva done invade_1roov.sd 5 similiar to contains MER8.t2 MER8 repetitive element;
5465	1				8.0E-06 AF167441 1	IN	Mus musculus E-cadherin binding prolein E7 mRNA, complete cds
5525	1	31739			6.0E-06 Q02040	SWISSPROT	PROTEIN XE7
10060	L		1.98		6.0E-06 AW801912.1	EST HUMAN	ILS-UM0070-110400-063-502 UM0070 Homo sapiens cDNA
13142	1	31948		90-30'9	11418157 NT	INT	Homo sapiens calcium channel, voltage-dependent, alpha 11 subunit (CACNATI), mKNA
6186	1_		3.74		5.0E-06 AL 163246.2	LΝ	Homo sapiens chromosome 21 segment HS210046
6467	19634	32995	1.94		5.0E-06 U07561.1	TN	Human ABL gene, exon 1b and intron 1b, and putative M8604 Met protein (M8604 Met) gene, complete cds
7382	1	Ĺ	1.18		5.0E-06 AB007546.1	NT	Homo sapiens gene for LEC12, complete cds
8654	21734	L			5.0E-06 AW856972.1	EST_HUMAN	RC1-CT0302-120200-013-h02 CT0302 Homo saplens cDNA
8654	١.	L	95.0		5.0E-06 AW856972.1	EST HUMAN	RC1-CT0302-120200-013-h02 CT0302 Hamo sapiens CDNA
10307	L.	L			5.0E-06 AA313620.1	EST_HUMAN	EST185496 Colon carcinoma (HCC) call line nonto saprens curva 3 end
10731		l			5.0E-06 P06681	SWISSPROT	COMPLEMENT CZ PRECURSON (CACO CONVENTACE)
13011	25566	31957	5.49		5.0E-06 AI065045.1	EST HUMAN	HANGE I DUMBER 1958 IIVEL COUNT HIGH SEPTEMBER COUNTY
798	<u> </u>	77880	5.47		4.0F-06 R16267.1	EST HUMAN	yadbous it soares intant drain 1 Mib Honto sapiets obtain draine invace, where the container is contained in the petitive element, contains L1 repetitive element.
				<u>l</u>			xc63g12.x1 NCI_CGAP_Eso2 Homo septiens cDNA clone IMAGE.2589574 3' similar to contains Alu
869	14045	5 27110	4.73		4.0E-06 AW103354.1	EST HUMAN	repetitive element/contains element MENAT repetitive etailient.
1365	14519	27593	3.18		4.0E-06 AI334928.1	EST_HUMAN	tb33e09.x1 NCI_CGAP_HSCZ Hamo saptens dLiva didite invides.z0ddids 3
1365	14519	27594			4.0E-06 AI334928.1	EST_HUMAN	(BASEBLAY) NOT COATE TRUE ATTACKS LAWS and the Coate of the Coate of the Coate of the Coate of the Coate of the Coate of the Coate of the Coate of the Coate of the Coate of the Coate of the Coate of the Coate of the Coate of the Coate of the Coate of the Coate of the Coate of the Coate of the Coate of the Coate of the Coate of the Coate of the Coate of the Coate of the Coate of the Coate of the Coate of the Coate of the Coate of the Coate of the Coate of the Coate of the Coate of the Coate of the Coate of the Coate of the Coate of the Coate of the Coate of the Coate of the Coate of the Coate of the Coate of the Coate of the Coate of the Coate of the Coate of the Coate of the Coate of the Coate of the Coate of the Coate of the Coate of the Coate of the Coate of the Coate of the Coate of the Coate of the Coate of the Coate of the Coate of the Coate of the Coate of the Coate of the Coate of the Coate of the Coate of the Coate of the Coate of the Coate of the Coate of the Coate of the Coate of the Coate of the Coate of the Coate of the Coate of the Coate of the Coate of the Coate of the Coate of the Coate of the Coate of the Coate of the Coate of the Coate of the Coate of the Coate of the Coate of the Coate of the Coate of the Coate of the Coate of the Coate of the Coate of the Coate of the Coate of the Coate of the Coate of the Coate of the Coate of the Coate of the Coate of the Coate of the Coate of the Coate of the Coate of the Coate of the Coate of the Coate of the Coate of the Coate of the Coate of the Coate of the Coate of the Coate of the Coate of the Coate of the Coate of the Coate of the Coate of the Coate of the Coate of the Coate of the Coate of the Coate of the Coate of the Coate of the Coate of the Coate of the Coate of the Coate of the Coate of the Coate of the Coate of the Coate of the Coate of the Coate of the Coate of the Coate of the Coate of the Coate of the Coate of the Coate of the Coate of the Coate of the Coate of the Coate of the Coate of the Coate of the Coate of the Coate of the Coate of t
1503	ľ				4.0E-06 BF365612.1	EST_HUMAN	COV2-N 10046-200600-230-no N 10040 Holito Saprens CONA clone IMAGE 2710425 3
2339					4.0E-06 AW015401.1	EST HUMAN	ULT-FBIC-888-1-3001.81 NOT COART COART SAFATIO COART COART COART COART COART COART COART COART COART COART COART COART COART COART COART COART COART COART COART COART COART COART COART COART COART COART COART COART COART COART COART COART COART COART COART COART COART COART COART COART COART COART COART COART COART COART COART COART COART COART COART COART COART COART COART COART COART COART COART COART COART COART COART COART COART COART COART COART COART COART COART COART COART COART COART COART COART COART COART COART COART COART COART COART COART COART COART COART COART COART COART COART COART COART COART COART COART COART COART COART COART COART COART COART COART COART COART COART COART COART COART COART COART COART COART COART COART COART COART COART COART COART COART COART COART COART COART COART COART COART COART COART COART COART COART COART COART COART COART COART COART COART COART COART COART COART COART COART COART COART COART COART COART COART COART COART COART COART COART COART COART COART COART COART COART COART COART COART COART COART COART COART COART COART COART COART COART COART COART COART COART COART COART COART COART COART COART COART COART COART COART COART COART COART COART COART COART COART COART COART COART COART COART COART COART COART COART COART COART COART COART COART COART COART COART COART COART COART COART COART COART COART COART COART COART COART COART COART COART COART COART COART COART COART COART COART COART COART COART COART COART COART COART COART COART COART COART COART COART COART COART COART COART COART COART COART COART COART COART COART COART COART COART COART COART COART COART COART COART COART COART COART COART COART COART COART COART COART COART COART COART COART COART COART COART COART COART COART COART COART COART COART COART COART COART COART COART COART COART COART COART COART COART COART COART COART COART COART COART COART COART COART COART COART COART COART COART COART COART COART COART COART COART COART COART COART COART COART COART COART COART COART COART
3131					4.0E-06 AF198349.1	뉟	Gallus gailus Dadriz protein (Dadriz) Ilinava, Cariptoto Cus
4000	17157	7 30163	3 0.99		4.0E-06 AW848295.1	EST_HUMAN	13-C10214-130200-1/4-600 U 12-C1011 PIENT ORDINA SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVI

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Top Hit Descriptor	wig4c10.x1 NCI_CGAP_Brn26 Homo sapiens cDNA dons IMAGE:2432552 3' similar to contains element MER22 repetitive element ;	TRANSMEMBRANE PROTEASE, SERINE 2	Homo sapiens T cell receptor beta locus, TCRBV7S3A2 to I CRBV12S2 region	Homo sapiens SPP2 gene for secreted phosphoprotein 24 precursor, exons 1-8	Homo sapiens mRNA, chromosome 1 specific transcript KIAA0486	xs53e01.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2773368 3'	######################################	######################################	Homo sapiens PP1200 mRNA, complete cds	ek48g11.s1 Soeres_testis_NHT Homo sepiens oDNA done INAGE:1409252 3' similar to contains LTR1.t3 LTR1 repetitive element ;	wI22a05.x1 NCI_CGAP_Ut1 Homo saplens cDNA clone IMAGE:2425616 3' similar to TR:060734 060734   UNE-1 LIKE PROTEIN ;contains L1.t2 L1 repetitive element ;	hq84d12.x1 NCI_CGAP_HN13 Homo sapiens cDNA clone IMAGE:3124151 3	hq64412.x1 NCI_CGAP_HN13 Homo sapiens cDNA clone IMAGE:3124151 3'	yb78b10.r1 Stratagene ovary (#937217) Homo sapiens cDNA clone IMAGE:77275 5' similar to contains L1 repetitive element	Homo sapiens gene for alpha-1-microglobulin-bikunin, exons 1-5 (encoding alpha-1-microglobulin, N-	terminus.)	AU159412 THYRO1 Homo sapiens cDNA clone I HYRO1001602.3	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG	601336213F1 NIH MGC 44 Homo sapiens cluna dione lima de 30803 14 3	PAROTID SECRETORY PROTEIN PRECURSOR (PSP.)	RC04_T0001-261199-011-A03_LT0001 Homo saplens cDNA	HOMEOBOX PROTEIN GOOSECOID	POL POLYPROTEIN (CONTAINS: PROTEASE; REVERSE TRANSCRIPTASE; ENDONUCLEASE)	wa04e03.x1 NCI_CGAP_Kid11 Home eapiens oDNA done IMAGE:2237068 3' similar to contains MEK30.b1	MER30 repetitive element;	HISTIDINE-RICH GLYCOPRO I EIN PRECURSOR	KNOB-ASSOCIATED HIS ILDINE-RICH PRO-ILLING OF STREET PRO-ILLING OF STREET PRO-ILLING OF STREET PRO-ILLING OF STREET PRO-ILLING OF STREET PRO-ILLING OF STREET PRO-ILLING OF STREET PRO-ILLING OF STREET PRO-ILLING OF STREET	AV657555 GLC Homo sapiens cDNA clone GLC-DBU5 3
Top Hit Databese Source	EST_HUMAN	SWISSPROT	IN	NT	- IN	EST HUMAN	EST HUMAN	EST HUMAN	N	EST HUMAN	EST HUMAN	EST_HUMAN	EST_HUMAN	EST HUMAN		۲	EST_HUMAN	SWISSPROT	EST_HUMAN	SWISSPROT	EST_HUMAN	SWISSPROT	SWISSPROT		EST_HUMAN	SWISSPROT	SWISSPROT	EST_HUMAN
Top Hit Acession No.	4.0E-06 AI886939.1	015393	4.0E-06 AF009660.1	4.0E-06 AJ272265.1	4.0E-06 AB007955.1	0E-06 AW 299734.1	.0E-06 AA700562.1	3.0E-06/AA700562.1	.0E-06 AF202635.1	.0E-06 AA868218.1	3.0E-06 Al857779.4	3.0E-06 BE047094.1	3.0E-06 BE047094.1	.0E-06 T50266.1		.0E-06 X54816.1	3.0E-06 AU159412.1	3.0E-06 P08548	.0E-06 BE562964.1	.0E-06 P07743	3.0E-06 AW385262.1	2.0E-06 P54366	2.0E-06 P21414		2.0E-06 AI672138.1	2.0E-06 P04929	2.0E-06 P06719	2.0E-06 AV657555.1
Most Similar (Top) Hit BLAST E Value	4.0E-06	4.0E-06 015393	4.0E-06	4.0E-08	4.0E-06	4.0E-06	ຸ ຕ		3.0E-06	3.0E-06	3.0E-06	3.0E-06	3.0E-06	_ "		ຕ		Ĺ	3.0E-06	3				<u> </u>	``			
Expression Signal	1.89	89.0	4.49	1.28		1.33	1.31			180	2.67			80		5.52	0.82	2.14	0.81	0.75		2.22	6.39			1	1.81	6.0
ORF SEQ ID NO:	31041	36308	35620				28494			. 62		30040				30807	32814		34874		]_					28785		29786
Exon SEQ (D NO:	18059	1	ı	ı	L	١	1		15471	l		1		1	L	17819	19462	20456	21356		L		L	<u>l.</u>	15579	Ĺ	15755	ľ
Probe SEQ ID NO:	4929	9698	0006	6066	11735	13149	2232	2232	2340	2088	3330	3883	3883	4507		4684	6289	7377	8274	8883	12658	207	1599		2451	2537	2632	3607

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																_	_								<del>_</del> -		_	_	-	
Top Hit Descriptor	zp02e05.r1 Stratagene ovarian cancer (#937219) Homo sapiens cDNA clone IMAGE:595232 5'	UI-HI-Bi3-aky-g-05-0-UI.s1 NCI_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2736176 3'	Mus musculus gene for odorant receptor A18, complete cds	on34h01,s1 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1558609 3' similar to contains Afu repetitive	element;	te51f05.x1 Soares_NFL_T_GBC_S1 Homo sepiens cDNA clone IMAGE:2090241 3' similar to TR:Q13537 Q13537 MER37 TRANSPOSABLE ELEMENT, COMPLETE CONSENSUS SEQUENCE. ;	wjs0b04.x1 NCI_CGAP_Lym12 Homo sapiens cDNA clone IMAGE:2410063 3'	nv59c06.s1 NO_CGAP_GCB1 Homo saplens cDNA clone IMAGE:1234090 3' similar to contains L1.t3 L1	repetitive element ;	MR3-SN0067-120400-002-f02 SN0067 Homo saplens cDNA	A447R Heart Homo sapiens cDNA clone A447	<u>2027c11.s1 Soares, pinsal, gland, N3HPG Homo sapiens cDNA clone IMAGE.413300 3' similar to</u> TR:P70467 P70467 REVERSE TRANSCRIPTASE :	vu37c04.r1 Soares ovary tumor NbHOT Homo sapiens cDNA clone IMAGE:235974 5' similar to gb:X74929	KERATIN, TYPE II CYTOSKELETAL 8 (HUMAN);	Homo saplens glypican 3 (GPC3) gene, partial cds and flanking repeat regions	Homo sapiens gtypican 3 (GPC3) gene, partial cds and flanking repeat regions	t/18g10.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2141730 3'	yw69e03.s1 Soares_placenta_8to9weeks_2NbHP8to9W Homo saplens cDNA clone IMAGE:287212.3'	AV748969 NPC Homo capiens cDNA clone NPCAXD05 5'	PROTEIN MOV-10	hs92102.x1 NC_CGAP_Kld13 Homo sapiens cDNA clone IMAGE:3144699 3' similar to contains L1.t2 L1	repetitive etement;	ORGANIC CATION/CARNITINE TRANSPORTER 2 (SOLUTE CARRIER FAMILY 22, MEMBER 5) (HIGH-	AFFINITY SOUIDIM-DEPENDEN! CARNITINE COLIFAINSPORTER)	Mus musculus DowlmbE pratein (Dowlmbe) michae, complete cas	MEROZOITE SURFACE PROTEIN CMZ-8	Homo sapiens chromosome 21 segment HS21C078	zi06a12.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:429982 3' similar to	contains Alu repetitive element;	zi06at2.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sepiens cDNA clone IMAGE:4ZB982 3 similar to contains Alu repetitive element;
Top Hit. Database Source	EST_HUMAN	EST_HUMAN	ΙN		EST_HUMAN	EST HUMAN	EST_HUMAN		EST_HUMAN	EST_HUMAN	EST HUMAN	NAMIN TAB		EST_HUMAN	IN	FZ	EST_HUMAN	EST_HUMAN	EST_HUMAN	SWISSPROT		EST_HUMAN		SWISSPROT	L	SWISSPROT	IN		EST_HUMAN	EST_HUMAN
Top Hit Acession No.	2.0E-06 AA173518.1	2.0E-06 AW450215.1	2.0E-06 AB030896.1		2.0E-06 AA974932.1	2.0E-06 AI539448.1	2.0E-06 AIB19424.1		2.0E-06 AA688423.1	2.0E-06 AW869223.1	T12238.1	2 DE DE A A 772497 1		2.0E-06 H62051.1	2.0E-06 AF003529.1	2.0E-06 AF003529.1	2.0E-06 A1473450 1	2.0E-06 N30576.1	2.0E-06 AV748969.1	P23249		2.0E-06 BE328232.1		076082	1.0E-06 AF084364.1	P09125	1.0E-06 AL163278.2		1.0E-06 AA034141.1	1.0E-06 AA034141.1
Most Similar (Top) Hit BLAST E Value	2.0E-06/	2.0E-06 /	2.0E-06/		2.0E-08	2.0E-06	2.0E-08		2.0E-06	2.0E-06	2.0E-08 T12238.1	2 OF OR	22	2.0E-06	2.0E-06	2.0E-08		2.0E-06	2.0E-08	2.0E-06 P23249		2.0E-06					1.05-06			
Expression Signal	1.54	89.0	1.7		0.92	0.62	5.64		0.63	1.02	0.78	40.4	201	1.59	6.0	6.0	0.46	98'0	0.7	1.34		5.94		1.16	1.8	1.8			1.19	1.19
ORF SEQ ID NO:	30017	30026	30033			32766	33112		34183		34882			35872		36057		36527		31549	<u> </u>	i					27786		27837	27838
Exon SEQ ID NO:	17018	17027	17035		19389	19420	19733		20702	21184	21363	22446	2 2	22128	22491	22491	22510	ľ	1	ı		25473		_	13860	14635	14706		14756	14756
Probe SEQ ID NO:	3858	3868	3876		6214	6246	6571		7635	8102	8281	9500	2000	9049	9417	9417	9436	9902	10123	12548		12711		34	674	1482	1553		1603	1603

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	Top Hit Descriptor	DNA-DIRECTED RNA POLYMERASE III LARGEST SUBUNIT	Homo sapiens p47-phox (NCF1) gene, complete cds	Homo sapiens p47-phox (NCF1) gene, complete cds	Human ABL gene, exon 1b and intron 1b, and putative M8604 Met protein (M8804 Met) gene, complete cds	Homo sapiens chromosome 21 segment HS21C085	Homo sapiens chromosome 21 segment HS21C085	za27e08.s1 Soares fetal liver spleen 1NFLS Homo seplens cDNA clone IMAGE:293750 3'	MR1-BT0800-030700-002-c06 BT0800 Homo sapiens cDNA	MR3-FN0004-090600-001-e04 FN0004 Homo saplens cDNA	MR3-FN0004-090600-001-e04 FN0004 Homo sapiens cDNA	15 KDA SELENOPROTEIN PRECURSOR	CM0-BT0281-031199-087-h04 BT0281 Homo sapiens cDNA	FIBRINOGEN ALPHA/ALPHA-E CHAIN PRECURSOR	IL5-HT0730-020500-074-g01 HT0730 Homo sapiens cDNA	ol29c08.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1524878 3'	qp54e02.x1 NCI_CGAP_Co8 Homo sapiens cDNA clone IMAGE:1926842 3	qv23f06.x1 NCI_CGAP_Lym6 Homo sapiens cDNA clone IMAGE:1982435 3' similar to contains element MR repositive selement	2355e01.51 Soares fetal liver spicen 1NFLS Homo sapiens cDNA clone IMAGE:298472 3'	DYNEIN GAMMA CHAIN, FLAGELLAR OUTER ARM	Homo sapiens shox gene, alternatively spliced products, complete cds	Homo sapiens shox gene, alternatively spliced products, complete cds	zo 17e08.r1 Stratagene colon (#937204) Homo sapiens cDNA clone IMAGE:587174 6'	zx04d11.s1 Soares_tatal_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:785493 3' similar to gb:D26129 RIBONUCLEASE PANCREATIC PRECURSOR (HUMAN);	Homo sapiens chromosome 21 segment HS21C003	RC4-NT0054-120500-012-b03 NT0054 Homo sapiens cDNA	Homo sapiens ADP/ATP carrier protein (ANT-2) gene, complete cds	Homo saplens glypican 3 (GPC3) gene, partial cds and flanking repoat regions	Homo sapiens glypican 3 (GPC3) gene, partial cds and flanking repeat regions	Homo sapiens chromosome 21 segment HS21C080	Homo sapiens chromosome 21 segment HS21C081	ql82g07.x1 Soares_NhHMPu_S1 Homo sepiens cDNA clone IMAGE:1878876 3
2.6	Top Hit Database Source	SWISSPROT	N	NT	Ę	N	NT		EST_HUMAN	EST_HUMAN	EST HUMAN	SWISSPROT	EST_HUMAN	SWISSPROT	EST_HUMAN	EST_HUMAN	EST HUMAN	ECT HIMAN	EST HUMAN	SWISSPROT	노	LN	EST_HUMAN	EST HUMAN	IN	EST HUMAN	NT.	LN	NT	TN	LN	EST_HUMAN
	Top Hit Acessian No.	P27625	1.0E-06 AF184614.1	1.0E-06 AF184614.1	1.0E-06 U07561.1	1.0E-06 AL163285.2	1.0E-06 AL163285.2	1.0E-08 N65946.1	1.0E-06 BF333015.1	1.0E-06 BE834518.1	1.0E-06 BE834518.1	060613	1.0E-06 BE063527.1	P02671	1.0E-06 BE185330.1	1.0E-06 AA912623.1	1.0E-06 Al347010.1	4 05 06 4	1.0E-06 N74635 1	1.0E-06 Q39575	1.0E-06 U82688.1	1.0E-06 U82688.1	1.0E-06 AA132611.1	1 0F-06 AA449257.1	1.0E-06 AL 163203.2	1.0E-06 AW890941.1	1.0E-06 L78810.1	9.0E-07 AF003529.1	9.0E-07 AF003529.1	9.0E-07 AL163280.2	9.0E-07 AL163281.2	8.0E-07 AI288696.1
	Most Similar (Top) Hit BLAST E Value	1.0E-06 P27625	1.0E-06	1.0E-06	1.0E-06	1.0E-06	1.0E-06	1.0E-08	1.0E-05	1.0E-06	1.0E-06	1.0E-06 O60613	1.0E-06	1.0E-06 P02671	1.0E-06	1.0E-06	1.0E-06	1010	10 F	1.0E-06	1.0E-06	1.0E-06	1.0E-06	1 0E-06	1.0E-06	1.0E-06	1.0E-08	9.0E-07	9.0E-07	9.0E-07	9.0E-07	8.0E-07
	Expression Signal	0.99	4.49	4.49	16.97	1.18	1.18	0.72	5.14	0.94	0.94	1.04	0.72	7.53	0.73	0.99	1.12	10.4	100	0.61	3.47	3.47	5.22	3.55	2.19	3.1	8.24	1.85	1.95	0.09	1.83	423
	ORF SEQ ID NO:			28304	30610			Ĺ		31607	31608			33569			35079							<u> </u>			32041					31008
	Exon SEQ ID NO:	14768	ı	l l	17629	!_	L.			18630	L	L		_	1	21272	1		027700	1	1_	1	L			L	_	L	┸	L	1 '	18023
	Probe SEQ ID NO:	1615	2050	2050	4489	5215	5215	5342	5405	5430	5430	5592	6915	7012	7923	8180	8468	1	68	9226	0884	9884	8929	900	10705	11949	12589	371	377	8602	11525	4893

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													_	_		_	_	-	_						_
Top Hit Descriptor	ql82g07.x1 Soares_NhHMPu_S1 Hamo sepiens cDNA clone IMAGE:1878876 3'	POL POLYPROTEIN [CONTAINS: PROTEASE; REVERSE TRANSCRIPTASE; ENDONUCLEASE]	Homo sapiens UDP-glucuronosytransferase gene, complete cds	EST05660 Fetal brain, Stratagene (cat#936206) Homo sapiens cDNA clone HFBEN89	Homo sapiens chromosome 21 segment HS210080	Homo sapiens membrane intarleukin 1 receptor accessory protein (IL1RAP) gene, exons 10 and 11	Homo sepiens ATP-binding cassette, sub-family A (ABC1), member 8 (ABCA8), mRNA	Homo sapiens ATP-binding cassetts, sub-family A (ABC1), member 8 (ABCA8), mRNA	CM3-CT0277-221089-024-e11 CT0277 Homo saplens cDNA	Homo septiens HLA class III region containing tenascin X (tenascin-X) gene, partial cds; cytochrome P450 21- hydroxylase (CYP21B), complement component C4 (C4B) G11, helicase (SKI2W), RD, complement factor B (R6), and, complement component C2 (C2) genes.>	HYPOTHETICAL 24.1 KD PROTEIN IN LEF4-P33 INTERGENIC REGION	7g94f07x1 NCI_CGAP_Co16 Homo sapiens cDNA clone IMAGE:3314149 3' similar to TR:075920 075920	CM0-BT0281-031199-087-e03 BT0281 Homo saplens cDNA	CM4-NN1029-250300-121-h12 NN1029 Homo saplens cDNA	hu11h05.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3166329 3' similar to contains L1.b2 L1 L1 repetitive element ;	wh64f10.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2385547 3'	EST93615 Supt cells Homo sepiens cDNA 5' end	wh64/10.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IWAGE:2385547 3'	Homo saplens NOD1 protein (NOD1) gene, exons 4 through 14 and complete cds	Mus musculus OG-2 homeodomain protein (OG-2) gene, partial cds	tg06b05.71 NCI_CGAP_CLL1 Homo sapiens cDNA clone IMAGE:2107953 3' similar to contains Alu repetitive element,contains element A3R repetitive element;	Ig06b05x1 NC_CGAP_CIL1 Homo sapiens cDNA clone IMAGE:2107953 3' similar to contains Alu repetitive element, contains element A3R repetitive element;	xe31e02.X1 NCI_CGAP_Br18 Home capiens cDNA clone IMAGE:2568362 3' similar to gb:X15341 CYTOCHROME C OXIDASE POLYPEPTIDE VIA-LIVER (HUMAN);	ADAM-TS 1 PRECURSOR (A DISINTEGRIN AND METALLOPROTEINASE WITH THROMBOSPONDIN MOTIFS 1) (ADAMTS-1) (ADAM-TS-1)	S-ANTIGEN PRECURSOR
Top Hit Database Source	EST_HUMAN	SWISSPROT	IN	EST_HUMAN	LN	N	TN	NT	EST_HUMAN	L'A	SWISSPROT	FOT LIMAN	EST HUMAN	EST HUMAN	EST HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	NT	NT	EST HUMAN	EST HUMAN	EST HUMAN	SWISSPROT	SWISSPROT
Top Hit Acession No.	8.0E-07 A1288596.1	P21414	8.0E-07 AF135416.1	8.0E-07 T07770.1	8.0E-07 AL163280.2	7.0E-07 AF167341.1	F0055700 NT	TN 0075009	6.0E-07 AW855558.1	00 DO 00 DO 00 DO 00 DO 00 DO 00 DO 00 DO 00 DO 00 DO 00 DO 00 DO 00 DO 00 DO 00 DO 00 DO 00 DO 00 DO 00 DO 00 DO 00 DO 00 DO 00 DO 00 DO 00 DO 00 DO 00 DO 00 DO 00 DO 00 DO 00 DO 00 DO 00 DO 00 DO 00 DO 00 DO 00 DO 00 DO 00 DO 00 DO 00 DO 00 DO 00 DO 00 DO 00 DO 00 DO 00 DO 00 DO 00 DO 00 DO 00 DO 00 DO 00 DO 00 DO 00 DO 00 DO 00 DO 00 DO 00 DO 00 DO 00 DO 00 DO 00 DO 00 DO 00 DO 00 DO 00 DO 00 DO 00 DO 00 DO 00 DO 00 DO 00 DO 00 DO 00 DO 00 DO 00 DO 00 DO 00 DO 00 DO 00 DO 00 DO 00 DO 00 DO 00 DO 00 DO 00 DO 00 DO 00 DO 00 DO 00 DO 00 DO 00 DO 00 DO 00 DO 00 DO 00 DO 00 DO 00 DO 00 DO 00 DO 00 DO 00 DO 00 DO 00 DO 00 DO 00 DO 00 DO 00 DO 00 DO 00 DO 00 DO 00 DO 00 DO 00 DO 00 DO 00 DO 00 DO 00 DO 00 DO 00 DO 00 DO 00 DO 00 DO 00 DO 00 DO 00 DO 00 DO 00 DO 00 DO 00 DO 00 DO 00 DO 00 DO 00 DO 00 DO 00 DO 00 DO 00 DO 00 DO 00 DO 00 DO 00 DO 00 DO 00 DO 00 DO 00 DO 00 DO 00 DO 00 DO 00 DO 00 DO 00 DO 00 DO 00 DO 00 DO 00 DO 00 DO 00 DO 00 DO 00 DO 00 DO 00 DO 00 DO 00 DO 00 DO 00 DO 00 DO 00 DO 00 DO 00 DO 00 DO 00 DO 00 DO 00 DO 00 DO 00 DO 00 DO 00 DO 00 DO 00 DO 00 DO 00 DO 00 DO 00 DO 00 DO 00 DO 00 DO 00 DO 00 DO 00 DO 00 DO 00 DO 00 DO 00 DO 00 DO 00 DO 00 DO 00 DO 00 DO 00 DO 00 DO 00 DO 00 DO 00 DO 00 DO 00 DO 00 DO 00 DO 00 DO 00 DO 00 DO 00 DO 00 DO 00 DO 00 DO 00 DO 00 DO 00 DO 00 DO 00 DO 00 DO 00 DO 00 DO 00 DO 00 DO 00 DO 00 DO 00 DO 00 DO 00 DO 00 DO 00 DO 00 DO 00 DO 00 DO 00 DO 00 DO 00 DO 00 DO 00 DO 00 DO 00 DO 00 DO 00 DO 00 DO 00 DO 00 DO 00 DO 00 DO 00 DO 00 DO 00 DO 00 DO 00 DO 00 DO 00 DO 00 DO 00 DO 00 DO 00 DO 00 DO 00 DO 00 DO 00 DO 00 DO 00 DO 00 DO 00 DO 00 DO 00 DO 00 DO 00 DO 00 DO 00 DO 00 DO 00 DO 00 DO 00 DO 00 DO 00 DO 00 DO 00 DO 00 DO 00 DO 00 DO 00 DO 00 DO 00 DO 00 DO 00 DO 00 DO 00 DO 00 DO 00 DO 00 DO 00 DO 00 DO 00 DO 00 DO 00 DO 00 DO 00 DO 00 DO 00 DO 00 DO 00 DO 00 DO 00 DO 00 DO 00 DO 00 DO 00 DO 00 DO 00 DO 00 DO 00 DO 00 DO 00 DO 00 DO 00 DO 00 DO 00 DO 00 DO 00 DO 00 DO 00 DO 00 DO 00 DO 00 DO 00 DO 00 DO 00 DO 00 DO 00 DO 00 DO 00 DO 00 DO 00 DO 00 DO 00 DO 00 DO	P41479	0 00 07 0000000 4	6.0E-07 BE063509 1	6.0E-07 AW903222.1	6.0E-07 BE222390.1	5.0E-07 AI831893.1	5.0E-07 AA380630.1	5.0E-07 AI831893.1	5.0E-07 AF149774.1	5.0E-07 U65067.1	5.0E-07 Al393981.1	5.0E-07 AI393981.1	5.0E-07 AW 070885.1	5 0F-07 09W UO1	P09593
Most Similar (Top) Hit BLAST E Value	8.0E-07	8.0E-07 P21414	8.0E-07	8.0E-07	8.0E-07	7.0E-07	7.0E-07	7.0E-07	6.0E-07	70 10 0	6.0E-07 P41479	20 30 9	6.0E-07	6.0E-07	6.0E-07	5.0E-07	5.0E-07	5.0E-07	5.0E-07	5.0E-07	5.0E-07	5.0E-07	5.0E-07	5.05.07	5.0E-07 P09593
Expression Signal	4.23	8.17	8.44	5.84	6.1	0.97	98.0	98'0	3.47	· · ·	1 74		1 45	1.72	1.32	1.04	2.39	0.73	0.97	1.33	1.7.1	1.7.1	16.93	100	20.0
ORF SEQ ID NO:	31009					28167	31906		28205	6	71007	0000	1						30886	32767	33487	1	1		
Exon SEQ ID NO:	18023	19192	21273	24907	25143	15057	18830	18830	15105	2000	17236	3	1		25992	13649	١.	l	17904	19421	20075		20578	1	1
Probe SEQ ID NO:	4893	6007	8191	11921	12183	1914	5636	2636	1962	ğ	8 8	9	1215	124	13229	336	1082	3096	4769	6247	7210	7210	7503	0470	8687

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Single Exoll Flores Expressed in technical	Top Hit Descriptor	CM-BT178-220499-014 BT178 Homo sapiens cDNA	COLLAGEN ALPHA 1(!) CHAIN PRECURSOR	Homo sapiens Xq pseudoautosomal region; segment 1/2	Homo sapiens chromosome 21 segment HS210085	QV0-CT0383-210400-204-612 CT0383 Homo sapiens cDNA	ws84h05.x1 NCI_CGAP_Co3 Homo sapiens cDNA clone IMAGE:2504697 3	Homo sapiens SPP2 gene for secreted phosphoprotein 24 precursor, exons 1-5	HISTONE DEACETYLASE 5 (HDS) (HIST ONE DEACETYLASE WIDNA)	HISTONE DEACETYLASE 5 (HD5) (HISTONE DEACETTLASE WILDAT)	Homo sapiens chromosome Zi segment HSZTUOU/	xy49g11.x1 NCI_CGAP_Lu34.1 Homo sapiens cDNA done IMAGE:2835346.3	601676748F1 NIH_MGC_Z1 Homo sapiens cUNA cloro IMACE: 399901 3	601576748F1 NIM_MGC_21 Homo sapiens CUNA clone IMAGE:3838651 5	Homo sapiens chromosome 21 segment HS21C018	w/81b08.x/ NCI_CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2389703 3	wi81b08.x1 NC_CGAP_Kid12 Homo saplens cUNA clone INA GET2389703 3	PM1-BN0083-030300-003-e12 BN0083 Homo sapiens cUNA	601649083F1 NIH_MGC_73 Homo sapiens cDNA clone IMAGE:3832924 5	Homo sapiens deleted in lymphocytic leukemia, 1 (DLEU1), mRNA	Human microfibril-associated glycoprotein (MFAP2) gene, pulative promoter region and alternatively spiliced	untranslated exons	Homo sapiens Xq pseudoautosomai region; segment 1/2	Human polymorphic microsatellite DINA	Human IgK subgroup I germline gene, exons 1 and 2, v-region 016 aliete	ni56b09.s1 NCI_CGAP_Ov2 Homo sapiens cDNA clone IMAGE:980825 similar to contains Alu repeuvve	derieu (Aufleins Line in representation and in the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the	Human polymorphic migrostatum Liva	MR0-BN0115-020300-001-f11 BN0115 Homo sapiens culvA	MRO-BN0115-020300-001-f11 BN0115 Home sapiens CUNA	yd50f12,r1 Soares fetal Iiver spieen 1NFLS Homo sapiens cuiva cione iiwakee ii 11093 o	HYPOTHETICAL 63.8 KD PROTEIN IN GUIT-RIMT IN LENGENIC REGION PRECUNSON	OVOSTATIN PRECURSOR (OVOMACROGLOBOLIN)	AV650201 GLC Homo septens aDNA done GLCCCD01 3	We86b12.X1 Soares NFL_1 GBC_S1 Homo septens convision agreement and a septens convision and a septens convision and a septens convision and a septens convision and a septens convision and a septens convision and a septens convision and a septens convision and a septens convision and a septens convision and a septens convision and a septens convision and a septens convision and a septens convision and a septens convision and a septens convision and a septens convision and a septens convision and a septens convision and a septens convision and a septens convision and a septens convision and a septens convision and a septens convision and a septens convision and a septens convision and a septens convision and a septens convision and a septens convision and a septens convision and a septens convision and a septens convision and a septens convision and a septens convision and a septens convision and a septens convision and a septens convision and a septens convision and a septens convision and a septens convision and a septens convision and a septens convision and a septens convision and a septens convision and a septens convision and a septens convision and a septens convision and a septens convision and a septens convision and a septens convision and a septens convision and a septens convision and a septens convision and a septens convision and a septens convision and a septens convision and a septens convision and a septens convision and a septens convision and a septens convision and a septens convision and a septens convision and a septens convision and a septens convision and a septens convision and a septens convision and a septens convision and a septens convision and a septens convision and a septens convision and a septens convision and a septens convision and a septens convision and a septens convision and a septens convision and a septens convision and a septens convision and a septens convision and a septens convision and a septens convision and a septens convision and a septens convision and a septens
EXCIT LODGS	Top Hit Database Source	EST_HUMAN C	SWISSPROT		TN TN	EST HUMAN C	T_HUMAN	٦		ISSPROT	١			T_HUMAN	_		EST_HUMAN \		T_HUMAN						NT		ESI HUMAIN	_			٦	П	$\neg$	7	EST_HUMAN
allille	Top Hit Acesson No.	5.0E-07 Al908587.1		5.0E-07 AJ271735.1		5.0E-07 AW862537.1		5.1				4.0E-07 AW419134.1	4.0E-07 BE901975.1	4.0E-07 BE901976.1	4.0E-07 AL163218.2		4.0E-07 AI765528.1	4.0E-07 BE001828.1	4.0E-07 BE967557.1	11437071 NT		3.0E-07 U19719.1	3.0E-07 AJ271735.1	3.0E-07 M99149.1	3.0E-07 M64857.1		-	١	3.0E-07 BE005077.1	3.0E-07 BE005077.1	3.0E-07 T84704.1	3.0E-07 P38739	3.0E-07 P20740	3.0E-07 AV650201.1	3.0E-07 AI797236.1
	Most Similar (Top) Hit BLAST E Value	5.0E-07	5.0E-07 P11087	5.0E-07	5.0E-07	5.0E-07	4.0E-07	4.0E-07	4.0E-07 Q9Z2V6	4.0E-07 Q9Z2V6	4.0E-07	4.0E-07	4.0E-07	4.0E-07	4.0E-07	4.0E-07	4.0E-07	4.0E-07	4.0E-07	4.0E-07		3.0E-07	3.0E-07	3.0E-07	3.0E-07		3.0E-07	3.0E-07	3.0E-07	ļ			3.0E-07		
	Expression Signal	5.47	5.69	2.08	1.2	3.06	1.66	0.8	76.0	76.0	0.51	6.4	0.53	0.53	0.56	3.88	3,88	1.89	1.32	1.71		5.38	3.59	1.43	3.62		232	1.14	4.99	4.99	76.0		0.64		0.7
	ORF SEQ ID NO:	37217	38493				30261		33963	33964	34709		36976			37881	37882							27633				28621	28789	28790		29414	L	30970	
	SEQ ID NO:	23612	24795	24868	25968	25966	1	١	L	20495	21189	22328	23367	23367	23566	24248	L	24553	1	25788	1_	13650	L	1	14808	1		15492	15665		L	L	L	1	18015
	Probe SEQ ID NO:	10577	11805	11880	12256	12918	4106	7328	7417	7417	8107	9251	10332	10332	10531	11179	11179	11495	11919	13207		454	596	1405	1655		2104	2361	2540	2546	3099	3228	4802	4849	4885

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
5175	18297	31259	1.43	3.0E-07	.0E-07 T57850.1	EST_HUMAN	yc14h09.s1 Stratagene lung (#837210) Homo sapiens cDNA clone IMAGE:80705 3' similar to similar to gb:M62982 ARACHIDONATE 12-LIPOXYGENASE (HUMAN)
5175	18297	31260	1.43	3.0E-07	.0E-07 T57850.1	EST_HUMAN	yc14h09.s1 Stratagene lung (#837210) Homo sapiens cDNA clone IMAGE:80705 3' similar to similar to gb:M62982 ARACHIDONATE 12-LIPOXYGENASE (HUMAN)
5783	ļ		1	<b>"</b>	.0E-07 O88807	SWISSPROT	PROTEIN-ARGININE DEIMINASE TYPE IV (PEPTIDYLARGININE DEIMINASE IV) (PAD-R4) (PEPTIDYLARGININE DEIMINASE TYPE ALPHA)
9009	ľ		0.7	3.0E-07	3.0E-07 O42280	SWISSPROT	WNT-14 PROTEIN PRECURSOR
6842	ľ		5.09	["	1.0E-07 AA815175.1	EST_HUMAN	cc04c10.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1339890 3'
7678	20743	34224	3.53	3.0E-07	3.0E-07 AW797168.1	EST_HUMAN	QV1-UM0036-200300-115-g02 UM0036 Homo sapiens cDNA
7841	20896		1.3		.0E-07 AI591065.1	EST_HUMAN	tw28f11.x1 NCJ_CGAP_Ov35 Home sapiens cDNA clone IMAGE:226f037 3' sImilar to contains Alu repetitive element,contains element MSR1 MSR1 repetitive element;
9330	22406	35959	0.48		3.0E-07 P33240	SWISSPROT	CLEAVAGE STIMULATION FACTOR, 64 KD SUBUNIT (CSTF 64 KD SUBUNIT) (CF-1 64 KD SUBUNIT)
8330	22406	35960	0.48	.,	3.0E-07 P33240	SWISSPROT	CLEAVAGE STIMULATION FACTOR, 64 KD SUBUNIT (CSTF 64 KD SUBUNIT) (CF-1 64 KD SUBUNIT)
13194			4.26		3.0E-07 AJ132352.1	TN	Rettus norvegicus mRNA for 45 kDa secretory protein, partial
8	13267	26270			2.0E-07 AF262988.1	NT	Homo sapiens TRF2-interacting telomeric RAP1 protein (RAP1) mRNA, complete cds
158			90'9		2.0E-07 L77569.1	NT	Homo sapiens DiGeorge syndrome critical region, telomeric end
158	13383	26414	90.9		2.0E-07 L77569.1	NT	Homo sapiens DiGeorge syndrome critical region, telomeric end
186	13408		35.88		2.0E-07 U38849.1	NT	Fugu rubripes beta-cytoplasmic(vascular) actin gene, complete cds
767	13948		1.48	,	2.0E-07 AF003530.1	NT	Home saplens homeobox protein CDX4 (CDX4) gene, complete cds and flanking repeat regions
767	13948		1.48		2.0E-07 AF003530.1	NT	Homo sapiens homeobox protein CDX4 (CDX4) gene, complete cds and flanking repeat regions
977	13959		. 1.36		2.0E-07 P11369	SWISSPROT	RETROVIRUS-RELATED POL POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE ; ENDONUCLEASE]
	14139	27200	232		2.0E-07 AA223260.1	EST HUMAN	2/08b07.s1 Stratagene NT2 neuronal precursor 937230 Homo capiens cDNA clone IMAGE:650869 3' similar to gb:L31860 GLYCOPHORIN A PRECURSOR (HUMAN);contains Alu repetitive element,
730	<u> </u>	<u> </u>			2 0E-07 TR3042 4	EST HIMAN	yc15g04.s1 Stratagene lung (#937210) Homo sapiens cDNA clone IMAGE:80790 3' similar to contains L1 mesetiiwe element :
1100	┸	1			2.0E.071026768	SWISSPROT	I/6 AUTOANTIGEN
200					2 0E 07 009704	SWISSPROT	HYPOTHETICAL 72.5 KD PROTEIN C2F7.10 IN CHROMOSOME I
	L				2 NE A7 BE134307 4	EST HIMAN	R01818B18E1 NIH MGC 58 Homo sapiens cDNA clone IMAGE:4044891 57
3/20	1	1			2 0E 07 AF125348 4	P LV	Homo sabians caveolin 1 (CAV1) gene, exon 3 and partial cds
8//8	- 1	29940	7		AF 123340.J	TOT LINEAN	TOWA NIM 023 26 DAD 468-414 NIM 1023 Home sanians cDNA
523	8 18360		0.6		2.0E-07 AW902219.1	ESI HUMAN	CVS-NN 1025-200400-100-1111 NN 1025-110110 September 20147

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Probe (2007 D)         Exp. (2007 D)         Probability (2007 B)         Probability (2007 B)         Probability (2007 B)         Probability (2007 B)         Probability (2007 B)         Probability (2007 B)         Probability (2007 B)         Probability (2007 B)         Probability (2007 B)         Probability (2007 B)         Probability (2007 B)         Probability (2007 B)         Probability (2007 B)         Probability (2007 B)         Probability (2007 B)         Probability (2007 B)         Probability (2007 B)         Probability (2007 B)         Probability (2007 B)         Probability (2007 B)         Probability (2007 B)         Probability (2007 B)         Probability (2007 B)         Probability (2007 B)         Probability (2007 B)         Probability (2007 B)         Probability (2007 B)         Probability (2007 B)         Probability (2007 B)         Probability (2007 B)         Probability (2007 B)         Probability (2007 B)         Probability (2007 B)         Probability (2007 B)         Probability (2007 B)         Probability (2007 B)         Probability (2007 B)         Probability (2007 B)         Probability (2007 B)         Probability (2007 B)         Probability (2007 B)         Probability (2007 B)         Probability (2007 B)         Probability (2007 B)         Probability (2007 B)         Probability (2007 B)         Probability (2007 B)         Probability (2007 B)         Probability (2007 B)         Probability (2007 B)         Probability (2007 B)         Probability (2007 B)<	-			_	_	_		<del>-</del>	_			_	_		_	-,	. 7	_	_			_	_	_	_	$\neg$	7	_	-	т	_	
Exon NO:-         CNF SEQ. Expression Signal         Most Similar IT pp Hit Acession Signal         Most Similar IT pp Hit Acession Value SIGNOS           18650   D NO:-         31638   1.52   2.0E-07 AW889066.1         No.           25829   33229   0.73   2.0E-07 AW889066.1         2.0E-07 AW889066.1           21744   3.87   3.87   2.0E-07 AW889066.1         2.0E-07 AW889066.1           21744   3.87   3.87   2.0E-07 AW882507.1         2.0E-07 AW882507.1           23739   37342   1.01   2.0E-07 AW882507.1         2.0E-07 AW882507.1           23739   37342   1.01   2.0E-07 AW882507.1         2.0E-07 AW882507.1           23739   37342   1.01   2.0E-07 AW882507.1         2.0E-07 AW882507.1           23739   37342   1.01   2.0E-07 AW882507.1         2.0E-07 AW882507.1           23739   37342   1.01   2.0E-07 AW882507.1         2.0E-07 AW882507.1           24056   2.0E-07 AW882507.1         2.0E-07 AW882507.1           25066   1.0E-07 AW78862.1         1.0E-07 AW78862.1           14291   1.0E-07 AW78862.1         1.0E-07 AW78862.1           17650   30536   4.69   1.0E-07 AW78862.1         2.0E-07 AW78862.1           20142   33560   4.69   1.0E-07 AW78862.1         2.0E-07 AW78862.1           20881   34382   0.69   1.0E-07 AW78862.1         2.0E-07 AW78862.1           20881   34382   0.69   1.0E-07 AW78862.1         2.0E-07 AW78862.1           21491   35020   2.29   1.0E-07 AW78862.1<		Top Hit Descriptor	RC3-NN0066-260400-021-g11 NN0066 Homo sapiens cDNA	UI-H-BI3-ake-b-01-0-UI.s1 NCI_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2734008 31	qg56d05.x1 Soares_testis_NHT Hamo saptens cDNA clane IMAGE:1839177 3'	AV729390 HTC Homo sapiens cDNA done HTCAEG02 5'	zk27g09.s1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:471808 3'	Homo sapiens chromosome 21 segment HS21C103	CM4-NN0003-280300-124-e06 NN0003 Homo saplens cDNA	COMPLEMENT FACTOR B PRECURSOR (C3/C5 CONVERTASE) (PROPERDIN FACTOR B)   (GLYCINE-RICH BETA GLYCOPROTEIN) (GBG) (PBF2)	COMPLEMENT FACTOR B PRECURSOR (C3/C5 CONVERTASE) (PROPERDIN FACTOR B) (c) YOINE-RICH BETA GLYCOPROTEIN) (GBG) (PBF2)	PM0-HT0339-260100-006-H07 HT0339 Homo serviers dDNA	7785711 v5 Stratanene lung cardnoma 937218 Homo saplens cDNA clone IMAGE:565029 3' similar to	contains THR.b2 THR repetitive element;	Homo sapiens chromosome 21 segment HS21C082	GLYCOPROTEIN GPV	Homo sapiens chromosome 21 segment HS21C082	AV718662 GLC Homo sapiens cDNA clone GLCFNF04 5'	AV718882 GLC Homo sapiens cDNA clone GLCFNF04 5'	Homo sapiens chromosome Xq28 melanoma antigen family A2a (MAGEA2A), melanoma antigen family A12	(MAGEA12), melanoma antigen family A2b (MAGEA2B), melanoma antigen family A3 (MAGEA3), caltractin	(CALT), NAD(P)H dehydrogenase-like protein (NSDHL), and LI>	[1243d06.y1 NCI_CGAP_Bm52 Homo sapiens cDNA clone IMAGE:2291339 5	Iz43d06.y1 NCI_CGAP_Bm52 Homo sepiens cDNA clone IMAGE:2291339 5	w43c07.s1 Soares fetal liver spicen 1NFLS Homo sapiens cDNA clone IMAGE:245484 3	PM4-TN0024-030800-002-b05 TN0024 Homo sepiens cDNA	PM4-TN0024-030800-002-b05 TN0024 Homo sapiens cDNA	Hano sapiens chranosome 21 segment HS21C081	ENTEROPEPTIDASE (ENTEROKINASE)	ENTEROPEPTIDASE (ENTEROKINASE)	zi51e10.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:434346 3	ADAM-TS 8 PRECURSOR (A DISINTEGRIN AND METALLOPROTEINASE WITH THROMBOSPONDIN MOTIFS 8) (ADAMTS-8) (ADAM-TS8) (METH-2)
Exon NO:         Check SEQ Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal			EST HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	NT	EST_HUMAN	SWISSPROT	SWISSPROT	EST HIMAN	NC III	EST_HUMAN	Ϋ́	SWISSPROT	۲	EST HUMAN	EST_HUMAN			INT	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST HUMAN	EST_HUMAN	NT	SWISSPROT	SWISSPROT	EST_HUMAN	SWISSPROT
Exon NO: 19850         ORF SEQ 31638         Expression 1,52         Most 1,52           19857         3329         0,73           21744         3,87         1,11           23002         37329         0,73           21927         3,87         1,11           23002         37322         1,11           23002         37322         1,11           23002         37322         1,01           23002         37322         1,01           23002         37322         1,01           23002         37342         1,01           23002         37342         1,01           23739         37342         1,01           23739         37342         1,01           23739         37342         1,01           14291         27784         2,91           14291         27784         2,91           14291         30534         2,91           17650         30536         4,69           20142         33560         4,69           20142         33561         4,69           20881         34325         0,69           20981         34326         0,69	,	Top Hit Acession No.	AW898066.1	AW448968.1	AI208715.1	AV729390.1	AA035198.1	AL163303.2	AW892507.1	P00751	D00754	DE483747 4	1000110	AI732462.1	AL163282.2	P09256	AL163282.2	AV718662.1	AV718682.1			U82671.2	BE047871.1	BE047871.1	N55081.1	BF375909.1	BF375909.1	AL163281.2	P97435	P97435	AA693576.1	P57110
Exon ORF SEQ Express NO: Signal NO: Signal NO: Signal NO: Signal NO: Signal NO: Signal NO: Signal NO: Signal NO: Signal NO: Signal NO: Signal NO: Signal NO: Signal NO: Signal NO: Signal NO: Signal NO: Signal NO: Signal NO: Signal NO: Signal NO: Signal NO: Signal NO: Signal NO: Signal NO: Signal NO: Signal NO: Signal NO: Signal NO: Signal NO: Signal NO: Signal NO: Signal NO: Signal NO: Signal NO: Signal NO: Signal NO: Signal NO: Signal NO: Signal NO: Signal NO: Signal NO: Signal NO: Signal NO: Signal NO: Signal NO: Signal NO: Signal NO: Signal NO: Signal NO: Signal NO: Signal NO: Signal NO: Signal NO: Signal NO: Signal NO: Signal NO: Signal NO: Signal NO: Signal NO: Signal NO: Signal NO: Signal NO: Signal NO: Signal NO: Signal NO: Signal NO: Signal NO: Signal NO: Signal NO: Signal NO: Signal NO: Signal NO: Signal NO: Signal NO: Signal NO: Signal NO: Signal NO: Signal NO: Signal NO: Signal NO: Signal NO: Signal NO: Signal NO: Signal NO: Signal NO: Signal NO: Signal NO: Signal NO: Signal NO: Signal NO: Signal NO: Signal NO: Signal NO: Signal NO: Signal NO: Signal NO: Signal NO: Signal NO: Signal NO: Signal NO: Signal NO: Signal NO: Signal NO: Signal NO: Signal NO: Signal NO: Signal NO: Signal NO: Signal NO: Signal NO: Signal NO: Signal NO: Signal NO: Signal NO: Signal NO: Signal NO: Signal NO: Signal NO: Signal NO: Signal NO: Signal NO: Signal NO: Signal NO: Signal NO: Signal NO: Signal NO: Signal NO: Signal NO: Signal NO: Signal NO: Signal NO: Signal NO: Signal NO: Signal NO: Signal NO: Signal NO: Signal NO: Signal NO: Signal NO: Signal NO: Signal NO: Signal NO: Signal NO: Signal NO: Signal NO: Signal NO: Signal NO: Signal NO: Signal NO: Signal NO: Signal NO: Signal NO: Signal NO: Signal NO: Signal NO: Signal NO: Signal NO: Signal NO: Signal NO: Signal NO: Signal NO: Signal NO: Signal NO: Signal NO: Signal NO: Signal NO: Signal NO: Signal NO: Signal NO: Signal NO: Signal NO: Signal NO: Signal NO: Signal NO: Signal NO: Signal NO: Signal NO: Signal NO: Signal NO: Signal NO: Signal NO: Signal NO: Signal NO: Signal N		Most Similar (Top) Hit BLAST E Value	2.0E-07	2.0E-07	2.0E-07	2.0E-07	2.0E-07	2.0E-07	2.0E-07	2.0E-07	208.07	205.0	4.0L-01	2.0E-07	Ì		1.0E-07	1.0E-07	1.0E-07				1.0E-07	1.0E-07	L						1.0E-07	
Exon ORF SEQ ID ID ID ID ID ID ID ID ID ID ID ID ID		Expression Signal	1.52	0.73	3.39	3.87	1.11	1.4	6.34	101	107	90 6	7.80	2.38	0.76	2.08	1.24	2.91	2.91			0.8	4.69	4.69	7.6	0.69	0.69	1.24	2.76	2.76	2.7	
		ORF SEQ ID NO:	L			ł	l					l														l				L	L	
		Exon SEQ ID NO:	18660	25829	19957	21744	21972	23002	23509	23739	002.00	20100	70000	25967	14291	14704	14291	17550	17550			•	1		1	20881	١.	L	ł	ì	ı	1 1
			5460	8884	6802	8664	8893	6963	10474	10706	902.04		2130	12226	1126	7888	3838	4408	4408			6832	9002	7006	7662	7826	7826	7854	8410	8410	9155	9470

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	93' similar to contains MER18.t3	5,			3'	3' similar to TR:095722 095722			3901953'		2 3' cimilar to contains OFR.t2			2328273 3			ne NHTBC_cn15c02 random	ne NHTBC_cn15c02 random		e cds; and unknown gene						80398 5'		
Top Hit Descriptor	hu28h06.x1 NCI_CGAP_Mei15 Homo sapiens cDNA clone IMAGE:3171419 3' similar to contains MER18.t3 MER18 repetitive element;	602137714F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4274426 5'	EST185054 Brain IV Homo saplens cDNA	Homo sapiens chromosome 21 segment HS21C082	qx89e03.x1 NCI_CGAP_GC8 Homo sapiens cDNA clone IMACE:2009692 3'	hr53c11.x1 NC _CGAP_Kld11 Homo saplens cDNA clone IMACE:3132212 3' cimilar to TR:O95722 O95722  DJ1163J1.1;	H. saplens ALAD gene for porphobilinogen synthase	Human lambda-immunoglobulin constant region complex (germline)	te51b06.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2090195 3'	AV734819 cdA Homo sapiens cDNA clone cdABFB06 5'	wn30a07 xt NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2446832 3' cimilar to containe OFR.t2 OFR renetitive element :	Homo saplens chromosome 21 segment HS21C101	Homo sapiens partial steerin-1 gene	wd16b05x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2328273 3'	601590133F1 NIH_MGC_7 Homo saplens cDNA clone IMAGE:3943976 5	601590133F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3943976 5	on 5002 x1 Normal Human Trabecular Bone Cells Homo sepiens cDNA clone NHTBC_cn15002 random	cn15c02.x1 Normal Human Trabecular Bone Cells Homo saplens cDNA clone NHTBC_cn15c02 random	EST382776 MAGE resequences, MAGK Homo saplens cDNA	Homo capiens jun dimerization protein gene, partial cds; cfos gene, complete cds; and unknown gene	Homo sapiens microsomal epoxide hydrolase (EPHX1) gene, complete cds	ANKYRIN 1 (ERYTHROCYTE ANKYRIN)	Rat mRNA for ribosomal protein L31	DYNEIN HEAVY CHAIN (DYHC)	DYNEIN HEAVY CHAIN (DYHC)	yc11e12.r1 Stratagene lung (#837210) Homo sapiens cDNA clone IMAGE:80398 5'	cong3.P11.A5 conorm Homo sapiens cDNA 3'	Rattus norvegicus Munc13-1 mRNA, complete ods
Top Hit Database Source	EST_HUMAN	EST_HUMAN	<b>EST_HUMAN</b>	LN	EST_HUMAN	EST HUMAN	LN LN	LN	EST_HUMAN	EST HUMAN	FOT HIMAN	NT	\ V	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST HUMAN	EST_HUMAN	LN	LN	SWISSPROT	TN	SWISSPROT	SWISSPROT	EST_HUMAN	EST_HUMAN	NT
Top Hit Acession No.	1.0E-07 BE327843.1	1.0E-07 BF674524.1	1.0E-07 AA386311.1	1.0E-07 AL163282.2	1.0E-07 Al341136.1	1.0E-07 BE048770.1	1.0E-07 X64467.1	1.0E-07 X51755.1	9.0E-08 AI539362.1	9.0E-08 AV734819.1	0 0E-08 & 1804052 4	9.0E-08 AL163301.2	9.0E-08 AJ251973.1	8.0E-08 AI911352.1	8.0E-08 BE795469.1	8.0E-08 BE795469.1	8.0E-08 AI752367.1	8.0E-08 AI752367.1	8.0E-08 AW970693.1	8.0E-08 AF111167.2	8.0E-08 AF253417.1	7.0E-08 Q02357	7.0E-08 X04809.1	7.0E-08 P15305	7.0E-08 P15305	7.0E-08 T65891.1	7.0E-08 AI535743.1	7.0E-08 U24070.1
Most Similar (Top) Hit BLAST E Value	1.0E-07	1.0E-07	1.0E-07	1.0E-07	1.0E-07	1.0E-07	1.0E-07	1.0E-07	9.0E-08	9.0E-08	80-300	90E-08	90E-08	8.0E-08	8.0E-08	8.0E-08	8.0E-08	8.0E-08	8.0E-08	8.0E-08	8.0E-08	7.0E-08					7.0E-08	7.0E-08
Expression Signal	0.6	2.35	1.23	1.22	2.35	3.37	1.45	2.1	0.75	2.04			2.51	2.09	1.01	1.57	5.35	5.35		0.48					0.88		1.73	4.1
ORF SEQ ID NO:	36436	36776	36784		38771	31761			33982								35557	35558		37445		26345		<u> </u>	29840	31413		38658
SEQ ID NO:	22856	1	1	23716	l	L		_	L	23129		L		1	14241	16798	22016	22016	L	23821	1	L	14546	16829	16829	18445	١ :	
Probe SEQ ID NO:	9816	10140	10149	10682	12085	12506	12659	12852	7433	10091	14.457	11965	12456	622	1075	3634	8937	8937	9827	10788	11523	87	1392	3666	3666	6332	11052	11970

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Top Hit Descriptor	AIN (DYHC)	AIN (DYHC)	Homo sapiens chromosome 21 segment HS21C048	Homo sapiens chromosome 21 segment HS21C048	MR0-HT0166-191199-004-g09 HT0166 Homo saplens cDNA	Homo sapiens KIAA1074 protein (KIAA1074), mRNA	Homo sapiens chromosome 21 segment HS21C048	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG	ob56c05.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1335368 3' sImilar to contains MER12.b3 MER12 repetitive element;	RETROVIRUS-RELATED POL POLYPROTEIN (CONTAINS: REVERSE TRANSCRIPTASE;		Homo sapiens chromosome 21 segment HS210009	Homo sapiens chromosome 21 segment HS21C103	nh03b09.s1 NCI_CGAP_Thy1 Homo saplens cDNA clone IMAGE:943193 similar to contains Alu repetitive		COMPLEMENT C2 PRECURSOR (C3/C5 CONVERTASE)	QV0-CT0225-131099-034-a12 CT0225 Homo sapiens cDNA	DORSAL-VENTRAL PATTERNING TOLLOID PROTEIN PRECURSOR	DORSAL-VENTRAL PATTERNING TOLLOID PROTEIN PRECURSOR	DKFZp434J0426_r1 434 (synonym: htes3) Homo saplens cDNA clone DKFZp434J0426 5	oz05e02.x1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1674458 3' similar to	e element;	Homo sapiens shox gene, alternativaly spliced products, complete cds	URIDINE PHOSPHORYLASE (UDRPASE)	TRANSMEMBRANE PROTEASE, SERINE 2	Cricetulus griseus ribosomal transcription factor (UBF2) mRNA, complete cds	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG	of78d12.s1 Soares_total_fetus_Nb2HF8_9w Homo saptens cDNA clone IMAGE:1622903 3'	er/22d10.x1 Gessler Wilms tumor Homo capiene oDNA clone IMAGE:1699411 3' similar to contains Alu	Hearts element with the tapeaute element,	2/76b08.r1 Scares_testis NHT Horno septiens cDNA clone IMAGE://2824/ 5 similar to Inc. G305579 G505579 NA/CA,K-EXCHANGER.;
	DYNEIN HEAVY CHAIN (DYHC)	DYNEIN HEAVY CHAIN (DYHC)	Homo sapiens chron	Homo sapiens chron	MR0-HT0166-19118	Homo sapiens KIAA	Homo sapiens chron	LINE-1 REVERSE 1	ob56c05.s1 NCI_CGAP_GCB1 Homo MER12.b3 MER12 repetitive element;	RETROVIRUS-REL	ENDONUCLEASE	Homo sapiens chron	Homo sapiens chron	nh03b09.s1 NCI_CC	element;	COMPLEMENT C2	QV0-CT0225-13109	DORSAL-VENTRA	DORSAL-VENTRA	DKFZp434J0426_r1	oz05e02.x1 Soares	contains Alu repetitive element;	Homo sapiens shox	URIDINE PHOSPH	TRANSMEMBRAN	Cricetulus griseus ri	LINE-1 REVERSE	ot78d12.s1 Soares	an22d10.x1 Gessler	ו בלבנווואם מכונופוול כי	#76b08.r1 Soares_testis_NHT Hords G505579 NA/CA,K-EXCHANGER.
Top Hit Database Source	SWISSPROT	SWISSPROT	NT	NT	EST_HUMAN	NT	NT	SWISSPROT	EST HUMAN		SWISSPROT	LN	NT		<b>EST_HUMAN</b>	SWISSPROT	EST_HUMAN	SWISSPROT	SWISSPROT	EST_HUMAN		EST HUMAN	L	SWISSPROT	SWISSPROT	.⊥N	SWISSPROT	EST_HUMAN	100	EST HOMAN	EST_HUMAN
Top Hit Acession No.	P15305	215305	6.0E-08 AL163248.2	6.0E-08 AL163248.2	6.0E-08 BE144398.1	7662473 NT	6.0E-08 AL163248.2	P08547	6.0E-08 AA827075.1		P11369	6.0E-08 AL163209.2	5.0E-08 AL163303.2		5.0E-08 AA493851.1	P06681	5.0E-08 AW851878.1	P25723	P25723	4.0E-08 AL079581.1		4.0E-08 AI078417.1	4.0E-08 U82668.1	P52624	015393	4.0E-08 L42571.1	P08547	4.0E-08 AI016342.1		4.0E-08 AI050027.1	4.0E-08 AA393627.1
Most Similar (Top) Hit BLAST E Value	7.0E-08 P15305	7.0E-08 P15305	80-30.9	80E-08	80E-08	80E-08	80E-08	6.0E-08 P08547	6.0E-08		6.0E-08 P11369	6.0E-08	5.0E-08		5.0E-08	5.0E-08 P06681	5.0E-08	4.0E-08 P25723	4.0E-08 P25723	4.0E-08		4.0E-08	4.0E-08	4.0E-08 P52624	4.0E-08 015393	4.0E-08	4.0E-08 P08547	4.0E-08		4.0E-08	۱
Expression Signal	1.84	1.84	3.3	3.3	1.77	0.68	1.15	0.59	0.55		2.16	1.43	2.17		3.93	4.55	1.77	.1.03	1.03	1.06		1.01	0.65	1.07	6.0	1.13	1.56	0.85		4.75	5.16
ORF SEQ ID NO:	29839			ļ			30487				38390		26350		28576		32077													37241	38037
Exan SEQ ID NO:	16829	16829		1	15564	ı	17506		22594	1 .		24812	13322	<u></u>	15441	25144	25271	l_	14948	16127		16308	17180	19698	L	_	Ĺ.,		<u>.                                    </u>	23632	24391
Probe SEQ ID NO:	12978	12978	840	8	2436	3129	4363	8137	9529		11701	11823	87		2309	12185	12382	1799	1799	2950		3132	4054	9635	8668	9340	9845	10536		10597	11328

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Probe SEQ ID NO:	Exen SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Vælue	Top Hit Acession No.	Top Hit Dafabase Source	Top Hit Descriptor
11328	24381	38038	5.16	4.0E-08	4.0E-08 AA393627.1	EST_HUMAN	Z76b08.rl Soares_testis_NHT Homo sepiens cDNA clone IMAGE:728247 5' similar to TR:G505579 G605579 NA/CA,K-EXCHANGER.;
11349	24411	38064		4.0E-08	4.0E-08 BF692493.1	EST_HUMAN	602248024F1 NIH_MGC_62 Homo sapiens cDNA clone IMAGE:4333300 5
11349	24411	L	11.86	4.0E-08	4.0E-08 BF692493.1	EST_HUMAN	602248024F1 NIH_MGC_62 Homo saplens cDNA clone IMAGE:4333300 5
12190	26108			4.0E-08	4.0E-08 W 76159.1	EST HUMAN	za86g03.r1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:345556 5' strillar to contains L1.t1 L1 repetitive element;
12804	25588		201	4.0E-08	4.0E-08 AI343353.1	EST HUMAN	tb95a11.x1 NCI_CGAP_Co16 Homo sapiens cDNA clone IMAGE:2062076 3' similar to contains MER18.b3   MER18 MER18 meretitive element ;
							bb79a10.y1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3048570 5' similar to TR:Q9Z158 Q9Z158
5728	18921	32215	227	3.0E-08	3.0E-08 BE018348.1	EST_HUMAN	SYNTAXIN 17.;
7115	18541	31498	6.01	3.0E-08	3.0E-08 AI792737.1	EST_HUMAN	qs76f11.y5 NCI_CGAP_Pr28 Home saplens cDNA clone IMAGE:1944045 5'
7711	l	_	1.43	3.0E-08	3.0E-08 AL163246.2	ΙN	Homo sapiens chromosome 21 segment HS21C046
7928	20978		3.32	3.0E-08	3.0E-08 AI436352.1	EST_HUMAN	th93h09.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2126273 3° sImilar to TR:Q13537 Q13537 MER37 TRANSPOSABLE ELEMENT, COMPLETE CONSENSUS SEQUENCE. ;
10102	Ł		0.63	3.0E-08	3.0E-08 AF055066.1	LN	Homo sapions MHC class 1 region
11276	1	37983			3.0E-08 AI218001.1	EST_HUMAN	qh21a04.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1845294 31
11957	l	38646	1.32		3.0E-08 AF111167.2	LN.	Homo sapiens jun dimerization protein gene, partial cds; cfos gene, complete cds; and unknown gene
2,01	ı		33 85		3 0F-08 R18420 1	EST HUMAN	yg02/04.r1 Soares infant brain 1NIB Homo sapiens cDNA done IMAGE:30948 6' similar to contains Alu repetitive element;
2 2	1		4 16		2 0E-08 AW302996.1	EST HUMAN	xr87f06x1 NCI_CGAP_Lu26 Hamo sepiens cDNA clone IMAGE:2767139 3'
386	1		5.76		2 DE-08 AA425598 1	EST HUMAN	zw48f07.r1 Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:773317 5' similar to contains Au repetitive element,contains element MER16 repetitive element;
66	L	28732			2.0E-08 AF198349.1	F	Gallus gallus Dach2 protein (Dach2) mRNA, complete cds
677	L				2.0E-08 AW886438.1	EST HUMAN	MR0-OT0080-240200-001-g08 OT0080 Homo saplens cDNA
677	13863	26894			2.0E-08 AW886438.1	EST HUMAN	MR0-OT0080-240200-001-008 OT0080 Homo seplens cDNA
1014	L				2.0E-08 BE280477.1	EST_HUMAN	601156321F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3138893 5'
1373	L	27602	1.46		2.0E-08 AL163247.2	NT	Homo sapiens chromosome 21 segment HS21C047
1774	L				2.0E-08 AW841890.1	EST_HUMAN	IL5-CN0024-030300-026-C01 CN0024 Homo sapiens cDNA
1780	14929		2.08		2.0E-08 BE734871.1	EST_HUMAN	601570463F1 NIH_MGC_21 Homo saplens cDNA clone IMAGE:3845199 6
1902	L	1.5	6.7		2.0E-08 AW270271.1	EST_HUMAN	xp43f11.x1 NCI_CGAP_HN11 Homo saplens cDNA clone IMAGE:2743149 3'
2608	}		1.86		2.0E-08 K00216.1	NT	Sheep His-RNA-GUG
3279	1	3 29474	5.61		2.0E-08 O42280	SWISSPROT	WNT-14 PROTEIN PRECURSOR

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Top Hit Desariptor	WNT-14 PROTEIN PRECURSOR	RC3-ST0197-161099-012-b03 ST0197 Homo sapiens cDNA	Homo sapiens shox gene, alternatively spliced products, complete cds	aa28c07.rt NCI_CGAP_GCB1 Homo saplens cDNA clone IMAGE:814380 5' similar to contains L1.t2 L1 monatrive element:	Fe-77-08 v2 NC; CGAP CM 1 Home seriens cDNA clone IMAGE:2919327 3' similar to contains Alu	repetitive element;	al80h11.s1 Soares_testis_NHT Homo sapiens cDNA clone 1377189 3'	xd32c04.x1 NC _CGAP_Ov23 Homo saplens cDNA clone IMAGE:2595462 3' similar to contains MER18.b3 MER18 MER18 repetitive element ;	POL POLYPROTEIN [CONTAINS: PROTEASE; REVERSE TRANSCRIPTASE; ENDONUCLEASE]	ab02g06.s1 Stratagene fetal retina 937202 Homo sapiens cDNA clone IMAGE:839674 3'	AU139978 PLACE1 Homo sapiens cDNA clone PLACE1011719 5'	w/2f02.r/ Scares fetal liver spleen 1NFLS Homo saplens cDNA clone IMAGE:248283 5' similar to contains 1 TR4 h3 I TR4 reputitive element :	22200 4 Consequence commence ANEI S Home continue CDNA close MARCE: 248283 5' civilar to contains	yr zivz. i Soarso reta inter sproci intra Eo fronto Spronto Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Co	Homo saplens chromosome 21 segment HS21C084	Homo sapiens hypothetical protein FLJ11342 (FLJ11342), mRNA	POL POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE ; ENDONUCLEASE]	PROTEIN GRAINY-HEAD (DNA-BINDING PROTEIN ELF-1) (ELEMENT I-BINDING ACTIVITY) (TRANSCRIPTION FACTOR NTF-1)	PROTEIN GRAINY-HEAD (DNA-BINDING PROTEIN ELF-1) (ELEMENT I-BINDING ACTIVITY)	(TRANSCRIPTION FACTOR NTF-1)	Homo saplens caveolin 1 (CAV1) gene, exon 3 and partial cds	PM2-HT0130-150999-001-f12 HT0130 Homo saplens cDNA	TCBAPID5232 Pediatric pre-B cell acute lymphoblastic feukemia Baylor-HGSC project=TCBA Homo	sepiens cDNA clone TCBAP5232	TCBAP105232 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA Homo		Homb sapiens hyperion gene, exons 1-50	52 KD RO PROTEIN (SJOGREN SYNDROME TYPE A ANTIGEN (SS-A)) (RO(SS-A))	Homo sapiens chromosome 21 segment HS21C102
Top Hit Database Source	SWISSPROT	EST_HUMAN	LN	EST HIMAN	Т	EST_HUMAN	EST_HUMAN	EST HUMAN	SWISSPROT	EST HUMAN	EST_HUMAN	ENT LINAAN	NOIN DE	EST_HUMAN	N	LΝ	SWISSPROT	SWISSPROT		SWISSPROT	F	EST HUMAN		EST_HUMAN	DOT LINAAN	NOMES I	L	SWISSPROT	N
Top Hit Acession No.	D42280	2.0E-08 AW813620.1	2.0E-08 U82668.1	2 OF OB \$ \$459040 1	T.OLOGOUTO.	2.0E-08 AW 572881.1	2.0E-08 AA813204.1	2 0F-08 AW088924.1	P10272	2.0E-08 AA490121.1	2.0E-08 AU139978.1	0 DC 00 N 20007 4	A LOCAL .	2.0E-08 N78097.1	2.0E-08 AL163284.2	11431676 NT	P31792	P13002		P13002	1.0E-08 AF125348.1	1.0E-08 BE141959.1		1.0E-08 BE246844.1	7 7 70 70 70 70 70 70 70 70 70 70 70 70	DE 240044.1	5.7		1.0E-08 AL163302.2
Most Similar (Top) Hit BLAST E Value	2.0E-08 O42280	2.0E-08	2.0E-08	10 c		2.0E-08	2.0E-08	2.0F-08	2.0E-08 P10272	2.0E-08	2.0E-08	00 110 0	2.00-00	2.0E-08	2.0E-08	2.0E-08		1.0E-08 P13002		1.0E-08 P13002	1.0E-08	1.0E-08				1	1.0E-08		
Expression Signal	5.61	1.63	0.62	4 48	2	3.5	0.85	-	1.11	1.5	0.89	000	3	0.83	1.77	1.8	1.05	133		1.33	1.66	2.97		0.95		CR:O	4.51		0.62
ORF SEQ ID NO:	29475		30332			·	32247	32457	L				3/30	37382			27770	27907		27908				29453		1			34826
Exon SEQ ID: NO:	16453	17120	17339	<u> </u>	1	18200	_	]	L	<u> </u>	L	I	1//3	123771	ļ	ı	ļ	l	ļ	14824	1	J		16435		)		H	21306
Probe SEQ ID NO:	3279	3962	4189	2004	2707	5072	5753	5055	8193	8301	9286	0.0,	10/36	10738	12476	13065	1539	1872		1672	1816	2110		3261		3261	5716	7948	8224

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Top Hit Descriptor	Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ublqultin-conjugating enzyme E2D 3 (UBE2D3) genes, complete cds	Homo saplens mannosidase, beta A, Iysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D3) genes, complete cds	ot35a05.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1618736 3'	S-ANTIGEN PROTEIN PRECURSOR	PM2-BT0546-210100-004-d02 BT0548 Homo sapiens cDNA	TRICARBOXYLATE TRANSPORT PROTEIN PREGURSOR (CITRATE TRANSPORT PROTEIN) (CTP) (TRICARBOXYLATE CARRIER PROTEIN)	BONE MORPHOGENETIC PROTEIN 1 PRECURSOR (BMP-1)	Homo sapiens major histocompatibility locus class III region	Human lambda∹mmunoglobulin constant region complex (germilne)	MR4-ST0240-240700-013-g04 ST0240 Homo saplens cDNA	Hano sapiens chromosome 21 segment HS21C079	Hano sapiens chromasame 21 segment HS21C079	ye58a12.s1 Soares fetal liver spleen 1NFLS Homo sepiens cDNA clone IMAGE:121918 3	qd42e07.x1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:1732164 3' similar to contains MSR1.t1 MSR1 repetitive element;	CM0-NN1004-100300-273-506 NN1004 Homo sapiens cDNA	op74d08.s1 Soares_NFL_T_GBC_S1 Homo saplens cDNA clone IMAGE:15825753'	Homo sapiens DNA for 3-ketoacy-CoA thiclase beta-subunit of mitochondrial trifunctional protein, exon 2, 3	Human familial Alzhelmer's disease (STM2) gene, complete cds	745e10.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:3524443 3' similar to contains MER29.b2 MER29 repetitive element ;	zr80c05.r1 Soares_NhHMPu_S1 Homo saplens cDNA clone IMAGE:681992 5' similar to contains L1.t2 L1	repetitive element :	Human tysosomal membrane gtycoprotein-2 (LAMP2) gene, 5' end and flanking region	601111173F1 NIH_MGC_18 Homo sapiens cDNA clone IMAGE:3351834 5'	z58e07.s1 Sogres retina N2b4HR Homo sapiens cDNA clone IMAGE:381156 3' similar to contains L1.t2 L1	repetitive element;	ye58a12.s1 Soares fetal liver spieen TNFLS Homo sapiens cluiva cione liviadue: 121916 3	DKFZp434C0514_r1 434 (synonym: ntes3) Homo sepiens cunk cione UNFZp434Cu314 3	PM1-HT0527-160200-001-h05 H10527 Homo sapiens cUNA
Top Hit Database Source	Ł	Į.	EST_HUMAN	SWISSPROT	EST_HUMAN	SWISSPROT	SWISSPROT		TN.	T_HUMAN	- LN	Į.	EST_HUMAN	EST_HUMAN	EST_HUMAN		TN	NT	EST_HUMAN		EST_HUMAN	TN	EST_HUMAN		T	٦	Т	EST_HUMAN
Top Hit Acesslon No.	.0E-08 AF224669.1	.0E-08 AF224669.1	.0E-08 AI015304.1	.0E-08 P09593	.0E-08 BE072572.1	.0E-08 P79110	.0E-08 P98063	.0E-08 AF044083.1	.0E-08 X51755.1	.0E-08 BF375398.1	3.0E-09 AL163279.2	9.0E-09 AL163279.2	9.0E-09 T97950.1	3.0E-09 A1183500.1	3.0E-09 AW 900159.1	3.0E-09 AA938892.1	7.0E-09 D86842.1	7.0E-09 U50871.1	.0E-09 BF108755.1		7.0E-09 AA256200.1	7.0E-09 L09709.1	7.0E-09 BE254850.1		7.0E-09 AA058626.1	7.0E-09 T97950.1	6.0E-09 AL040439.1	6.0E-09 BE169421.1
Most Similar (Top) Hit BLAST E Value	1.0E-08	1.0E-08	1.0E-08	1.0E-08	1.0E-08	1.0E-08	1.0E-08	1.0E-08	1.0E-08	1.0E-0B	9.0E-09	9.0E-09	9.0E-09	8.0E-09	8.0E-09	8.0E-09	7.0E-09	7.0E-09	7.0E-09		7.0E-09	7.0E-09	7.0E-09		7.0E-09	7.0E-09	6.0E-09	6.0E-09
Expression Signal	0.54	0.54	2.27	0.56	0.85	28.0	0.87	3.55	3.06	1.26	4.17	4.17	0.63	8.1	2.54	2.53	1.98	96.0	0.58		0.99	2.86	1.95		0.76	2.01		6.2
ORF SEQ ID NO:	34927	]			36043		Ì					30482		33960									37028					31195
SEQ ID	21402	1	1	1	22480		1	24648	ı	25925	17500	17500	23302	l	1	1	16856		1_		21319	ı		ı				18223
Probe SEQ ID NO:	8320	8320	8744	9405	9406	10171	10778	11595	12581	13137	4357	4357	10267	7414	8189	9189	3695	4115	8088		8237	9460	10386		10554	10910	2221	5095

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	Top Hit Descariptor	xn85h08.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2701311 3'	MR3-HT0446-260300-201-h12 HT0446 Homo sapiens cDNA	Homo sapiens fibroblast growth factor receptor 3 (achondroplasia, thanatophoric dwarfism) (FGFR3) mRNA	Homo sapiens testis-specific kinase substrate (TSKS) gene, complete cds	745e10.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:3524443 3' similar to contains MFR29.b2 MFR29 receitive element:	HUMGS0003762 Human adult (K. Okubo) Homo sapiens cDNA	RC2-HT0252-120200-014-h10 HT0252 Homo sapiens cDNA	Homo sapiens chromosome 21 segment HS21C084	EST68746 Fetal lung II Homo sapiens cDNA 5' end	Human germline T-cell receptor beta chain Dopamine-beta-hydroxylase-like, TRY1, TRY2, TRY3, TCRBV27S1P, TCRBV22S1A2N1T, TCRBV3S1A1T, TCRBV7S1A1N2T, TCRBV5S1A1T, TCRBV13S3, TCRBV6S7P, TCRBV7S3A2T, TCRBV13S2A1T, TCRBV8S2A2PT, TCRBV7S2A1N4T, TCRBV13S9/13S>	OLFACTORY RECEPTOR-LIKE PROTEIN CORS	PM2-UM0053-240300-005-c09 UM0053 Homo saplens cDNA	zx60e09.s1 Soares_testis_NHT Homo saplens cDNA clone IMAGE:795880 3'	Homo sapiens chromosome 21 segment HS21 C082	Homo sapiens chromosome 21 segment HS21C086	Homo sapiens hypothetical protein (AF038169), mRNA	EST58385 Infant brain Homo sapiens cDNA 5' end sImilar to similar to heat shock protein, 90 kDa	zw04c06.r1 Soares_NhHMPu_S1 Homo sapiens cDNA clane IMAGE:768298 5'	yd11a07.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:66804 3'	wm94f10x1 NCI_CGAP_Ut2 Hamo sapiens cDNA clane IMAGE:2443627 3'	234s12.fl Soares_NHIMPu_S1 Homo sapiens cDNA clone IMAGE:665278 5' similar to gb:L07807 DYMAMIN.1 /HI IMAN):	http9e09.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3163120 3' similar to contains MER18.t3	MER18 repetitive element;	hu09e09.x1 NCI_CGAP_Lu24 Homo sapiens cDNA done IMAGE:3166120 3' cimitar to contains MER18.t3 MER18 repetitive element;	PROTEIN MOV-10	hu09e09.x1 NCI_CGAP_Lu24 Home sapiens cDNA clone IMAGE:3166120 3' similar to contains MER18.t3 MER18 repetitive element;
	Top Hit Database Source	EST_HUMAN	EST HUMAN	TN	Į.	FST HIMAN	EST HUMAN	EST HUMAN	N	EST_HUMAN	l- Z	SWISSPROT	EST HUMAN	EST HUMAN	TN	LΝ	LNT	EST HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	ENT HIMAN	NUMOI TO	EST_HUMAN	EST HUMAN	SWISSPROT	EST_HUMAN
	Top Hit Acession No	6.0E-09 AW 195784.1	6.0E-09 BE161653.1	4503710 NT	6.0E-09 AF200923.2	8 0E-09 BE108755 1	6.0E-09 C01803.1	5.0E-09 BE149264.1	5.0E-09 AL163284.2	5.0E-09 AA359454.1	5 0F-09 (168059 1	P37071	5.0E-09 AW799667.1	5.0E-09 AA460142.1	4.0E-09 AL163282.2	4.0E-09 AL163285.2	9558718 NT	4.0E-09 AA350878.1	4.0E-09 AA495747.1	4.0E-09 T64942.1	4.0E-09 A1886401.1	4 OF 00 4 A 40 E 4 4 2 4	177100100	3.0E-09 BE222239.1	3.0E-09 BE222239.1	P23249	3.0E-09 BE222239.1
	Most Similar (Top) Hit BLAST E Value	6.0E-09	6.0E-09	6.0E-09	60E-09	S OF JO	6.0E-09	5.0E-09	5.0E-09	5.0E-09	5.0F-09	5 0F-09 P37071	5.0E-09	5.0E-09	4.0E-09	4.0E-09	4.0E-09	4.0E-09	4.0E-09	4.0E-09	4.0E-09	4 OF 00	4.01	3.0E-09	3.0E-09	3.0E-09 P23249	3.0E-09
	Expression Signal	9.33	1.11	2.18	3.4	79	1.37	3.47	7.4	2.22	C	0 63	3.25	1.87	1.64	2.75	1.86	5.32	0.53	1.02	9.51	1 44	1	4.51	1.06	0.99	0.9
	ORF SEQ ID NO:	31711		36014		37692					21593				L		27732							28682			
	SEQ ID NO:	18695	1	22452	L		1_	14600	L	L	18507	L		1_		L	1	L.	21113	<u>!_</u>	1_	l	<u> 」</u>	15555	l	1	1 1
	Probe SEQ ID NO:	5496	8775	7289	10483	10080	12089	1447	1900	6540	88 98	8785	10300	11944	534	987	1497	2500	8030	8719	11330	14970	200	2427	2619	2716	3408

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Top Hit Descriptor	zv54a04.r1 Scares_testis_NHT Homo sapiens cDNA clone IMAGE:757422 5	H.sapiens PADPRP-I gene for NAD(+) ADP-ribosytransferase	Homo sapiens eukaryotic initiation factor 4AI (EIF4A1) gene, partial cds	258.1 KDA PROTEIN C210RF5 (KIAA0933)	hx80s02 x1 NCI_CGAP_Kld11 Homo saplens cDNA clone IWAĢE:3194090 3' similar to TR:O55091 О55091 IMPACT PROTEIN ;	Homo sapiens chromosome 21 segment HS210047	HYPOTHETICAL 13.1 KD PROTEIN B0310.4 IN CHROMOSOME X	712c08.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo saplens cDNA clone IMAGE:3527030 3'	72c08x1 Scares_NSF_F8_9W_OT_PA_P_S1 Homo saptens cDNA done IMAGE:3527030 3'	H.saplens PADPRP-I gene for NAD(+) ADP-ribosyltransferase	Hamo sapiens chromosame 21 segment HS210084	DKFZp761B1710_r1 761 (synonym: hamy2) Homo sapiens cDNA clone DKFZp761B1710 5	258.1 KDA PROTEIN C210RF5 (KIAA0833)	BRAIN-SPECIFIC ANGIOGENESIS INHIBITOR 2 PRECURSOR	qi07d09.x1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:1855793 3'	Human transposon-like element mRNA	ot47b09.s1 Scares_testis_NHT Homo sapiens cDNA clone IMAGE:1619897 3'	Homo sapiens chromosome 21 segment HS21C049	EST66142 Kidney IX Homo sapiens cDNA 5' end similar to EST containing L1 repeat	263106.r1 Seares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:796187 5 similar to contains	Alu repetitive element; 52411 Himan ratina cDNA randomly national cublibrary Homo canians cDNA	ch88a10 x1 Spares NFI T GBC S1 Homo sapiens cDNA clone IMAGE:1854114 3'	Homo sapiens Xg pseudoautosomal region; segment 1/2	AV688642 GKC Homa saplens cDNA clone GKCACA11 5'	H. sapiens PADPRP-1 gene for NAD(+) ADP-ribosy/transferase	nc11c02.r1 NCI_CGAP_Pr1 Homo sapiens cDNA clone IMAGE:1007810 similar to contains Alu repetitive	element;	zd79d03.s1 Soares_fetal_heart_NbHH19W_Homo sapiens cDNA clone IMAGE:346863 3' similar to	GD:LOZSSZ PEKOXISOME PKOLITEKATOK ACTIVATED KECEPTOK ALPHA (HOWAN);	Homo sapiens CCAAT-box-binding transcription factor (CBF2) mRNA	Homo sapiens CCAAT-box-binding transcription factor (CBF2) mRNA
Top Hit Database Source	EST_HUMAN 2		1NT	SWISSPROT	EST_HUMAN (	Γ	SWISSPROT	Г	П	П	LN	EST HUMAN	SWISSPROT	Г	EST_HUMAN (	IN LN	EST_HUMAN	LN⊥	EST_HUMAN	Г	EST HUMAN	Т	Т	Г	L L	Т	EST_HUMAN		T_HUMAN		
Top Hit Acession No.	2.1	3.0E-09 X16674.1	3.0E-09 AF175325.1	29Y3R5	3.0E-09 BE465780.1	3.0E-09 AL163247.2		13.1	3.0E-09 BF109943.1	X16674.1	2.0E-09 AL163284.2	2.0E-09 AL118573.1			2.0E-09 Al263479.1	2.0E-09 M23161.1	2.0E-09 A1004062.1		2.0E-09 AA357407.1		2.0E-09 AA461430.1	2.0E-09 M2003732 1		_		İ	2.0E-09 AA226070.1		1.0E-09 W 78152.1	5031624 NT	5031624 NT
Most Similar (Top) Hit BLAST E Value	3.0E-09	3.0E-09	3.0E-09	3.0E-09 Q9Y3R5	3.0E-09	3.0E-09	3.0E-09 Q10940	3.0E-09	3.0E-09	2.0E-09 X16674.1	2.0E-09	2.0E-09	2.0E-09 Q9Y3R5	2.0E-09 O60241	2.0E-09	2.0E-09	2.0E-09	2.0E-09	2.0E-09		2.05.09	20E-00	2.0E-09	20E-09	2.0E-09		2.0E-09		1.0E-09	1.0E-09	1.0E-09
Expression Signal	0.7	0.62	3.47	1.19	1.1	1.87	0.46	3.15	3.15	96.0	4.7	10.71	2.24	3.01	6.0 ·	0.62	0.67	0.75	0.88		8.81	0.00	1.2	0.85	20.06		1.86		1.19	1.43	1.43
ORF SEQ ID NO:			30666	30751	34682	37096	37448	37978	37979		27511		28661		30272	31348	32333				34155	١	ľ						1		27354
Exon SEQ ID NO:	16631	17361	17684	17770	21166	23488	23825	24340	24340	14013	14443	14843	15534	17204	17273	18383	13027	19452	20234	i	20679	ı	21988		_	<u> </u>	26188	1		- 1	14298
Probe SEQ ID NO:	3464	4212	4546	4634	8084	10453	10792	11272	11272	835	1287	1691	2403	4048	4119	5264	5837	6278	6919		7609	707	8909	10824	12745		12830		1019	1133	1133

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Top Hit Descriptor	qy64e11.x1 NCI_CGAP_Bm25 Homo saplens cDNA clone IMAGE:2016812 3' similar to contains MER12.t2 MER12 repetitive element ;	Homo saplens basic transcription factor 2 p44 (btf2p44) gene, partial cds, neuronal apoptosis inhibitory protein (naip) and survival motor neuron protein (smn) genes, complete cds	Homo saplens nucleolar phosphoprotein B23 (NPM1) mRNA, complete cds	Homo sapiens nucleolar phosphoprotein B23 (NPM1) mRNA, complete cds	601058602F1 NIH_MGC_10 Homo saplene cDNA clone IMAGE:3445177 51	zh35b03.s1 Soares_pineal_gland_N3HPG Homo sapiens cDNA clone IMAGE:414029 3' similar to contains. Alu repetitive element;contains element MER22 repetitive element ;	dm44g12.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1543942.3	Homo sapiens chromosome 21 segment HS21C083	Human breakpoint cluster region (BCR) gene, complete cds	GIRCUMSPOROZOITE PROTEIN PRECURSOR (CS)	wd39005.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2330481 3' similar to contains	MEK25.tt MEK25 repetitive element.	Homo sapiens chromosome 21 segment HSZ1CU83	Homo saplens GTP binding protein 1 (GTPBF1), mKNA	yb51g12.s1 Stratagene fetal spleen (#937205) Homo sapiens cUNA cione ilWAGE: 14730 3	Homo sapiens TESTIN 2 and TESTIN 3 genes, complete cds, alternatively spuiced	MR0-SN0040-050500-002-c07 SN0040 Homo sapiens cDNA	we78hG3x1 Soares_Dieckgraafe_colon_NHCD Homo sapiens cDNA clone IMAGE:2347253 3' similar to SW:RL29_HUMAN P47914 60S RIBOSOMAL PROTEIN L29 ;contains element PTR5 repetitive element ;	है48509.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo saplens cDNA clone IMAGE:2144537 3' stmilar to TR:000372 000372 PUTATIVE P150. ;	Homo sepiens MCM4 (MCM4) and DNA-PKcs (PRKDC) genes, partial cds	QV1-BT0631-150200-071-f01 BT0631 Homo saplens cDNA	EST89564 Small intestine I Homo sapiens cDNA 5' end	Homo sapiens lens major intinsic protein (MIP) gene, complete cds	Homo sapiens TPA Inducible protein (LOC61686), mRNA	Homo saplens TPA inducible protein (LOC51586), mRNA	LYSP100 PROTEIN (LYMPHOID-RESTRICTED HOMOLOG OF SP100)	LINE-1 REVERSE TRANSCRIP LASE HOMOLOG	H.sepiens DHFR gene, exon 3
Top Hit Database Source	EST_HUMAN N	I a	TN TN	TN	EST_HUMAN 6	EST_HUMAN A	T_HUMAN	LN	ı. ₩	SWISSPROT		HOMAN			HUMAN		EST_HUMAN N	EST_HUMAN			EST HUMAN						ISSPROT	Ę
Top Hit Acession No.	.0E-09 Al356086.1				.0E-09 BE535440.1	.0E-09 AA719297.1	1.0E-09 AA921958.1	1.0E-09 AL163283.2	1.0E-09 U07000.1	P26694		1.0E-09 AI688474.1	1.0E-09 AL163283.2	11418127 NT	1.0E-09 T57368.1	1.0E-09 AF260225.1	9.0E-10 AW867740.1	9.0E-10 AI870071.1	9.0E-10 Al452982.1	8.0E-10 U63630.2	8.0E-10 BE080748.1		U36308.2		7706225 NT	Q13342	P08547	7.0E-10 X00856.1
Most Similar (Top) Hit BLAST E Value	1.0E-09	1.0E-09	1.0E-09	1.0E-09	1.0E-09	1.0E-09	1.0E-09	1.0E-09	1.0E-09	1.0E-09 P26694		1.0E-09	1.0E-09	1.0E-09	1.0E-09	1.0E-09	9.0E-10	9.0E-10	9.0E-10	8.0E-10	8.0E-10	8.0E-10	8.0E-10	7.0E-10	7.0E-10			
Expression Signal	1.15	2.02	6.17	6.17	0.99	6.15	9.0	0.85	1.29	3.34		0.92	2.72	1.7.1	1.42	1.66	1.52	3.74	4.98				2.51	21.38			20.25	2.25
ORF SEQ ID NO:		29146	L	29185		}		31882		1		35206		31668			27564	28092			29607	L	L	26941	L	27890		29341
Exon SEQ ID NO:	15696	16131	L	L.	Ĺ	<u> </u>	L	l	L	Ł	1	21665	23555	26120	ᆫ	26020	L	16074	l _	L	L	L	L	L	1_	L	15749	16332
Probe SEQ ID NO:	2571	8	2992	2002	3103	4920	5341	5620	5952	6272		8584	10520	12642	12767	13132	1337	2895	6973	151	3423	4318	10170	719	719	1651	2626	3157

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Top Hit Descriptor	EST51247 Gall bladder II Homo sapiens cDNA 5' end	IL3-HT0619-110700-209-D12 HT0619 Homo saplens cDNA	DNA-DIRECTED RNA POLYMERASE II LARGEST SUBUNIT	Homo sapiens presentin-1 gene, exons 1 and 2	Homo saplens presentlin-1 gene, exons 1 and 2	Homo sapiens ASCL3 gene, CEGP1 gene, C11orf14 gene, C11orf15 gene, C11orf16 gene and C11orf17	eueb	tf02d07.x1 NCI_CGAP_Pr28 Homo sapiens cDNA clone IMAGE:2095021 3	MUCIN 2 PRECURSOR (INTESTINAL MUCIN 2)	RC3-CT0254-031099-012-g12 CT0254 Hamo sapiens cDNA	E-SELECTIN PRECURSOR (ENDOTHELIAL LEUKOCYTE ADHESION MOLECULE 1) (ELAM-1) (LEUKOCYTE-ENDOTHELIAL CELL ADHESION MOLECULE 2) (LECAM2) (CD62E)	E-SELECTIN PRECURSOR (ENDOTHELIAL LEUKOCYTE ADHESION MOLECULE 1) (ELAM-1)	(LEUKOCYTE-ENDOTHELIAL CELL ADHESION MOLECULE 2) (LECAM2) (CD62E)	ENTEROPEPTIDASE PRECURSOR (ENTEROKINASE)	EST384012 MAGE resequences, MAGL Homo saplens cDNA	DKFZp434N219_r1 434 (synonym: htes3) Homo saplens cDNA clone DKFZp434N219 5	HYPOTHETICAL GENE 48 PROTEIN	Homo sapiens WRN (WRN) gene, complete cds	601822184F1 NIH_MGC_75 Homo sapiens cDNA clone IMAGE:4042413 5'	HYPOTHETICAL 67,9 KD PROTEIN ZK888,8 IN CHROMOSOME III	HYPOTHETICAL 67.9 KD PROTEIN ZK688.8 IN CHROMOSOME III	Macaca tonkeana isolate 569tonkpeona NADH dehydrogenase subunit 4L gene, complete cds; and NADH dehydrogenase subunit 4 gene, mitochondrial genes encoding mitochondrial proteins, partial cds	og09000.x1 Soares, placenta, 8to8weeks, 2NbHP8to9W Homo sapiens cDNA clone IMAGE:1759049 3' similar to contains LTR8.b2 LTR8 repetitive element;	hg58g03.xt NCL_CGAP_GC6 Homo sepiens cDNA clone IMAGE:2949844 3' similar to contains Alu	repealive evenient,	Homo sapiens chromosome z1 segment HSZICTUS	Homo sapiens mannosidase, beta A, Iysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D3) genes, complete cds	UI-H-BI2-ahl-a-07-0-UI.s1 NG_CGAP_Sub4 Homo saplens cDNA clone IMAGE:2727061 3'	aq63h11.x1 Stantey Frontal SN pool 2 Homo sapiens cDNA done IMAGE:2035653
Top Hit Database Source	EST_HUMAN E	EST_HUMAN		INT IN	LN		T	EST_HUMAN t	SWISSPROT	EST HUMAN F	SWISSPROT		SWISSPROT (	SWISSPROT	Г	EST_HUMAN	SWISSPROT	Į.	EST_HUMAN (	SWISSPROT		LN	EST HUMAN		HOMAN	Z	<u> </u>	П	EST_HUMAN
Top Hit Acession No.	7.0E-10 AA345220.1	7.0E-10 BF352883.1	P35084	7.0E-10 AF029701.2	7.0E-10 AF029701.2		6.0E-10 AJ400877.1	6.0E-10 A1424405.1	Q02817	8.0E-10 AW853719.1	P33730		P33730	P98073	Ļ	5.0E-10 AL046804.1	001033	5.0E-10 AF181897.1	5.0E-10 BF105159.1			5.0E-10 AF091415.1	4.0E-10 AI221083.1	, 001, 021, 4	4.0E-10 AW 594 / 09.1	4.0E-10 AL163303.2	4.0E-10 AF224669.1	4.0E-10 AW 293243.1	4.0E-10 AI267342.1
Most Similar (Top) Hit BLAST E Value	7.0E-10	7.0E-10	7.0E-10 P35084	7.0E-10	7.0E-10		6.0E-10	6.0E-10	6.0E-10 Q02817	6.0E-10	6.0E-10 P33730		6.0E-10 P33730	6.0E-10 P98073	6.0E-10	5.0E-10	5.0E-10 Q01033	5.0E-10	5.0E-10	5.0E-10 P34678	5.0E-10 P34678	5.0E-10	4.0E-10	2, 10,	4.0E-10	4.0E-10	4.0E-10	4.0E-10	4.0E-10
Expression Signal	4.06	1.37	1.65	1.54	1.54		8.44	1.63	1.88	3.15	960		96.0	0.48	1.95	5.29	1.14	4.1	1.85	2.24	2.24	1.31	1.09	,	4,1	6.79	17.76	0.71	1.12
ORF SEQ ID NO:	32841	34124			34765		27171	28971	30733		35602		35603	36458			29745	31202		36374	36375	38725			ı	28877	33871	37039	37305
Exen SEQ ID NO:	19486	20646	20889	21245	21245			15859	72421	17994	22062	L	22062	L	L	L	16729	18233	20550	l	22801	25021	t	ł		15763	20409		Lil
Probe SEQ ID NO:	6314	7574	7834	8163	8163		936	2742	4615	4861	8983		8983	9834	12223	780	3564	5105	7475	92.26	9736	12040	114		2062	2640	7327	10398	10862

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Top Hit Descriptor	PM1-HT0521-120200-001-008 HT0521 Homo sepiens cDNA	PM1+HT0521-120200-001-f08 HT0521 Home capiens cDNA	yy32f06.s1 Soares melanocyte 2NbHM Homo sapiens cDNA clone IMAGE:272963 3' similar to contains L1.t1 L1 repetitive element;	Homo sapiens extracellular glycoprotein lacritin precursor, gene, complete cds	Homo sapiens chromosome 21 segment HS21C003	Homo sapiens chromosome 21 segment HS21C003	Human XRCC1 DNA repair gene, genomic	yz11g08.s1 Soares_multiple_sclerosls_2NbHMSP Homo sepiens cDNA clone IMAGE:2827823'	RHOMBOID PROTEIN (VEINLET PROTEIN)	ba76d08.y1 NIH_MGC_20 Homo saplens cDNA clone IMAGE:2906319 5'	AV743302 CB Homo sapiens cDNA clone CBFBGD08 5	AV743302 CB Hamo sapiens aDNA clane CBFBGD08 5'	ys74b12.s1 Soares retina N2b4HR Homo sepiens cDNA clone IMAGE:2205113' similar to contains MER29	repetitive element;	IL3-CT0219-160200-064-B06 CT0219 Homo saplens cDNA	IL3-CT0219-160200-064-806 CT0219 Homo sapiens cDNA	Homo sapiens FRA3B common fragile region, diadenosine triphosphate hydrolase (FHIT) gene, exon 5	yc11e12.r1 Stratagene lung (#937210) Homo sapiens cDNA clone IMAGE:80398 5'	nz36g03.s1 NCI_CGAP_GCB1 Homo saplens cDNA clone IMAGE:1289908 3	IL3-HT0618-110500-136-E07 HT0618 Homo sapiens cUNA	MAJOR CENTROMERE AUTOANTIGEN B (CENTROMERE PROTEIN B) (CENP-B)	MAJOR CENTROMERE AUTOANTIGEN B (CENTROMERE PROTEIN B) (CENT-B)	Homo sapiens basic transcription factor 2 p44 (btt2p44) gene, partial cds, neuronal apoptosis innibitory	protein (halp) and survival motor neuron protein (strin) genes, comprete	802136640F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:42/33/7 5	(HPRG)	Homo sapiens cytochrome P450 polypeptide 43 (CYP3A43) gene, partial cds; cytochrome P450 polypeptide	4 (CYP3A4) and cytochrome P450 polypeptide 7 (CYP3A7) genes, complete cds; and cytochrome F450	polypeptide 5 (CYP3A5) gene, partial cds	601586208F1 NIH MGC 7 Homo saptens cDNA clone IMAGE:3940824 5	POL POLYPROTEIN (CONTAINS) PROTEASE; REVERSE TRANSCRIPTASE; RIBONOCLEASE HJ	POL POLYPROTEIN (CONTAINS: PROTEASE; REVERSO INAINSORITIASE, INDOINCOLLANDE !!)
Top Hit Database Source	П	EST HUMAN	EST HUMAN	T	LN	N	LΝ	EST_HUMAN			EST_HUMAN	EST_HUMAN			EST_HUMAN	EST_HUMAN	TN		EST_HUMAN	EST_HUMAN	SWISSPROT	SWISSPROT		LN.	EST_HUMAN	SWISSPROT		_	LN L	EST_HUMAN	SWISSPROT	SWISSPROT
Top Hit Acescion No.	4.0E-10 BE169208.1	4.0E-10 BE169208.1	3.0E-10 N36113.1	3.0E-10 AY005150.1	3.0E-10 AL163203.2	3.0E-10 AL163203.2	3.0E-10 1.34079.1	3.0E-10 N50109.1	P20350	3.0E-10 BE302970.1	3.0E-10 AV743302.1	3.0E-10 AV743302.1		3.0E-10 H87208.1	3.0E-10 AW850731.1	3.0E-10 AW850731.1	3.0E-10 AF020503.1	3.0E-10 T65891.1	3.0E-10 AA769294.1	3.0E-10 BE179517.1	2.0E-10 P48988	2,0E-10 P48988		2.0E-10 U80017.1	2.0E-10 BF675047.1	2.0E-10 Q28640			2.0E-10 AF280107.1	2.0E-10 BE791082.1	2.0E-10 P26809	2.0E-10 P26809
Most Similar (Top) Hit BLAST E Value	4.0E-10	4.0E-10	3.0E-10	3.0E-10	3.0E-10	3.0E-10	3.0E-10	3.0E-10	3.0E-10 P20350	3.0E-10	3.0E-10	3.0E-10		3.0E-10	3.0E-10	3.0E-10	3.0E-10	3.0E-10	3.0E-10	3.0E-10	2.0E-10	2,0E-10		2.0E-10	2.0E-10	2.0E-10						
Expression Signal	0.54	0.54	2.24	5.3	0.94	0.94	0.89	0.78	2.06	3.62	1.42	1.42		1.57	1.52	1.52	0.78	1.95	96.0	1.87	2.08	2.08		1.66	0.84	2.3			1.56			0.58
ORF SEQ ID NO:	37450	37451	27173		30777			L				34496		35546		35873				31977	26278	26279							32905			34808
Exon SEQ ID NO:	23827	23827	14112	14537	17793	17793	18463	L		L	20987	20987		22007	l	22326	22606	L.	L	25619	13274	13274		15089	16227	ı	L		19549	20610	ı	
Probe SEQ ID NO:	10794	10794	88	1382	4657	4657	3350	5571	6332	6481	7937	7887		8928	9249	9249	9541	10679	10820	12941	36	36		1946	3051	5924			6380	7537	8203	8203

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Probe SEQ ID NO: 11639 1637 1637 2849 3889 3889 3847 4245 4245 4245 4245 4245 4245 8434 8434 8855	Exan SEQ ID NO: 0.00   NO: 0.00   NO: 0.00   NO: 0.00   NO: 0.00   NO: 0.00   NO: 0.00   NO: 0.00   NO: 0.00   NO: 0.00   NO: 0.00   NO: 0.00   NO: 0.00   NO: 0.00   NO: 0.00   NO: 0.00   NO: 0.00   NO: 0.00   NO: 0.00   NO: 0.00   NO: 0.00   NO: 0.00   NO: 0.00   NO: 0.00   NO: 0.00   NO: 0.00   NO: 0.00   NO: 0.00   NO: 0.00   NO: 0.00   NO: 0.00   NO: 0.00   NO: 0.00   NO: 0.00   NO: 0.00   NO: 0.00   NO: 0.00   NO: 0.00   NO: 0.00   NO: 0.00   NO: 0.00   NO: 0.00   NO: 0.00   NO: 0.00   NO: 0.00   NO: 0.00   NO: 0.00   NO: 0.00   NO: 0.00   NO: 0.00   NO: 0.00   NO: 0.00   NO: 0.00   NO: 0.00   NO: 0.00   NO: 0.00   NO: 0.00   NO: 0.00   NO: 0.00   NO: 0.00   NO: 0.00   NO: 0.00   NO: 0.00   NO: 0.00   NO: 0.00   NO: 0.00   NO: 0.00   NO: 0.00   NO: 0.00   NO: 0.00   NO: 0.00   NO: 0.00   NO: 0.00   NO: 0.00   NO: 0.00   NO: 0.00   NO: 0.00   NO: 0.00   NO: 0.00   NO: 0.00   NO: 0.00   NO: 0.00   NO: 0.00   NO: 0.00   NO: 0.00   NO: 0.00   NO: 0.00   NO: 0.00   NO: 0.00   NO: 0.00   NO: 0.00   NO: 0.00   NO: 0.00   NO: 0.00   NO: 0.00   NO: 0.00   NO: 0.00   NO: 0.00   NO: 0.00   NO: 0.00   NO: 0.00   NO: 0.00   NO: 0.00   NO: 0.00   NO: 0.00   NO: 0.00   NO: 0.00   NO: 0.00   NO: 0.00   NO: 0.00   NO: 0.00   NO: 0.00   NO: 0.00   NO: 0.00   NO: 0.00   NO: 0.00   NO: 0.00   NO: 0.00   NO: 0.00   NO: 0.00   NO: 0.00   NO: 0.00   NO: 0.00   NO: 0.00   NO: 0.00   NO: 0.00   NO: 0.00   NO: 0.00   NO: 0.00   NO: 0.00   NO: 0.00   NO: 0.00   NO: 0.00   NO: 0.00   NO: 0.00   NO: 0.00   NO: 0.00   NO: 0.00   NO: 0.00   NO: 0.00   NO: 0.00   NO: 0.00   NO: 0.00   NO: 0.00   NO: 0.00   NO: 0.00   NO: 0.00   NO: 0.00   NO: 0.00   NO: 0.00   NO: 0.00   NO: 0.00   NO: 0.00   NO: 0.00   NO: 0.00   NO: 0.00   NO: 0.00   NO: 0.00   NO: 0.00   NO: 0.00   NO: 0.00   NO: 0.00   NO: 0.00   NO: 0.00   NO: 0.00   NO: 0.00   NO: 0.00   NO: 0.00   NO: 0.00   NO: 0.00   NO: 0.00   NO: 0.00   NO: 0.00   NO: 0.00   NO: 0.00   NO: 0.00   NO: 0.00   NO: 0.00   NO: 0.00   NO: 0.00   NO: 0.00   NO: 0.00   NO: 0.00   NO: 0.00   NO: 0.00	ORF SEQ ID NO: 27874 29768 30379 30379 30346	Expression Signed 1.06 1.06 1.33 3.37 1.03 3.37 1.03 1.05 1.05 1.05 1.05 1.05 1.05 1.05 1.05	Mosts Van	Similar Sirrier No. 3) Hit Top Hit Acession ST E No. 2.0E-10 BF434565.1 2.0E-10 BF434565.1 2.0E-10 BF434565.1 2.0E-10 BF434565.1 2.0E-10 AW852001.1 2.0E-10 AW852001.1 2.0E-10 AW852001.1 2.0E-10 AW852001.1 2.0E-10 AL041685.1 2.0E-10 AL041685.1 2.0E-10 U52111.2 2.0E-10 U52111.2 2.0E-10 U52111.2 2.0E-10 U52111.2 2.0E-10 U52111.2 2.0E-10 AN98520.1 2.0E-10 AN98520.1 2.0E-10 AN98520.1 2.0E-10 AN98520.1 2.0E-10 AN98520.1 2.0E-10 AN98520.1 2.0E-10 AN98520.1	Top Hit Databese Source Source Source EST HUMAN EST HUMAN EST HUMAN EST HUMAN EST HUMAN EST HUMAN NT NT NT NT NT NT EST HUMAN EST HUMAN EST HUMAN EST HUMAN EST HUMAN EST HUMAN EST HUMAN	Top Hit Descriptor  7678d08.x1 NCI_CGAP_Kid11 Homo saplens cDNA clone IMAGE.3642303 3' similar to contains I.1.t3 L1 repetitive element;  MRCI_SGAS_GOAP_GOAP_LIGHT Homo saplens cDNA clone IMAGE.2043695 3' MRCI_SGAS_GOAP_GOAP_GOAP_GOAP_GOAP_GOAP_GOAP_GOAP
10406	1, 1				1.0E-10 AA081868.1	EST HUMAN	zn23g06.r1 Stratagene neuroepithelium NT2RAMI 937234 Homo sapiens cDNA clone IMAGE:548314 5' ov85h03.x1 Soares fetal liver spleen 1NFLS S1 Homo sapiens cDNA clone IMAGE:1672661 3'
11154 12165 272 2171	1 1.1.1	1 11			1.0E-10 AI038280.1 1.0E-10 X87344.1 8.0E-11 BE145800.1 9.0E-11 AL134395.1	NT EST HUMAN	Oyosinos.XI Soates_teta_tive_pheal_intrice_si nono squets contraction and 14 H.saplens DMA, DMB, HLA-Z1, IPP2, LMP2, TAP1, LMP7, TAP2, DOB, DQB2 and RING8, 9, 13 and 14 genes IL2-HT0203-291099-016-c08 HT0203 Home sapiens cDNA DKFZp547D225_r1 547 (syncnym: hfbr1) Home sapiens cDNA done DKFZp547D225 5
2171	ш	28434	1 6.02		9.0E-11 AL134395.1	EST_HUMAN	DKFZp547D225_r1 547 (syncrym: hfbr1) Homo sapiens cDNA clone DKFZp547D225 5

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Top Hit Descriptor	DKFZp547D225_r1 547 (synonym: hfbr1) Homo sapiens cDNA clone DKFZp547D225 5'	DKFZp547D225_r1 547 (synonym: hfbr1) Homo sapiens cDNA clone DKFZp547D225 5	ae78f01.s1 Stratagene schizo brain S11 Homo sapiens cDNA clone IMAGE:970297 3'	RC6-BT0627-140200-011-E06 BT0627 Hamo sapiens cDNA	EST27872 Cerebellum If Homo saplens cDNA 5' end	EST27872 Cerebellum II Homo sapiens cDNA 5' end	C16635 Clontech human acrts pctyA+ mRNA (#572) Homo sepiens cDNA clone GEN-506B08 5	yn53111.s1 Soares adult brain N2b5HB55Y Homo saplens cDNA clone IMAGE:172173 3' similar to contains	L1 repetitive element;	yw46e06.s1 Weizmann Olfactory Epithelium Homo sapiens cDNA clone IMAGE:255298 31	ba60g04.x1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:2900982.3'	X451/11X1 NCI_CGAP_Bm50 Home sapiens cDNA clone IMAGE:2821061 3' similar to contains MER10.t1	MER10 repetitive element;	EST34392 Embryo, 6 week I Hano sapiens cDNA 5' end	Homo sapiens SNCA isoform (SNCA) gene, complete cds, alternatively spliced	RETROVIRUS-RELATED POL POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE;	ENDONUCLEASE]	Human matrix Gla protein (MGP) gene, complete cds	Human matrix Gla protein (MGP) gene, complete cds	Homo sapiens chromosome X region from filamin (FLN) gene to glucose-6-phosphate dehydrogenase	(G8PD) gene, complete cds's	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG	AV727859 HTC Homo sapiens cDNA clone HTCASC06 5	CM0-BT0281-031199-087-a03 BT0281 Homo sapiens cDNA	Homo saplens chromosome 21 segment HS21C083	Homo sapiens chromosome 21 segment HS21C083	Homo saplens chromosome 21 segment HS21C013	Homo saplens protocadherin beta 3 (PCDHB3), mRNA	zu01b12.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:730559 5'	601507531F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3909295 51	Homo sapiens chromosome 21 segment HS21C047	HUMSUPY069 Human brain cDNA Homo sapiens cDNA clone 069	PRE-MRNA SPLICING FACTOR RNA HELICASE PRP2
	П			EST_HUMAN_R			EST_HUMAN C		П	EST_HUMAN y	EST_HUMAN   b		П	EST HUMAN E		<u>α</u>	SWISSPROT	H	TN 라			SWISSPROT	EST_HUMAN A	EST_HUMAN C	IN	F			T HUMAN	EST_HUMAN 6	NT I	П	SWISSPROT
Top Hit Acession No.	9.0E-11 AL134395.1	9.0E-11 AL134395.1	9.0E-11 AA775985.1	9.0E-11 BE079780.1	9.0E-11 AA324960.1	9.0E-11 AA324960.1	9.0E-11 C16635.1		8.0E-11 H19971.1	8.0E-11 N23712.1	8.0E-11 AW674316.1		8,0E-11 AW 166158.1	7.0E-11 AA330642.1	7.0E-11 AF163864.1		P11369	6.0E-11 M55270.1	6.0E-11 M55270.1		6.0E-11 L44140.1	P08547	6.0E-11 AV727859.1	6.0E-11 BE063509.1	5.0E-11 AL163283.2	5.0E-11 AL163283.2	5.0E-11 AL163213.2	11416799 NT	AA4360	4.0E-11 BE885900.1	4.0E-11 AL163247.2	4.0E-11 D44666.1	4.0E-11 P20095
Most Similar (Top) Hit BLAST E Value	9.0E-11	9.0E-11	9.0E-11	9.0E-11	9.0E-11	9.0E-11	9.0E-11		8.0E-11	8.0E-11	8.0E-11		8.0E-11	7.0E-11	7.0E-11		7.0E-11 P11369	6.0E-11	6.0E-11	i	6.0E-11	6.0E-11 P08547	6.0E-11	6.0E-11	5.0E-11	5.0E-11	5.0長-11	5.0E-11	4.0E-11	4.0E-11	4.0E-11	4.0E-11	4.0E-11
Expression Signal	2.98	2.98	8.0	3.05	1.17	1.17	2.45		10.53	5.37	99.0		0.62	2.09	2.61		1.37	6.19	6.19		0.91	3.5	66.9	0.5	-	1.24	1.92	11.57	1.38	9.84	1.26	0.81	3.29
ORF SEQ ID NO:	29657	29658	30741		37002	37003	32072			30300	32415			27717	35307		,	26661	26662		33424	34431	35179		26250	26250		l		29074	_		33154
Exon SEQ ID NO:	16637	16637	1	18886	23392	1	l	ı	16360	1	19101		19965	14632	21775	Ι.	23469	13620	<u> </u>		20014	l		22579	1	13250	1_	L			L	17875	19765
Probe SEQ ID NO:	3470	3470	4622	5692	10357	10357	12556		3185	4154	5913		6811	1479	8695		10434	425	425		6862	7870	8559	9514	12	3450	6646	7699	1433	2851	3034	4740	6605

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	80	Expression Signal 0.85 0.85 0.85 0.85 0.85 0.85 0.85 0.85		AST E No. 1919 Hit Acession AST E No. 2.0E-11 AA581028.1 ES 2.0E-11 BF582945.1 ES 2.0E-11 AF029308.1 NT 2.0E-11 AV885874.1 ES 2.0E-11 AV885874.1 ES 2.0E-11 AV885874.1 ES 2.0E-11 AV885874.1 ES 2.0E-11 AV885874.1 ES 2.0E-11 AV885874.1 ES 2.0E-11 AV885874.1 ES 2.0E-11 AV885874.1 ES 2.0E-11 AV885874.1 ES 2.0E-11 AV885874.1 ES 2.0E-11 AV885874.1 ES 2.0E-11 AV88587.2 NT 1.0E-11 AV8858.1 ES 2.0E-11 AV8858.1 ES 2.0E-11 AV8858.1 ES 2.0E-11 AV8858.1 ES 2.0E-11 AV8858.1 ES 2.0E-11 AV8858.1 ES 2.0E-11 AV8858.1 ES 2.0E-11 AV8858.1 ES 2.0E-11 AV8858.1 ES 2.0E-11 AV8858.1 ES 2.0E-11 AV8858.1 ES 2.0E-11 AV8858.1 ES 2.0E-11 AV8858.1 ES 2.0E-11 AV8858.1 ES 2.0E-11 AV8858.1 ES 2.0E-11 AV8858.1 NT 1.0E-11 AV8858.1 NT 1.0E-11 AV8858.1 NT 1.0E-11 AV8858.1 NT 1.0E-11 AV8858.1 NT 1.0E-11 AV8858.1 NT 1.0E-11 AV8858.1 NT 1.0E-11 AV8858.1 NT 1.0E-11 AV8858.1 NT 1.0E-11 AV8858.1 NT 1.0E-11 AV8858.1 ES 2.0E-11 AV8858.1 NT 1.0E-11 AV8858.1 NT 1.0E-11 AV8858.1 NT 1.0E-11 AV8858.1 NT 1.0E-11 AV8858.1 NT 1.0E-11 AV8858.1 NT 1.0E-11 AV8858.1 NT 1.0E-11 AV8858.1 NT 1.0E-11 AV8858.1 NT 1.0E-11 AV8858.1 NT 1.0E-11 AV8858.1 NT 1.0E-11 AV8858.1 NT 1.0E-11 AV8858.1 NT 1.0E-11 AV8858.1 NT 1.0E-11 AV8858.1 NT 1.0E-11 AV8858.1 NT 1.0E-11 AV8858.1 NT 1.0E-11 AV8858.1 NT 1.0E-11 AV8858.1 NT 1.0E-11 AV8858.1 NT 1.0E-11 AV8858.1 NT 1.0E-11 AV8858.1 NT 1.0E-11 AV8858.1 NT 1.0E-11 AV8858.1 NT 1.0E-11 AV8858.1 NT 1.0E-11 AV8858.1 NT 1.0E-11 AV8858.1 NT 1.0E-11 AV8858.1 NT 1.0E-11 AV8858.1 NT 1.0E-11 AV8858.1 NT 1.0E-11 AV8858.1 NT 1.0E-11 AV8858.1 NT 1.0E-11 AV8858.1 NT 1.0E-11 AV8858.1 NT 1.0E-11 AV8858.1 NT 1.0E-11 AV8858.1 NT 1.0E-11 AV8858.1 NT 1.0E-11 AV8858.1 NT 1.0E-11 AV8858.1 NT 1.0E-11 AV8858.1 NT 1.0E-11 AV8858.1 NT 1.0E-11 AV8858.1 NT 1.0E-11 AV8858.1 NT 1.0E-11 AV8858.1 NT 1.0E-11 AV8858.1 NT 1.0E-11 AV8858.1 NT 1.0E-11 AV8858.1 NT 1.0E-11 AV8858.1 NT 1.0E-11 AV8858.1 NT 1.0E-11 AV8858.1 NT 1.0E-11 AV8858.1 NT 1.0E-11 AV8858.1 NT 1.0E-11 AV8858.1 NT 1.0E-11 AV8858.1 NT 1.0E-11 AV8858.1 NT 1.0E-11 AV8858.1 NT 1.0E-11 AV8858.1 NT 1.0E-11 AV8858.1 NT		Top Hit Descriptor  ne8sh05.r1 NCI_CGAP_GC1 Homo sepiens cDNA clone IMAGE;797433 5' similar to SW;PR16_YEAST P15608 PRE_MRNA SPI_CIONG FACTOR RNA HELICASE PRP16; P15703.r1 NCI_CGAP_GC3 Homo sepiens cDNA clone IMAGE;79742565 3' OLFACTORY RECEPTOR_LIKE PROTEIN CORNS OLFACTORY RECEPTOR_LIKE PROTEIN CORNS OLFACTORY RECEPTOR_LIKE PROTEIN CORNS OLFACTORY RECEPTOR_LIKE PROTEIN CORNS OLFACTORY RECEPTOR_LIKE PROTEIN OLF1) RG4-OT0072-170400-013-c11 OT0072 Homo sepiens cDNA RC4-OT0072-170400-013-c11 OT0072 Homo sepiens cDNA RC3-ON0027-21010-011-c01 CN0027 Homo sepiens cDNA Homo sepiens SEC14 (5. cerevisies)-like 2 (SEC14L2), mRNA Homo sepiens shromosome 21 segment HS21C079 Homo sepiens chromosome 21 segment HS21C079 Homo sepiens chromosome 21 segment HS21C079 Homo sepiens homogentisete 1,2-dlx0ygenese gene, complete cds OXYSTEROL-BINDING PROTEIN Homo sepiens homogentisete 1,2-dlx0ygenese gene, complete cds EST190196 Liker, hepstoceliular carcinome Homo sepiens cDNA 6' end similar to EST containing Alu repeat
Ll	Ц			1.0E-11 BE004315.1	EST HUMAN	CM0-BN0105-170300-292-d12 BN0105 Homo sapiens cDNA
11	18647 31625	14.68		1.0E-11 AL163247.2	EST HUMAN	Homo sapiens chromosome 21 segment HS21C047 7p57d01.x1 NCI_CGAP_Pr28 Homo sapiens cDNA clore IMAGE:3649945 3' similar to contains MER10.b3 MER10 repetitive element :
1_				4886546 NT	NT =	Homo sapiens PHD finger protein 2 (PHF2) mRNA
L			L	1.0E-11 R13174.1	EST_HUMAN	yf73d08.r1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:28166 51
L			Ш	1.0E-11 BF365119.1	EST_HUMAN	QV4-NN1149-250900-423-e03 NN1149 Homo septens cDNA

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Probe SEQ ID NO:	Exen SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
9248	22325	35871	1.49	-	.0E-11 BF365119.1	EST_HUMAN	QV4-NN1149-250900-423-e03 NN1149 Homo saplens cDNA
10626	23660		0.54	ļ.	.0E-11 AL163302.2	NT	Homo sapiens chromosome 21 segment HS21C102
11566	24621	38302	2.02	<u>L</u>	.0E-11 BF680078.1	EST_HUMAN	602154807F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4295977 5'
12903	<u> </u>		1.37		1	EST_HUMAN	HSAAACADH P, Human foetal Brain Whole tissue Homo saplens cDNA
3017	L.			)	9.0E-12 P20742	SWISSPROT	PREGNANCY ZONE PROTEIN PRECURSOR
10002	23040	36632	1.17	9.0E-12	9.0E-12 AL163300.2	NT	Homo sapiens chromosome 21 segment HS21C100
10002	23040	36633	1.17	9.0E-12	9.0E-12 AL163300.2	NT	Homo sapiens chromosome 21 segment HS21C100
9539	ļ.	L	0.88			EST_HUMAN	IL5-BT0578-130300-036-G12 BT0578 Homo sapiens cDNA
12408	1		4.68		8.0E-12 AJ271736.1	NT	Homo sapiens Xq pseudoautosomal region; segment 2/2
4783	17918	30905	1.57		7.0E-12 Q05904	SWISSPROT	34 KD SPICULE MATRIX PROTEIN PRECURSOR (LSM34)
11831	24711	38402	6.8		7.0E-12 AA704735.1	EST_HUMAN	z/23g01.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:451152 3'
13225	25903		1.18		7.0E-12 D16473.1	. IN	Human mRNA, Xq terminal portion
3637	١		96.0		5.0E-12 AV730554.1	EST_HUMAN	AV730554 HTF Homo saplens cDNA clone HTFAW F06 5
							rz88f11.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1302573 3' sImilar to contains Alu
4468	17608	30586	9.23	_	3.0E-12 AA732518.1	EST_HUMAN	repetitive element;
90	3,0	۱.			2 00 4 1 4 2 4 4	COT LIBRANI	165912.x1 Soares_NSF_F8_9W_OT_PA_F31 Home sapiens cDNA clone IMAGE:2146438 3' similar to
97.00	1	35811			3 0F-12 AF003249 1	TN TN	Morone saxatilis myosin heavy chain FM3A (FM3A) mRNA, complete cds
3	1						oction 1 st NCI CGAP GCB1 Homo seniens cDNA clone IMAGE: 1367588 similar to contains MER29.t2
9675	22637		1.81	6.0E-12	6.0E-12 AA847898.1	EST_HUMAN	MER29 repetitive element;
13205	_		1.25		6.0E-12 AW 885845.1	EST_HUMAN	RC4-OT0072-060400-012-f11 OT0072 Homo sapiens cDNA
1068	14234	27293	2:37		5.0E-12 T06573.1	EST_HUMAN	EST04462 Fetal brain, Stratagene (cat#936206) Homo sapiens cDNA clone HFBDV33
3477	16644	29663	1.28		5.0E-12 BE047779.1	EST_HUMAN	tz42b05.y1 NCI_CGAP_Bm52 Homo sapiens cDNA clone IMAGE:2291217 5'
3821	16981	29984	7.44		5.0E-12 AJ271736.1	NT	Homo sapiens Xq pseudoautosomal region; segment 2/2
6145	19323		6.13		5.0E-12 AL163278.2	LN	Homo sapiens chromosome 21 segment HS21C078
6145	19323	32667	6.13		5.0E-12 AL163278.2	TN	Homo sapiens chromosome 21 segment HS21C078
6620	19780	33168	96'6		5.0E-12 AW974760.1	EST_HUMAN	EST386850 MAGE resequences, MAGN Homo sapiens cDNA
7176	<u> </u>	33462	1.06		5.0E-12 AL040739.1	EST_HUMAN	DKFZp434B1615_s1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434B1615 3'
7187	20052	33462	0.93		5.0E-12 AL040739.1	EST_HUMAN	DKFZp434B1615_s1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434B1615 3'
	L				2 7 40 000 40 00	NAME TO TO	Z01g12.s1 Soares_fetal_heart_NbHH19W Homo sepiens cDNA clone IMAGE:375718.3' similar to contains   14 rs 14 renefittiue alement :
8424	21505	32032			AH033/40.	מאוסו וכש	L. D. L. I PECULY CHAINE, TO DESCRIPTION
8867	ı		0.55		_	EST HUMAN	RC1-010086-220300-011-b07 U10086 Homo sapiens cunA
9195	١,		0.77			EST_HUMAN	DKFZp434J0426_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434J0426 5
9308	22384	35936	2.52		5.0E-12 AJ271735.1	LN L	Homo sapiens Xq pseudoautosomal region; segment 1/2

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Top Hit Descriptor	<u>OLFACTORY RECEPTOR 1D2 (OLFACTORY RECEPTOR-LIKE PROTEIN HGMP07E) (OLFACTORY RECEPTOR 17-4) (OR17-4)</u>	Homo sapiens chromosome 21 segment HS21C103	Homo sapiens chromosome 21 segment HS21C102	Raftus norvegicus Deleted In colcorectal cancer (rat homolog) (Dcc), mRNA	zj74g11.s1 Soares_feta[]Iver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:460676 3'	zj74g11.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:460676 3'	b28h05.x1 NCI_CGAP_Lu24 Homo sapiens cDNA done IMAGE:2270745 3' similar to TR:Q13539 Q13539 MARINER TRANSPOSASE ;	nad21b03.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3366077 3' similar to contains MER7.b2 MER7 repetitive element :	Homo carions S164 none partial cds: PS1 and hypothetical protein genes complete cds: and S171 dene	national source, the same case, the same injures in the case of the same same case, the case of the same case, the same case of the same case of the same case of the same case of the same case of the same case of the same case of the same case of the same case of the same case of the same case of the same case of the same case of the same case of the same case of the same case of the same case of the same case of the same case of the same case of the same case of the same case of the same case of the same case of the same case of the same case of the same case of the same case of the same case of the same case of the same case of the same case of the same case of the same case of the same case of the same case of the same case of the same case of the same case of the same case of the same case of the same case of the same case of the same case of the same case of the same case of the same case of the same case of the same case of the same case of the same case of the same case of the same case of the same case of the same case of the same case of the same case of the same case of the same case of the same case of the same case of the same case of the same case of the same case of the same case of the same case of the same case of the same case of the same case of the same case of the same case of the same case of the same case of the same case of the same case of the same case of the same case of the same case of the same case of the same case of the same case of the same case of the same case of the same case of the same case of the same case of the same case of the same case of the same case of the same case of the same case of the same case of the same case of the same case of the same case of the same case of the same case of the same case of the same case of the same case of the same case of the same case of the same case of the same case of the same case of the same case of the same case of the same case of the same case of the same case of the same case of the same case of the same case of the same case	Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22, segment 3/3	Homo sapiens Bruton's tyrosine kinase (BTK), alpha-D-galactosidase A (GLA), L44-like ribosomal protein	(L44L) and FTP3 (FTP3) genes, complete cds	hd13d01.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2908377 3' similar to TR:014517	014517 SMRP.;	hd13d01.x1 Soares_NR_T_GBC_S1 Homo saplens cDNA clone IMAGE:2909377 3' similar to TR:014517. 044547 SMRP:	Home conjugate chamber of commant HC9470f8	Unio sapieis dilicinoscine a i seglinenti i con con con con con con con con con con	Homo sapiens serine paimilioy transferase, subunit il gene, complete cus, and unin lowi genes	SERINE PROTEASE HEPSIN	Human prostate specific antigen gene, 5' flanking region	Human prostate specific antigen gene, 5' flanking region	IL5-UN0071-120400-065-e05 UM0071 Homo saplens cDNA	Mus musculus keratin-associated protein 6.2 (Krtap6-2), mRNA	Ret U3A small nuclear RNA	Rat U3A small nuclear RNA	CM0-BT0281-031199-087-a03 BT0281 Homo sapiens cDNA	TBX15 PROTEIN (T-BOX PROTEIN 15)	TBX15 PROTEIN (T-BOX PROTEIN 15)	EST383946 MAGE resequences, MAGL Homo sapiens cDNA	EST06060 Infant Brain, Bento Scares Homo saplens cDNA done HIBBA13 5' end
Top Hit Database Source	SWISSPROT	Į.			EST_HUMAN	EST HUMAN	EST_HUMAN	EST HUMAN	T	Ę	LN LN		F		EST_HUMAN	ECT LIMAN	Τ		7	ISSPROT	LN	. LN	EST_HUMAN			Ę	EST_HUMAN	SWISSPROT	SWISSPROT	EST_HUMAN	EST_HUMAN
Top Hit Acession No.	P34982	5.0E-12 AL163303.2	5.0E-12 Al.163302.2	6978754 NT	4.0E-12 AA700326.1	4.0E-12 AA700326.1	4.0E-12 AI68984.1	4 0F-12 BF445140.1		4.0E-12 AF109907.1	4.0E-12 AJ229043.1		4.0E-12 U78027.1		3.0E-12 AW341683.1	2 OC 10 VW241662 1	A1 400000 0	3.0E-12 AL163268.2	3.0E-12 AF111168.2	035453	3.0E-12 U37672.1	3.0E-12 U37672.1	2.0E-12 AW802131.1	6754495 NT	2.0E-12 J01884.1	2.0E-12 J01884.1	2.0E-12 BE063509.1	070306	2.0E-12 O70306	2.0E-12 AW971857.1	2.0E-12 T08169.1
Most Similar (Top) Hit BLAST E Value	5.0E-12 P34982	5.0E-12	5.0E-12	5.0E-12	4.0E-12	4.0E-12	4.0E-12	4.0F-12		4.0E-12	4.0E-12		4.0E-12		3.0E-12	300	200-16	3.05-12	3.0E-12	3.0E-12 O35453	3.0E-12	3.0E-12	2.0E-12	2.0E-12	2.0E-12	2.0E-12	2.0E-12	2.0E-12 O70306	2.0E-12	2.0E-12	2.0E-12
Expression Signal	122	4.8	69.0	9.0	3.29	3.42	0.88	0.74		18.4	4.33		2.11		2.58	c c	2,30	0.78	1.44	0.5	2.32	2.32	1.24	0.93	1.29	1.29	2.03	0.71	0.71	2.08	3.85
ORF SEQ ID NO:	36247		37213	37449	26505	26505	30860		†	_	38050				26839	080	2007	31363	31806	35193	37606			29736	30365	30366		31123	31124		33870
Exon SEQ ID NO:	22678	23517	23608	23826	13474	13474	17871	20853	1	21518	ı	ı	25458		13816	6.00					23975	23976	1			1		1_	L	19766	2040B
Probe SEQ ID NO:	9623	10482	10573	10793	254	255	4742	7977		8437	11338		12684		831	8	3	5276	5568	8570	10891	10891	1685	3556	4230	4230	4541	5018	5018	9099	7326

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Table 4
Single Exon Probes Expressed in Placenta

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			,		6:10		
Probe SEO ID 8 NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
							Human germline T-cell receptor beta chain Dopamine-beta-hydroxylase-like, TRY1, TRY2, TRY3, TCRBV27S1P, TCRBV22S1A2N1T, TCRBV8S1A1T, TCRBV7S1A1N2T, TCRBV5S1A1T, TCRBV13S3, TCRBV7S2A1N4T, TCRBV7S2A1N4T, TCRBV7S2A1N4T, TCRBV7S2A1N4T, TCRBV7S2A1N4T, TCRBV7S2A1N4T, TCRBV7S2A1N4T, TCRBV7S2A1N4T, TCRBV7S2A1N4T, TCRBV7S2A1N4T, TCRBV7S2A1N4T, TCRBV7S2A1N4T, TCRBV7S2A1N4T, TCRBV7S2A1N4T, TCRBV7S2A1N4T, TCRBV7S2A1N4T, TCRBV7S2A1N4T, TCRBV7S2A1N4T, TCRBV7S2A1N4T, TCRBV7S2A1N4T, TCRBV7S2A1N4T, TCRBV7S2A1N4T, TCRBV7S2A1N4T, TCRBV7S2A1N4T, TCRBV7S2A1N4T, TCRBV7S2A1N4T, TCRBV7S2A1N4T, TCRBV7S2A1N4T, TCRBV7S2A1N4T, TCRBV7S2A1N4T, TCRBV7S2A1N4T, TCRBV7S2A1N4T, TCRBV7S2A1N4T, TCRBV7S2A1N4T, TCRBV7S2A1N4T, TCRBV7S2A1N4T, TCRBV7S2A1N4T, TCRBV7S2A1N4T, TCRBV7S2A1N4T, TCRBV7S2A1N4T, TCRBV7S2A1N4T, TCRBV7S2A1N4T, TCRBV7S2A1N4T, TCRBV7S2A1N4T, TCRBV7S2A1N4T, TCRBV7S2A1N4T, TCRBV7S2A1N4T, TCRBV7S2A1N4T, TCRBV7S2A1N4T, TCRBV7S2A1N4T, TCRBV7S2A1N4T, TCRBV7S2A1N4T, TCRBV7S2A1N4T, TCRBV7S2A1N4T, TCRBV7S2A1N4T, TCRBV7S2A1N4T, TCRBV7S2A1N4T, TCRBV7S2A1N4T, TCRBV7S2A1N4T, TCRBV7S2A1N4T, TCRBV7S2A1N4T, TCRBV7S2A1N4T, TCRBV7S2A1N4T, TCRBV7S2A1N4T, TCRBV7S2A1N4T, TCRBV7S2A1N4T, TCRBV7S2A1N4T, TCRBV7S2A1N4T, TCRBV7S2A1N4T, TCRBV7S2A1N4T, TCRBV7S2A1N4T, TCRBV7S2A1N4T, TCRBV7S2A1N4T, TCRBV7S2A1N4T, TCRBV7S2A1N4T, TCRBV7S2A1N4T, TCRBV7S2A1N4T, TCRBV7S2A1N4T, TCRBV7S2A1N4T, TCRBV7S2A1N4T, TCRBV7S2A1N4T, TCRBV7S2A1N4T, TCRBV7S2A1N4T, TCRBV7S2A1N4T, TCRBV7S2A1N4T, TCRBV7S2A1N4T, TCRBV7S2A1N4T, TCRBV7S2A1N4T, TCRBV7S2A1N4T, TCRBV7S2A1N4T, TCRBV7S2ANAT, TCRBV7S2ANAT, TCRBV7S2ANAT, TCRBV7S2ANAT, TCRBV7S2ANAT, TCRBV7S2ANAT, TCRBV7S2ANAT, TCRBV7S2ANAT, TCRBV7S2ANAT, TCRBV7S2ANAT, TCRBV7S2ANAT, TCRBV7S2ANAT, TCRBV7S2ANAT, TCRBV7S2ANAT, TCRBV7SANAT, TCRBV7SANAT, TCRBV7SANAT, TCRBV7SANAT, TCRBV7SANAT, TCRBV7SANAT, TCRBV7SANAT, TCRBV7SANAT, TCRBV7SANAT, TCRBV7SANAT, TCRBV7SANAT, TCRBV7SANAT, TCRBV7SANAT, TCRBV7SANAT, TCRBV7SANAT, TCRBV7SANAT, TCRBV7SANAT, TCRBV7SANAT, TCRBV7SANAT, TCRBV7SANAT, TCRBV7SANAT, TCRBV7SANAT, TCRBV7SANAT, TCRBV7SANAT, TCRBV7SANAT, TCR
8686	21766	35298	0.59		DE-12 D86059.1	NT EST HUMAN	ac26d05,s1 Strategene ovary (#837217) Homo saplens cDNA clone IMAGE.857577 3'
12215	25166				1.0E-12 AW962164.1	EST_HUMAN	EST374237 MAGE resequences, MAGG Homo sapiens cDNA
12437	25310				.0E-12 AI738592.1	EST_HUMAN	w33h08.x1 NCI_CGAP_Co16 Homo sapiens cDNA clone IMAGE:2392095 3'
12600	26068		1.93	1.0E-12	.0E-12 AL163268.2	NT	Homo sapiens chromosome 21 segment HS21C068
12788	26166		1.19	-	.0E-12 P44836	SWISSPROT	PROBABLE TONB-DEPENDENT RECEPTOR HI0712 PRECURSOR
12951	25661		2.82		.0E-12 AF224669.1	TN	Homo sepiens mannosidase, beta A, Iysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D3) genes, complete cds
4056	17212	30223		٦	9.0E-13 AB029900.1	¥	Homo sapiens CST gene for cerebroside sulfotransferase, exon 1, 2, 3, 4, 5
9801	22841	L		9.0E-13	9.0E-13 N69653.1	EST_HUMAN	za28b06.s1 Soares fetal liver spicen 1NFLS Homo sapiens cDNA clone IMAGE:283651 3'
735	13917	L		8.0E-13	8.0E-13 U29185.1	LN-	Homo saplens prion protein (PIP) gene, complete cds
736	13917	26958		L	8.0E-13 U29185.1	N	Homo sapiens prion protein (PrP) gene, complete cds
							Homo sapiens basic transcription factor 2 p44 (btt2p44) gene, partial cds, neuronal apoptosis Inhibitory
1885	15029	28136			8.0E-13 U80017.1	LN.	protein (naip) and survival motor neuron protein (smn) genes, complete cds
8303	21385		0.63		8.0E-13 AI884398.1	EST_HUMAN	wm31h09x1 NCI_CGAP_Ut4 Homo sapiens cDNA clone IMAGE:2437601 3
ജയ	21385				8.0E-13 AI884398.1	EST_HUMAN	wm31h09x1 NCI_CGAP_Ut4 Homo sapiens cDNA clone IMAGE:2437601 3'
						L.	Homo sapiens Bruton's tyrosine kinase (BTK), alpha-D-galactosidase A (GLA), L44-like ribosomal protein
10350	08557		2.82		8.0E-13 U/0027.1	FOCOCIANO	(L-HA) alla II i a (I I I ) yanay unipera wa On HAOTODO DECEDITOD I IKE DODITEN OLE
8429	21510		0.77		7.0E-13 C95155	SWISSPRO	OCTACION NECESTORISME TANDER MOLE A CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE
12713	25474		32		7.0E-13 BE778223.1	EST HUMAN	B01463Z85F1 NIH_INGC_6/ Homo sapiens curv cigne invade: 3000 is 3
							POLYPEPTIDE N-ACETYLGALACTOSAMINYL I KANSFERASE (PROTEIN-UDP ACETYLGALACTOSAMINYL TRANSFERASE) (UDP-GALNAC:POLYPEPTIDE, N-
12976	25635		1.53		7.0E-13 Q10473	SWISSPROT	ACETYLGALACTOSAMINYLTRANSFERASE) (GALNAC-T1)
2168	15303	28430	5.65		6.0E-13 AL163207.2	LN.	Hamo sapiens chromosome 21 segment HS21C007
5239	18361		0.93		6.0E-13 AI267928.1	EST_HUMAN	qo44a09.x1 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1911352 3'
3399	16569		1.15		5.0E-13 R78338.1	EST_HUMAN	y82f04.r1 Soares placenta Nb2HP Homo sapians cDNA clone IMAGE:145759 5'
							z77a12.s1 Soares_testis_NHT Homo sepiens cDNA clone IMAGE:728350 3' similar to contains Alu
3484	16652				5.0E-13 AA435773.1	EST_HUMAN	repetitive element contains element MER22 repetitive element ;
7016	20152				5.0E-13 P08983	SWISSPROT	
11100	24173	37808			5.0E-13 P07313	SWISSPROT	
1916	15059		4.86		4.0E-13 AW378614.1	EST_HUMAN	PM2-HT0224-221099-001-611 HT0224 Homo saplens cDNA

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Homo saptems X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a), Ca2+/Calmodulin-dependent protein kinase I (CAMKI), creatine transporter (CRTR), y33g05.r1 Soares melanocyte 2NbHM Homo sapiens cDNA clone IMAGE:273080 5' similar to PIR:A32995 zn88h10.r1 Stratagene lung carcinoma 937218 Homo sapiens cDNA clone IMAGE:565315 5' similar to zn88h10.r1 Stratagene lung carcinoma 937218 Homo sapiens cDNA clone IMAGE:565315 5' similar to Homo saplens X-linked anhidroitic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat zw76g12.r1 Soares\_testis\_NHT Homo sapiens cDNA clone IMAGE:782182 5' similar to TR:G452763 #288c02.x1 NCI\_CGAP\_Brn25 Homo sapiens cDNA clone IMAGE:2565890 3' similar to TR:O75139 qn32d05,x1 NCI\_CGAP\_Kid5 Homo sapiens cDNA clone IMAGE:1899945 3' similar to contains Alu DKFZp434A0128\_r1 434 (synonym: htes3) Homo sepiens cDNA clone DKFZp434A0128 5 7B04H11 Chromosome 7 Fetal Brain cDNA Library Homo sapiens cDNA clone 7B04H1 zw68g08.r1 Soares\_testis\_NHT Homo sapiens cDNA clone IMAGE:781406 6 Homo septiens Xq pseudoautosomal region; segment 2/2 Homo septiens chromosoma 21 segment HS21C010 GM3-FT0100-140700-242-h08 FT0100 Homo septiens cDNA ob18402.s1 NGI\_CGAP\_Kid5 Homo septens cDNA clone IMAGE:1324035 3 zx48d07.r1 Soares\_testis\_NHT Homo saplens cDNA clone IMAGE:795469 5' PM3-HT0520-230200-002-08 HT0520 Homo saplens cDNA 2/78g10\_s1 Soares\_testis\_NHT Homo saplens cDNA clone IMAGE:728614 3' 2/78g10\_s1 Soares\_testis\_NHT Homo saplens cDNA clone IMAGE:728514 3' DNA-DIRECTED RNA POLYMERASE II LARGEST SUBUNIT (VERSION DNA-DIRECTED RNA POLYMERASE II LARGEST SUBUNIT (VERSION formo sapiene glypican 3 (GPC3) gene, partial cds and flanking repeat Fop Hit Descriptor Homo sapiens mRNA for KIAA1329 protein, partial cds CDM protein (CDM), adrenoleukodystrophy protein > CM-BT043-090299-075 BT043 Homo sapiens cDNA 432995 t complex sterlity protein - mouse contains THR.t2 THR repetitive element; contains THR.t2 THR repetitive element 075139 KIAA0644 PROTEIN. G462763 COR1 MRNA. repetitive element EST\_HUMAN EST\_HUMAN SWISSPROT EST\_HUMAN EST\_HUMAN EST\_HUMAN EST\_HUMAN EST\_HUMAN EST\_HUMAN EST\_HUMAN EST\_HUMAN EST\_HUMAN EST\_HUMAN **EST HUMAN** EST\_HUMAN EST\_HUMAN EST\_HUMAN Top Hit Database Source 눌 뉟 Top Hit Acession 3.0E-13 AW005639.1 4.0E-13 AA435819.1 4.0E-13 AA435819.1 3.0E-13 AA430310.1 3.0E-13 AA134017.1 3.0E-13 AA134017.1 AA454054.1 4.0E-13 AA431529.1 3.0E-13 Al904151.1 3.0E-13 AJ271736.1 4.0E-13 AA454054.1 4.0E-13 BE169131.1 4.0E-13 AB037750.1 4.0E-13 AL043810.1 4.0E-13 AA076907.1 3.0E-13 AF003528.1 3.0E-13 AA745844.1 BF372962.1 4.0E-13 AF003529.1 4.0E-13 AI289831.1 ģ 3.0E-13 U52111.2 4.0E-13 N44291.1 P18616 3.0E-13 3.0E-13 3.0E-13 (Top) Hit BLAST E Value 7. 0.68 0.73 88 1.06 1.38 4.4 96.0 1.53 2.28 3.69 24 1.09 1.08 <u>.</u> 0.47 Expression Signal 34669 32133 32134 32629 32189 ORF SEQ ID NO: 34337 35663 36850 38168 27737 28700 28957 33896 38167 29771 297 21149 15847 19294 14655 15673 16430 18851 18851 SEQ ID 15656 18897 20434 20844 20950 23262 13408 4664 15571 8067 2443 2548 2648 3256 7355 10226 5657 5657 6114 Probe SEQ ID 5704 788 7898 9042 9702 11439 184 2531 4869 3592

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Top Hit Descriptor	EST60487 Activated T-cells XX Homo sapiens cDNA 5' end similar to similar to serine protease P100, Ra- reactive factor	EST60487 Activated T-cells XX Homo sapiens cDNA 5' end similar to similar to serine protease P100, Rancedine factor	RC2-D 70007-110100-014-910 D 70007 Hano sapiens cDNA	HA0536 Human fetal liver cDNA library Homo saplens cDNA	CMQ-BT0281-031199-087-e03 BT0281 Homo saplens cDNA	Hamo sapiens chromosome 21 segment HS21 C048	Homo sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a), Ca2+/Calmodulin-dependent protein kinase I (CAMKI), creatine transporter (CRTR), CDM protein (CDM), adrendeukodystrophy protein >	Danio rario fibroblast growth factor receptor 4 mRNA, complete cds	Homo sapiens DNA polymerase delta small subunit (POLD2) gene, exons 1 through 11 and complete cds	Homo sapiens hypothetical protein PRO2130 (PRO2130), mRNA	Hamo sapiens hypothetical protein PRO2130 (PRO2130), mRNA	Homo sapiens S164 gene, partial cds; PS1 and hypothetical protein genes, complete cds; and S171 gene, partial cds	Homo saplens chromosome 21 segment HS21C078	CELL SURFACE GLYCOPROTEIN 1 PRECURSOR (OUTER LAYER PROTEIN B) (S-LAYER PROTEIN 1)	S. scrofa rps12 mRNA for ribosomal protein S12	Human PFKL gene for liver-type 6-phosphofractokinase (EC 2.7.1.11) exon 2	Homo sapiens N-myristoylitansferase 1 (NMT1), mRNA	Homo sapiens N-myristoyltransferase 1 (NMT1), mRNA	Homo sapiens mab-21 (C. elegans)-like 1 (MAB21L1) mRNA	CM0-NN0001-100300-274-e11 NN0001 Homo sapiens cDNA	FGF-1=fibroblast growth factor 1 [human, kidney, Genomic, 342 nt, segment 2 of 2]	Homo saplens LGMD2B gene	H.sapiens DMA, DMB, HLA-Z1, IPP2, LMP2, TAP1, LMP7, TAP2, DOB, DQB2 and RING8, 9, 13 and 14	genes	nw21g02.s1 NCI_CGAP_GCB0 Homo sapiens cDNA clone IMAGE:1241138.3' similar to contains THR.t3 THR repetitive element:	802038009F1 NCI_CGAP_Brn64 Home sapiens cDNA clone IMAGE:4185868 5
Top Hit Database Source	EST_HUMAN	H TXT	EST HUMAN	EST_HUMAN	EST_HUMAN	ΤN	۲	FZ	TN.	LN.	LN	١	LN LN	SWISSPROT	LN LN	N	LN	LN	LN	EST_HUMAN	N N	TN		LN	EST HIMAN	EST_HUMAN
Top Hit Acession No.	3.0E-13 AA352487.1	3 0F.13 AA352487 1	3.0E-13 AW935487.1	3.0E-13 A1064768.1	3.0E-13 BE063509.1	3.0E-13 AL163248.2	2.0E-13 U52111.2	2.0E-13 U23839.1	2.0E-13 AF239710.1	8924119 NT	8924119 NT	2.0E-13 AF109907.1	2.0E-13 AL163278.2	Q06852	2.0E-13 X79417.1	2.0E-13 X16912.1	10835072 NT	10835072 NT	5031896 NT	2.0E-13 AW892155.1	1.0E-13 S74129.1	1.0E-13 AJ007973.1		1.0E-13 X87344.1	1 0F-13 AA720574 1	1.0E-13 BF340987.1
Most Similar (Top) Hit BLAST E Value	3.0E-13	2 DE-13	3.0E-13	3.0E-13	3.0E-13	3.0E-13	2.0E-13	2.0E-13	2.0E-13	2.0E-13	2.0E-13	2.0E-13	2.0E-13	2.0E-13 Q06852	2.0E-13	2.0E-13	2.0E-13	2.0E-13	2.0E-13	2.0E-13	1.0E-13	1.0E-13		1.0E-13	1 0E-13	1.0E-13
Expression Signal	0.5	, c	0.58	3.1	3.41	1.62	3.52	2.06	8.93	0.61	0.61	1.68	2.07	4.34	0.58	5.73	9.0	9.0	2.41	22.49	1.34	5.53		1.4	2 64	1.32
ORF SEQ ID NO:	34865	34896			38008		26411		27521	l				32770	l	33704	33474	33475	37317			27151		27596		30833
Exen SEQ ID NO:	21350	21350	L			24886	13379	13470	14455	16245		16760	17372	19424	1	20267	20064	20064	23709	25274	L			14521	15210	
Probe SEQ ID NO:	8268	RACR	10401	10915	11301	11898	154	249	1289	3070	3070	3596	4224	6250	6335	6954	7189	7199	10675	12388	302	911		1367	2070	4715

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Top Hit Descriptor	nn24d01.s1 NCI_CGAP_Gas1 Homo saplens cDNA clone IMAGE:1084801 3' similar to contains Alu repetitive element;contains element MER24 repatitive element;	nn24d01.s1 NCI CGAP_Gas1 Homo sapiens cDNA done IMAGE:1084801 3' similar to contains Alu repolitive element, contains dement MER24 repetitive element;	MELANOMA-ASSOCIATED ANTIGEN B4 (MAGE-B4 ANTIGEN)	Mus musculus osteotesticular protein tyrosine phosphatase mRNA, complete cds	745e10.x1 Scares NSF_FB_9W_OT_PA_P_S1 Homo capiens cDNA clone IMAGE:3524443 3' similar to contains MFR29.b2 MER39 repetitive element:	AV716377 DCB Homo saplens cDNA clone DCBAIE03 5	Homo sapiens Xq pseudoautosomal region; segment 1/2	H.sapiens CD4 gene	al24c01.s1 Soares_testis_NHT Homo sepiens cDNA clone 1391232 3' similar to contains MER19.t1 MER19 repolitive element :	aj24001.s1 Soares_testis_NHT Homo sapiens cDNA clone 1391.232.3' similar to contains MER19.t1 MER19 parafiling element	RC4-CT0322-080100-013-d09 CT0322 Homo sapiens cDNA	Homo sapiens TFF gene duster for trefoil factor, complete cds	xo54h05.x1 NCI_CGAP_Ut1 Homo sapiens cDNA clone IMAGE:2707833 3'	igi24c01.s1 Soares_testis_NHT Homo sapiens cDNA clone 1391232.3' similar to contains MER19.t1 MER19 repetitive element;	Human DNA, SINE repetitive element	Seguinus oedipus gene for seminal vesicle secreted protein semenogelin l	hz71c09.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3213424 3'	y72e03,r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:1447963'	H. sapiens DNA for endogenous retroviral like element	zq17c10.s1 Stratagene fetal retina 937202 Homo saplens cDNA clone IMAGE:629970 3'	QV2-BT0258-261099-014-a01 BT0258 Homo sapiens cDNA	wc92h08.x1 NCI_CGAP_Co3 Homo sapiens cDNA clone IMAGE:2326143 3'	x667e10.x1 NCI_CGAP_Gas4 Homo saplens cDNA clone IMAGE:2623146 3' similar to contains MER10.t2 MER10 repetitive element :	Homo sapiens chromosome 21 segment HS21C085	Homo sapiens FRA3B common fragile region, diadenosine triphosphate hydrolase (FHIT) gene, exon 5
Top Hit Database Source	EST_HUMAN	EST HUMAN	SWISSPROT	ΓZ	EST HUMAN	EST HUMAN	N	FZ	EST HUMAN	TOT LIMAN	EST HUMAN	LN	EST_HUMAN	EST HUMAN	N	Ę	EST_HUMAN	EST_HUMAN	IN	EST HUMAN	EST_HUMAN	EST_HUMAN	EST HUMAN	L	Į.
Top Hit Acession No.	.0E-13 AA577812.1	.0E-13 AA577812.1	.0E-13 O15481	.0E-13 AF300701.1	0E-13 BF108755.1	.0E-13 AV715377.1	.0E-13 AJ271735.1	.0E-13 X87579.1	9.0E-14 AA781159.1	0 05-14 4 4 701450 4	9.0E-14 AW861577.1	AB038162.1	9.0E-14 AW513296.1	9.0E-14 AA781159.1	9.0E-14 D14547.1	9.0E-14 AJ002153.1	8.0E-14 BE468263.1	R76269.1	X89211.1	8.0E-14 AA219316.1	BE062558.1	8.0E-14 AI688118.1	7.0E-14 AW151673.1	7.0E-14 AL163285.2	6.0E-14 AF020603.1
Most Similar (Top) Hit BLAST E Value	1.0E-13	1.0E-13	1.0E-13	1.0E-13	1.0E-13	1.0E-13	1.0E-13	1.0E-13	9.0E-14	0 00 44	9.0E-14	9.0E-14	9.0E-14	9.0E-14	9.0E-14	9.0E-14	8.0E-14	8.0E-14	8.0E-14	8.0E-14	8.0E-14	8.0E-14	7.0E-14	7.0E-14	6.0E-14
Expression Signal	76.0	0.97	1.04	9.0	9.74	1.38	3.46	1.85	3.76	70,7	4.13	7.9	7.5	-	7.37	2.23	1.17	3.64	38.93	3,22	1.79	2.43	4.76	0.73	12.43
ORF SEQ ID NO:	34691	34692		37154	38431				26583		ł.	L	29360	26583	30057	30994			34605	36266		32048	_		26620
Exon SEQ ID NO:	21176	21176		23543			25605	25706	13554	١	15694	15925	16355	13554	17057	18010	16751	17222	21090	22698		25410	16044		13586
Probe SEQ (D NO:	8094	8094	10295	10508	11661	12206	12920	13077	343	770	2569	2811	3180	3310	3898	4879	3587	4066	9647	9760	11717	12611	1658	9120	378

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Top Hit Descriptor	Homo sapiens FRA3B common fregile region, diadenosine triphosphate hydrolase (FHIT) gene, exon 5	Hamo sepiens FRA3B common fragile region, diadenosine triphosphate hydrolase (FHIT) gane, exon 6	CANALICULAR MULTISPECIFIC ORGANIC ANION TRANSPORTER 1 (MULTIDRUG RESISTANCE- ASSOCIATED PROTEIN 2) (CANALICULAR MULTIDRUG RESISTANCE PROTEIN)	xb03b05.x1 NCI_CGAP_GU1 Homo seplens cDNA clone IMACE:2575185 3' similar to contains L1.t2 L1 repetitive element;	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG	S-ANTIGEN PROTEIN PRECURSOR	Hamo septens LGMD2B gene	Zk67a06.r1 Scares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:487858 5'	yy7sc12.s1 Soares_multiple_scierosis_ZNbHMSP Homo sapiens cDNA clone IMAGE:279190 3' similar to contains L1.13 L1 repetitive element;	H.sapiens DMA, DMB, HLA-Z1, IPP2, LMP2, TAP1, LMP7, TAP2, DOB, DQB2 and RING8, 9, 13 and 14	denes	TCAAP1D1470 Pediatric acute myalogenous leukemia cell (FAB M1) Baylor-HGSC project=TCAA Homo sapiens cDNA clone TCAAP1470	wm08c03.x1 NCI_CGAP_Ut4 Homo saplens cDNA clone IMAGE:2435332 3' similar to contains Atu	repetitive element	R.narvegicus mRNA for CPG2 protein	te91c12.x1 NCI_CGAP_Pr28 Homo sapiens cDNA clone INAGE:2094070 3' similar to TR:000519 000519   FATTY ACID AMIDE HYDROLASE;	te91c12.x1 NCL CGAP_Pr28 Homo sepiens aDNA clone IMAGE:2094070 3' similar to TR:000519 000519 FATTY ACID AMIDE HYDROLASE.:	EST185054 Brain IV Homo sapiens cDNA	yy07b10.r1 Soares melanocyte 2NbHM Homo sapiens cDNA clone IMAGE:270523 5	xp45f12.x1 NCI_CGAP_HN11 Home sapiens cDNA clone IMAGE:2743343 3' similar to centains Alu	repetitive element contains element MER9 repetitive element ;	Homo sapiens chromosome 21 segment HS210085	601435233F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3920169 5'	Homo sapiens Xq pseudoautosomal region; segment 2/2	Homo sapiens Xq pseudoautosomal region; segment 2/2	Homo saplens chromosome 21 segment HS21C103
Top Hit Database Source	LN	LN.	SWISSPROT	EST HUMAN	SWISSPROT	SWISSPROT	NT	EST_HUMAN	EST HUMAN		L'N	EST_HUMAN		EST HUMAN	LN	EST_HUMAN	EST HUMAN	EST HUMAN	EST HUMAN		EST_HUMAN	NT	EST HUMAN	ŊŢ	NT	LN
Top Hit Acession	6.0E-14 AF020503.1	6.0E-14 AF020503.1	263120	5.0E-14 AW073791.1	P08547	P04928	4.0E-14 AJ007973.1	4.0E-14 AA046502.1	4.0E-14 N46328.1		X87344.1	4.0E-14 BE242466.1		4.0E-14 Ai886224.1	X95466.1	3.0E-14 AI420786.1	3.0E-14 Al420786.1	3.0E-14 AA386311.1	3.0E-14 N42165.1		3.0E-14 AW 265354.1	3.0E-14 AL163285.2	3.0E-14 BE891550.1	2.0E-14 AJ271736.1	2.0E-14 AJ271736.1	2.0E-14 AL163303.2
Most Similar (Top) Hit BLAST E Vatue	6.0E-14	6.0E-14	5.0E-14 Q63120	5.0E-14	5.0E-14 P08547	4.0E-14 P04928	4.0E-14	4.0E-14	4.0E-14		4.0E-14 X87344.1	4:0E-14		4.0E-14	3.0E-14 X95466.1	3.0E-14	3.0E-14	3.0E-14	3.0E-14		3.0E-14	3.0E-14	3.0E-14	2.0E-14	2.0E-14	2.0E-14
Expression Signal	2.19	2.19	4.17	1.32	5.26	1.61	10.15	0.73	1.04		0.71	5.5		69.9	1.56	0.93	0.93	9.0	0.86		5.87	1.88	1.51	2.33	2.33	11.36
ORF SEQ ID NO:	36682	36663	26842	31254	L		28174		30533			38729			27204	33434	33435	J			31533		31853		26635	
Exen SEQ ID NO:	23065	23065	13818	18288	L	16030		17007	17549	1	21227	25024	ı		14145	20025	2002	}	L	1		26041	25894			16019
Probe SEQ ID NO:	10027	10027	88	5166	5650	1147	1928	3847	4407		8145	12043		12986	972	6873	6873	7173	8987		11512	12894	13212	401	401	708

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					2		
Probe SEQ ID NO:	Exan SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
				0000			
2461	15588		1.04	,	2.0E-14 AW372868.1	EST_HUMAN	RC5-BT0377-091299-031-D12 BT0377 Homo saplens cDNA
2535	15660		66'0	20E-14	7657529 NT	LN	Homo sapiens rhabdold tumor deletion region protein 1 (RTDR1), mRNA
2593	15718	1			2.0E-14 AL163209.2	N <sub>T</sub>	Homo saplens chromosome 21 segment HS21C009
5641	ı	31912			2.0E-14 BF380661.1	EST_HUMAN	1L2-UT0072-240800-142-D07 UT0072 Homo septens cDNA
							ta78h01 x2 NCI_CGAP_HSC2 Homo sapiens cDNA clone IMAGE:2050225 3' similar to contains L1.t3 L1
5738	18931	32229	1.03	•	.1	EST_HUMAN	repetitive element;
5838	19028		E	2.0E-14	2.0E-14 U01317.1	ΤN	Human beta globin region on chromosome 11
7023	20159		1.04	,	2.0E-14 BE000550.1	EST_HUMAN	RC3-BN0072-240200-011-a06 BN0072 Homo sapiens cDNA
7437	20514		1.06		2.0E-14 P56163	SWISSPROT	ZINC-FINGER PROTEIN NEURO-D4
7676	20741			`	2.0E-14 BE158761.1	EST HUMAN	IL2-HT0397-071299-024-D04 HT0397 Homo saplens cDNA
7676	20741		24,46		2.0E-14 BE158761.1	EST_HUMAN	IL2-HT0397-071299-024-D04 HT0397 Homo sapiens cDNA
		!					wr59g10.x1 NCI_CGAP_Uff Homo sapiens cDNA clone IMAGE:2492034 3' similar to contains Alu repetitive
10121	23159		0.56		2.0E-14 AI978795.1	EST_HUMAN	dement;
10630	23664	37273	0.51	2.0E-14	2.0E-14 AV741648.1	EST_HUMAN	AV741649 CB Homo sapiens cDNA clone CBFBBF04 5'
11019	24098		3.62		2.0E-14 AW139800.1	EST_HUMAN	UI-H-BI1-adw-a-10-0-UI.s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:27182343'
12890	26045		2.5		2.0E-14 AF008191.1	NT	Homo sapiens putative G6 protein (GR6) gene, complete cds
13163	15660		1.26	2.0E-14	7667529 NT	N	Homo sapiens mabdold tumor deletion region protein 1 (RTDR1), mRNA
1092	14257	27313	2:32		1.0E-14 AL163246.2	TN	Homo sapiens chromosome 21 segment HS21C046
1438	14591		7.01		1.0E-14 AL163268.2	ΓN	Homo sapiens chromosome 21 segment HS21C068
1438	14591		7.01		1.0E-14 AL163268.2	Z	Homo saplens chromosome 21 segment HS21C068
							Нотто sapiens chromosome X region from filamin (FLN) gene to glucose-6-phosphate dehydrogenase
2057	16198	_			1.0E-14 L44140.1	N-	(G6PD) gene, complete cds's
2258	15391		6.33		1.0E-14 AL163303.2	ΝΤ	Homo sapiens chromosome 21 segment HS21C103
2480	15607		6.44		1.0E-14 AF001689.1	NT	Homo saplens ribosomal protein L23A (RPL23A) gene, complete cds
3010	16186		1.41		1.0E-14 P05227	SWISSPROT	HISTIDINE-RICH PROTEIN PRECURSOR (CLONE PFHRP-II)
3236	16410				1.0E-14 BF335227.1	EST_HUMAN	RC2-CT0432-310700-013-a09_1 CT0432 Homo saplens cDNA
3236	16410	29425	3.14	L	1.0E-14 BF335227.1	EST_HUMAN	RC2-CT0432-310700-013-a09_1 CT0432 Homo sapiens cDNA
3992	17149					EST_HUMAN	ae89c12.s1 Stratagene schizo brain S11 Homo sapiens cDNA clone IMAGE:971350 3'
4596	17733				1.0E-14 AW 275852.1	EST_HUMAN	xq38h10.x1 NCI_CGAP_Luz8 Homo saplens cDNA clone IMAGE:2753059 3'
							Bos taurus xenobiotic/medium-chain fatty acid:CoA ligase form XI-III mRNA, nuclear mRNA encoding
5930	19116		1.98		1.0E-14 AF126145.1	NT	mitochondrial protein, complete ods
6813				1.0E-14	11437150 NT	INT	Homo sapiens prominin (mouse)-like 1 (PROML1), mRNA
6813					1	LN	Homo sapiens prominin (mouse)-like 1 (PROML1), mRNA
1607	14760	27839	1.81	9.0E-15	5 7427522 NT	NT	Home sapiens protein tyrosine phosphatase, receptor type, T (PTPRT), mRNA

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Probe SEQ (D	ဟ	ORF SEQ	Expression Signal	Most Similar (Top) Hit	Top Hit Acession		Top Hit Descriptor
Ö	Ö	5	1000 1000 1000 1000 1000 1000 1000 100	Value	ġ	Source	
	<u></u>						Homo sapiens transcription factor ICHM enhancer 3, JM11 protein, JM4 protein, JM5 protein, T54 protein, JM10 protein, A4 differentiation-dependent protein, triple LIM domain protein 6, and synaptophysin genes,
2242			1.38		9.0E-15 AF196779.1	۲	complete cds; and L-type calcium channel a>
7865	20732	34207	4.24	9.0E-15	9.0E-15 P21416	SWISSPROT	GAG POLYPROTEIN [CONTAINS: CORE PROTEINS P15, P12, P30, P10]
8206	21288	34810	1.24	9.0E-15	BE903559.1	EST_HUMAN	601677750F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3960156 5
13099	25718		2.87	9.0E-15	9.0E-15 AL163247.2	NT	Hano saplens chromosome 21 segment HS210047
2872	13687		1.53	8.0E-15	BE261482.1	EST_HUMAN	601148632F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3164023 5'
7331	20412	33874	1.13	7.0E-15	BF035327.1	<b>EST_HUMAN</b>	601458531F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3862086 5'
10650	23684		786	7.0E-15	0E-15 AW241958 1	NAMIN TRE	xn77d02.x1 Sogres_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2700483.3' similar to contains THR t2 THR constitue element
							257408.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:701583 5' similar to gb:L21934 STEROL
12270	25203		1.44	7.0E-15	7.0E-15 AA284465.1	EST_HUMAN	O-ACYLTRANSFERASE (HUMAN); contains L1:11 L1 repetitive element;
1018	14189	27250	7.51	6.0E-15	AJ271736.1	LN	Homo sapiens Xq pseudoautosomal region; segment 2/2
5263	18382		96.0	6.0E-15	AW901258.1	EST_HUMAN	CM4-NN1011-100300-110-d10 NN1011 Homo saplens cDNA
6041		32546	1.02	6.0E-15	X73462.1	۲	O.aries mRNA for hair keratin cysteine-rich protein
6041	19224	32547	1.02	6.0E-15	X73462.1	LN.	O. aries mRNA for hair keratin cysteine-rich protein
11583	26231		45.1	6.0E-15	AW836843.1	EST_HUMAN	QV1-LT0036-150200-070-c10 LT0036 Homo sapiens cDNA
423	13618	26658	3.57	5.0E-15	5.0E-15 AL163208.2	NT	Homo sepiens chromosome 21 segment HS21C008
				i			Human heredifary haemoctromatosis region, histone 24-lika protein gene, heredifary haemochromatosis
2819	15933	29044	1.76	5.0E-15	0E-15 U91328.1	۲	(HLA-H) gene, RoRet gene, and sodium phosphate transporter (NPT3) gene, complete cds
5003	4005		3	B 07 45	OT 45 D44200	100001110	RETROVIRUS-RELATED POL POLYPROTEIN (CONTAINS: REVERSE TRANSCRIPTASE;
440	_	26240	233	4 0F-15	03.2	- PALSON NO	Homo sablens chromosome 21 segment HS21C1C3
6804	L	33359	6.0	4.0E-15	Γ	LN.	Homo sapiens mRNA, chromosome 1 specific transcript KIAA0501
11316	21065	34577	2.11	4.0E-15	4.0E-15 AJ130894.1	NT	Homo sepiens mRNA for transcription factor
11316	21065	34578	2.11	4.0E-15	0E-15 AJ130894.1	LN TN	Homo sapiens mRNA for transcription factor
							LY1142F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA clone LY1142 5' similar to
4333			7.67	3.0E-15	3.0E-15 N89452.1		ANF(CARDIODILATIN)
5141	18264	31232	0.67	3.0E-15	3.0E-15 AA078097.1	EST_HUMAN	7P01F03 Chromosome 7 Placental cDNA Library Homo sapiens cDNA clone 7P01F03
5141	18264	31233	0.67	3.0E-15	AA078097.1	EST_HUMAN	7P01F03 Chromosome 7 Placental cDNA Library Homo sapiens cDNA clone 7P01F03
6953	- 1		1.11	3.0E-15		SWISSPROT	GLUTATHIONE PEROXIDASE RY2D1 PRECURSOR (ODORANT-METABOLIZING PROTEIN RY2D1)
7430		33978	3.13			NT	Mus musculus ultra high suffur keratin gene, complete cds
7430	20507	33979	3.13	ຕ	0E-15 M27685.1	N	Mus musculus ultra high suffur keratin gene, complete cds

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Top Hit Descriptor	oc36a07.s1 NCI_CGAP_GCB1 Homo saplens cDNA clone IMAGE:1351764 3' similar to contains MER19.t1 MER19 repatitive element;	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete ods)	lomo sapiens Xq pseudoautosomal region; segment 1/2	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced	Homo sapiens hypothetical protein FLJ20212 (FLJ20212), mRNA	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced	wf07706.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2349923 3' sImitar to TR:Q61043 Q61043 NINEIN.	601344253F1 NIH_MGC_8 Homo sapiens cDNA done IMAGE:3677268 5'	601344253F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3677268 5'	Homo sapiens ASCL3 gene, CEGP1 gene, C11orf14 gene, C11orf15 gene, C11orf16 gene and C11orf17 gene	zi77e03.s1 Soares_fetal_liver_spleen_1NFLS_S1 Hamo saplens cDNA clone IMAGE:460924 3'	za78d10.r1 Soares fetal lung NbHL19W Homo sapiens cDNA clone IMAGE;298675 5' similar to WP:F44F4.8 CE02227 TRANSPOSASE ;	Human DNA, SINE repetitive element	zt77g08.1 Spares_testis_NHT Home sapiens cDNA clone IMAGE:728414 5'	zi77g08.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:728414 5'	CM0-HT0244-201099-078-a12 HT0244 Homo saplens cDNA	CM0-HT0244-201099-078-a12 HT0244 Homo sapiens cDNA	Homo sapiens Xq pseudoautosomal region; segment 1/2	Homo septens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
Top Hit Database Source	EST_HUMAN	Ę	LN L	TN	Ĭ	LN	LN	Ę	Ę	EST HUMAN	Т	EST_HUMAN	۲N	EST_HUMAN	EST_HUMAN	LN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	Г	ŢN
Top Hit Acession No.	.0E-15 AA807128.1	.0E-15 AB026898.1	3.0E-15 AJ271735.1	2.0E-15 AF223391.1	.0E-15 AF223391.1		N 1026288	.0E-15 AF223391.1	.0E-15 AF223391.1	2.0E÷15 Al806335.1	2.0E-15 BE562352.1	2.0E-15 BE562352.1	2.0E-15 AJ400877.1	.0E-15 AA704195.1	2.0E-15 W05064.1	2.0E-15 D14547.1	2.0E-15 AA397758.1	2.0E-15 AA397758.1	2.0E-15 AW379465.1	2.0E-15 AW379465.1	.0E-15 AJ271735.1	2.0E-15 AF223391.1
Most Similar (Top) Hit BLAST E Value	3.0E-15	3.0E-15	3.0E-15	2.0E-15	2.0E-15	2.0E-15	2.0E-15	2.0E-15	2.0E-15	2.0E:15	2.0E-15	2.0E-15	2.0E-15	2.0E-15	2.0E-15	2.0E-15	2.0E-15	2.0E-15	2.0E-15	2.0E-15	2.0E-15	2.0E-15
Expression Signal	2.38	8.11	829	3.71	3.28	3.28	0.99	0.72	0.72	2.76	1.11	1.11	1.58	2.73	5.05	2.86	0.91	16.0	1.18	1.18	3.69	3.89
ORF SEQ ID NO:		37748		26511	26621	26622		29778	29779			32839		69688				32900		36232		29778
Exon SEQ ID NO:	23167	24112	26081	13479	13587	13587	14712	16763	16763	17880	19483	19483	20346	20498					22659	22659	24152	16763
Probe SEQ ID NO:	10129	11033	12620	260	379	379	1559	3599	3599	4745	6311	6311	7263	7421	7554	9107	9273	9273	9604	9604	11077	13016

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			,	_	_		_	_	-	-		_	_			_			_		_					_		_
Top Hit Descriptor	Homo sapiens calcium channel apha1E subunit (CACNA1E) gene, exons 7-49, and partial ods, alternatively spliced	623h05x1 NC_CGAP_Lu24 Homo seplens oDNA olone IMAGE:22707453' similar to TR:Q13539 Q13539 MARINER TRANSPOSASE;	hk40e02.y1 NCI_CGAP_Ov34 Homo sapiens cDNA done IMAGE-2999162 5'	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG	RC3-HT0649-100500-022-b05 HT0649 Homo sapiens cDNA	ye40e10.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:120234 3' similar to contains MER6 repotitive element	QV3-BT0569-270100-074-905 BT0569 Homo sapiens cDNA	DYNEIN BETA CHAIN, CILIARY	Homo sapiens chromosome 21 segment HS21C080	qf88h06.x1 Soarse_lectis_NHT Homo sapiens cDNA clone IMAGE:1755227 3'	qf68h06x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1755227 3'	Homo sapiens chromosome 21 segment HS21C007	Homo saplens spermidine synthase (SRM) mRNA	DYNEIN GAMMA CHAIN, FLAGELLAR OUTER ARM	oh37c03.s1 NCI_CGAP_Kid6 Homo sapiens cDNA clone IMAGE:1459972.3' similar to contains L1.t3 L1 promittive element	Home sapiens major histocompatibility locus class III region	tr31c05.x1 NCI_CGAP_Ov23 Homo sapiens cDNA clone IMAGE:2219912 3' similar to contains Alu repetitive	Bemerit;	1500 September 200 Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Co	d78a02x1 NCI_CGAP_Ktd3 Homo sapiens dDNA clone IMAGE:1865354 3' similar to contains MER10.t3	MER10 repetitive element;	q76a02x1 NCI_CGAP_Kid3 Homo sapiens cDNA clore IMAGE:1865354 3' similar to contains MER10.t3	MER10 repetitive element;	Hamo sapiens chemokine (C-C motif) receptor 8 (CCR8) mRNA	PROTEIN-ARGININE DEIMINASE TYPE IV (PEPTIDYLARGININE DEIMINASE IV) (PAD-R4) (PEPTIDYLARGININE DEIMINASE TYPE ALPHA)	PROTEIN-ARGININE DEIMINASE TYPE IV (PEPTIDYLARGININE DEIMINASE IV) (PAD-R4)	(PEPTIDYLARGININE DEIMINASE TYPE ALPHA)	ye28c12.r1 Strategene lung (#937210) Homo sapiens cDNA clone IMAGE:119062 5'
Top Hit Database Source	TN	EST_HUMAN	EST_HUMAN	SWISSPROT	EST_HUMAN	HOT HIMAN	EST HUMAN	SWISSPROT	N	EST_HUMAN	EST_HUMAN	NT	NT	SWISSPROT	NAMIL TOE	NT		HEST HUMAN	MANA FOR	NONOLICE	EST_HUMAN		EST_HUMAN	IN	SWISSPROT		SWISSPROT	EST HUMAN
Top Hit Acession No.	2.0E-15 AF223391.1	1.0E-15 Al689984.1	1.0E-15 BE043584.1	P08547	1.0E-15 BE182696.1	1 0F-15 T95763 1	1.0E-15 BE074217.1	P39057	1.0E-15 AL163280.2	1.0E-16 AI200976.1	1.0E-15 Al200976.1	1.0E-15 AL163207.2	4507208 NT	Q39575	1 0E-15 AAB64653 1	1.0E-15 AF044083.1		1.0E-15 AI/83944.1 ES	0.05 46 50669 4	1,00000.1	9.0E-16 AI244341.1		9.0E-16 AI244341.1	4885120 NT	088807		088807	7.0E-16 T94149.1
Most Similar (Top) Hit BLAST E Value	2.0E-15	1.0E-15	1.0E-15	1.0E-15 P08547	1.0E-15	1 0F-15	1.0E-15	1.0E-15 P39057	1.0E-15	1.0E-16	1.0E-15	1.0E-15	1.0E-15	1.0E-15 Q39575	1 0E-15	1.0E-15	1	1.0E-15	9.00	0.0	9.0E-16		9.0E-16	7.0E-16	7.0E-16   O88807		7.0E-16 O88807	7.0E-16
Expression Signal	3.89	3.09	1.42	1.18	0.61	172	1.96	0.79	66.0	4.94	4.94	0.78	96.0	66.0	0.04	3.04		13.05	44.		1.48		1.48	0.85	1.3		1.3	38.08
ORF SEQ ID NO:	67762			29396		33032		Ĺ						36127	36455			30244			38685			32315	34043		34044	
Exon SEQ ID NO:	16763	15948	16253		17619	19668								22564	22872	1		73867 77767	2/3/0		24980		-	19009	20571			25995
Probe SEQ ID NO:	13016	2834	3077	3211	4479	6502	7149	7184	8427	8615	8615	9239	9242	9448	9832	11057	, 0,0,	13104	44244		11995		11995	5819	7496		7496	13043

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Top Hit Descriptor	EST384702 MAGE resequences, MAGL Homo seplens cDNA	Mus musculus olfactory receptor cluster, OR37A, OR37B, OR37C, OR37E genes and OR37D pseudogene	0t80c04.s1 Scares_total_fetus_Nb2IFB_8w Homo saplens cDNA clone IMAGE:1623078 3' similar to contains element L1 repetitive element:	601885734F1 NIH_MGC_57 Homo septens cDNA clone IMAGE:4104129 5	Homo sapiens GTP binding protein 1 (GTPBP1), mRNA	Homo sapiens gene for TMEM1 and PWP2, complete and partial cds	QV1-UM0036-200300-115-g02 UM0036 Homo sepiens cDNA	QV1-UM0036-200300-115-g02 UM0036 Homo capiens cDNA	MYELIN-ÖLIGODENDROCYTE GLYCOPROTEIN PRECURSOR	PM4-BT0650-010400-002-009 BT0650 Homo saplens cDNA	PM4-BT0650-010400-002-909 BT0650 Homo sapiens cDNA	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG	Homo sapiens chromosome 21 segment HS21C084	Homo sapiens hypothetical protein FLJ10024 (FLJ10024), mRNA	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG	C05947 Human pancreatic islet Homo sapiens cDNA clone hbc5355	Homo sapiens Grb2-associated binder 2 (KIAA0571), mRNA	yf96511.r1 Soares Infant brain 1NIB Homo sapiens cDNA clone IMAGE:30489 5'	df45c01.y1 Morton Fetal Cochlea Homo saplens cDNA clone IMAGE:2486376 5'	df45c01.y1 Morton Fetal Cochlea Homo sapiens cDNA clone IMAGE:2486376 5	DKFZp434P037_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434P037 5'	Homo saplens TSX (TSX) pseudogene, exon 5	ZONADHESIN PRECURSOR	ENVELOPE GLYCOPROTEIN GP340 (MEMBRANE ANTIGEN) (MA) [CONTAINS: GLYCOPROTEIN GP2201	au76b08,y1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2782163 5' similar to	SW:KID1_MOUSE Q61751 RENAL TRANSCRIPTION FACTOR KID-1;	AV661393 GLC Homo sapiens cDNA clone GLCGSA013'	7B10F02 Chromosome 7 Fetal Brain cDNA Library Homo capiens cDNA clone 7B10F02	Homo sapiens glypican 3 (GPC3) gene, partial cds and flanking repeat regions	am98h05.s1 Stratagene schizo brain S11 Homo saplens cDNA clone IMAGE:1684185.3' similar to contains THR,b2 THR repetitive element;
Top Hit Database Source	EST_HUMAN	IN	EST HUMAN	Г		FN	EST_HUMAN		SWISSPROT	EST_HUMAN	Г	SWISSPROT	IN	Ę	SWISSPROT	EST_HUMAN		EST_HUMAN		Г	EST_HUMAN	Г	SWISSPROT	SWISSPROT	Т	EST_HUMAN		T_HUMAN	N	EST_HUMAN
Top Hit Acession No.	6.0E-16 AW972611.1	6.0E-16 AJ261154.1	5.0E-16 AA992178.1	5.0E-16 BF217368.1	11418127 NT	4.0E-16 AB001523.1	4.0E-16 AW797168.1	4.0E-16 AW797168.1	Q16653	4.0E-16 BE083875.1	4.0E-16 BE083875.1	P08548	4.0E-16 AL163284.2	11423191 NT	P08548	4.0E-16 C05947.1	6912469 NT	4.0E-16 R18591.1	3.0E-16 AW022862.1	3.0E-16 AW022862.1	3.0E-16 AL046445.1	3.0E-16 AF135446.1	028983	P03200		3.0E-16 AW160828.1	3.0E-16 AV661393.1	3.0E-16 AA077225.1	3.0E-16 AF003529.1	3.0E-16 AI002836.1
Most Similar (Top) Hit BLAST E Value	6.0E-16	5.0E-16	5.0E-16	5.0E-16	5.0E-16	4.0E-16	4.0E-16	4.0E-16	4.0E-16 Q16653	4.0E-16	4.0E-16	4.0E-16 P08548	4.0E-16	4.0E-16	4.0E-16 P08548	4.0E-16	4.0E-16	4.0E-16	3.0E-16	3.0E-16	3.0E-16	3.0E-16	3.0E-16 Q28983	3 OF-16 P03200		3.0E-16	3.0E-16	3.0E-16	3.0E-16	3.0E-16
Expression Signal	9.12	96:0	221	2.68	14.16	1.01	2.87	2.87	5.29	8.68	8.68	0.91	42.68	0.72	1.95	9.86	3.23	1.33	1.09	1.09	1.58	2.33	2.73	4.71		0.59	1.32	66.0	1.67	4.25
ORF SEQ ID NO:		27757	28973				28708	28709	29722	30394							32079		26395	26396			27720	76262		30830			32223	35473
Exen SEQ ID NO:	15342	14675	15862	L	25749	15444	15581	15581	16711	17405	17405	1,	ı	22552	25218	ļ	ł	25454		13361	13673	13682	14536	18217	L	17846	1	Į	18927	21837
Probe SEQ ID NO:	2208	1522	2745	11809	13152	2312	2453	2453	3546	4260	4260	5257	7890	9495	12293	12381	12392	12682	135	136	478	488	1483	3041		4711	5057	5392	5734	8858

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. Top Hit Descriptor	602246538F1 NIH_MGC_62 Homo sapiens cDNA clone IMAGE:4332032 5	Homo sapiens ADP/ATP carrier protein (ANT-2) gene, complete cds	DKFZp434L1623_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434L1623 5	Homo sapiens chromosome 21 segment HS210079	af06db4.s1 Scares_testis_NHT Homo saplens cDNA clone IMAGE:1030855 3'	Human SSAV-related endogenous retroviral LTR-like element	H. sapiens DNA for endogenous retroviral like element	og56/03.x1 Soares_testis_INHT Homo septens cDNA clone IMAGE:1839197 3' similar to contains MER29.t3 MER29 repetitive element :	RC3-BT0046-131199-003-H12 BT0046 Homo sapiens cDNA	HISTIDINE-RICH PROTEIN KE4	th Bert IXT NOT_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2141708 3' similar to contains element MER33 repositive element;	nz47f06,x5 NCI_CGAP_Pr12 Homo saplens cDNA clone IMAGE:1290947 similar to TR:054849 054849 HYPOTHETICAL 42.9 KD PROTEIN. [2] TR:008905 ; contains MER7.t1 MER7 repetitive element;	782h09.x1 NCI_CGAP_Pr28 Homo sepiens cDNA clone IMAGE:3303521 3'	7782h09.x1 NCI_CGAP_Pr28 Homo sapiens cDNA clone IMAGE:3303521 3'	CM4-PT0034-180200-506-e01 PT0034 Homo saplens cDNA	CM4-PT0034-180200-506-e01 PT0034 Homo saplens cDNA	Homo sapiens pitultary tumor fransforming gene protein (PTTG) gene, complete cds	af39g11.s1 Soeres_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:1034084 3' similar to contains OFR.t2 OFR repetitive element ;	QV0-BN0148-070700-293-e10 BN0148 Homo sapiens cDNA	Homo sapiens SNCA isoform (SNCA) gene, complete cds, atternatively spliced	Homo sapiens CCR8 chemokine receptor (CMKBR8) gene, complete cds	MITOGEN ACTIVATED PROTEIN KINASE KINASE KINASE 10 (MIXED LINEAGE KINASE 2) (PROTEIN KINASE MST)	Homo sapiens CCR8 chemokhe receptor (CMKBR8) gene, complete cds	QV2-PT0012-040400-124-e05 PT0012 Homo sapiens cDNA	CM1-NN1903-200300-153-601 NN1003 Hamo sapiens cDNA	tg22c11.x1 NG_CGAP_CLL1 Homo saplens cDNA clone IMAGE;2109524 3' similar to contains MER28.t2 MER28 repetitive element ;
Top Hit Database Source	r_HUMAN	. LN	T_HUMAN	NT	EST_HUMAN		I) IN	EST HUMAN	Т	П	EST HUMAN		Τ	1		L HUMAN	LN	EST HUMAN		Г	F	SWISSPROT	Γ	EST HUMAN	EST_HUMAN	EST_HUMAN
Top Hit Acesskan No.	3.0E-16 BF690617.1	3.0E-16 L78810.1	3.0E-16 AL043268.2	20E-16 AL163279.2	2.0E-16 AA621761.1	2.0E-16 J03061.1	2.0E-16 X89211.1	0F-16 AI208733.1	2.0E-16 BE061178.1	2.0E-16 Q31125	.0E-16 AI470723.1	2.0E-16.A1732837.1	2.0E-16 BE858026.1	2.0E-16 BE858026.1	2.0E-16 AW877214.1	2.0E-16 AW877214.1	.0E-16 AF200719.1	.0E-16 AA628592.1	I.0E-16 BF327942.1	1.0E-18 AF163864.1	.0E-16 U45983.1	.0E-16 002779	1.0E-16 U45983.1	1.0E-16 AW875651.1	.0E-17 AW900048.1	9.0E-17 Al392964.1
Most Similar (Top) Hit BLAST E Value	3.0E-18	3.0E-16	3.0E-16	20E-16	2.0E-16	2.0E-16	2.0E-16	2.0F-16	2.0E-16	2.0E-16	2.0E-16	2.0E-16	2.0E-16	2.0E-16	2.0E-16	``		1.0E-16	1.0E-16	1.0E-18	1.0E-16	1.0E-16	1.0E-16	1.0E-16	9.0E-17	
Expression Signal	1.09	2.59	3.62	1.03	96.0	1.14	1.62	1 27	0.64	0.68	86.0	1.67	0.81	0.81	0.76	0.78	2.28	22.93	3.42	0.6	18	2.96	5,39	0.81	2.08	2.15
ORF SEQ ID NO:			31557				30424	30718	1	33442		ļ			L		26438			32335		33252		36103		
Exon SEQ ID NO:	23132	23359			15586	15870	17437	l	ı	1	i	_	1		l	l	L	13630		1	19727	19862	1	L.	١.	20016
Probe SEQ ID NO:	10094	10324	13187	98	2469	2753	4294	4603	5299	6880	7893	8154	8352	8352	8724	8724	180	383	2028	5839	6565	8704	77.26	9483	3832	6864

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		_		_		,					_	-	_			_		_			_			_				<del>-</del>			
Top Hit Descriptor	xg49g12.x1 NCI_CGAP_Ut1 Homo sapiens cDNA clone IMAGE:2630950 3' similar to contains OFR.t2 OFR repetitive element;	Homo capiens pituitary tumor transforming gene protein (PTTG) gene, complete cds	QV0-OT0032-080300-155-d01 OT0032 Homo sepiens cDNA	Homo saplens chromosome 21 segment HS21C080	MR0-HT0559-060300-003-e04 HT0559 Homo saplens cDNA	AV730759 HTF Homo sepiens cDNA clone HTFAQB07 5'	Mus musculus apolipoprotein B editing complex 2 (Apobec2), mRNA	Homo sapiens putative MTAP (MTAP) mRNA, partial cds, alternatively spliced	Mus musculus WNT-2 gene, partial cds; putative ankyrin-related protein and cystic fibrosis transmembrane	conductance regulator (CFTR) genes, section 1 of 2 of the complete cds; and unknown gene	RC1-HN0003-220300-021-b04 HN0003 Homo saplens cDNA	h81d04.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2978695 3' similar to contains L1.t2	L1 repetitive element ;	MYELOID CELL SURFACE ANTIGEN CD33 PRECURSOR (GP67)	yc05h08.r1 Stratagene lung (#937210) Homo saplens cDNA clone IMAGE:79839 5'	yd26b04.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:109327 5'	x20e04.x1 NC_CGAP_Kid8 Homo sapiens cDNA clone IMAGE:2818622 3' similar to contains Alu repetitive	Homo capiens chromosome 21 segment HS21Ch47	ov45e04 x1 Soares testis NHT Homo saplens cDNA clone IMAGE:1640286 3' similar to TR:Q16530	Q16530 PMS3 MRNA ;contains MER10.t2 MER10 repetitive element;	xd89c09.x1 Soares_NFL_T_GBC_S1 Homo saplens cDNA done IMAGE:26047843'	MAS-RELATED G PROTEIN-COUPLED RECEPTOR MRG	hw05b04.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3181999 3'	PMO6b04.xf NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3181999 3'	za14b02.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:292491 3' similar to contains	PTR5.t3 PTR5 repetitive element ;	Homo sopiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes,	complete cas)	QV3-BN0047-270700-283-a12 BN0047 Homo saplens cDNA	QV3-BN0047-270700-283-a12 BN0047 Homo sepiens cDNA	Homo sapiens SEC14 (S. cerevisiae)-Ilike 2 (SEC14L2), mRNA
Top Hit Database Source	EST_HUMAN	LN	EST HUMAN	L	EST_HUMAN	EST_HUMAN	L	IN		LZ	EST_HUMAN		EST_HUMAN	SWISSPROT	EST_HUMAN	EST_HUMAN	POT UIMANI	NICKOLIN TO INC.		EST_HUMAN	EST_HUMAN	SWISSPROT	EST_HUMAN	EST_HUMAN		EST_HUMAN	ŀ	L	EST_HUMAN	EST_HUMAN	۲ <u>۷</u>
Top Hit Acessian No.	9.0E-17 AW150257.1	9.0E-17 AF200719.1	_	8.0E-17 AL163280.2		8.0E-17 AV730759.1	6753097	7.0E-17 AF216650.1		7.0E-17 AF229843.1	6.0E-17 AW983880.1		6.0E-17 AW662772.1	20138	T64110.1	T81043.1	4 05 47 0044 20465 4	4.0E-17 At 183247.0	11. 11. 11. 11.	4.0E-17 AI073546.1	3.0E-17 AW119123.1	P35410	3.0E-17 BE326522.1	3.0E-17 BE326522.1		3.0E-17 N68451.1	, 000000	3.0E-17 AB026898.1	3.0E-17 BF327012.1	3.0E-17 BF327012.1	11417968 NT
Most Similar (Top) Hit BLAST E Value	9.0E-17	9.0E-17	8.0E-17	8.0E-17	8.0E-17	8.0E-17	7.0E-17	7.0E-17		7.0E-17	6.0E-17		6.0E-17	6.0E-17 P20138	5.0E-17 T64110.1	5.0E-17 T81043.1	27 30 7	1.01		4.0E-17	3.0E-17	3.0E-17 P35410	3.0E-17	3.0E-17		3.0E-17	27 20 0	3.0E-17	3.0E-17	3.0E-17	3.0E-17
Expression Signal	3.56	2.35	2.43	0.78	4.09	1.73	2.58	3.11		7.91	5.62		2.06	0.54	2.37	1.81	00.7	1.32	2	1.82	1.85	1.17	1.91	1.91		1.12		5.19	0.72	0.72	4.2
ORF SEQ ID NO:					32187					33387	26463			37144	28234		OZUGC	١			28426		29897			35074		1		37235	
Exon SEQ ID NO:	21381	23464	14209	17156	25809		14640			19979	13431			23534	13234	20818	70704	ı	2	25226	15300		16893	16893		21544			23626		25201
Probe SEQ ID NO:	828	10429	1043	3998	5701	7425	1487	5438		6826	802		6443	10499	434	7759	Can	11782		12308	2165	3263	3732	3732		8463		9903	10591	10591	12268

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1					Sign Co	ביים ווספים	
Probe SEQ ID NO:	Exan SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
13155	25751		1.23	3.0E-17	3.0E-17 AV720204.1	EST_HUMAN	AV720204 GLC Homo sapiens cDNA clone GLCDIF08 5
							qt63a06.x1 NCI_CGAP_Eso2 Homo sapiens cDNA clone IMAGE:1959922.3' similar to contains Alu
363	13574	26605	2.65	2.0E-17	2.0E-17 AI270080.1	EST_HUMAN	repetitive element;
							qt63a06.x1 NCI_CGAP_Eso2 Homo sapiens cDNA clone IMAGE:1959922 3' similar to contains Alu
364	13574	26605	2.78	2.0E-17	2.0E-17 AI270080.1		repetitive element,
1012	14184		1.43	2.0E-17	2.0E-17 AA722932.1	EST_HUMAN	zg81d04.s1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:399751 3'
2518	15644	28765			2.0E-17 Q28983	SWISSPROT	ZONADHESIN PRECURSOR
2518			2.59		2.0E-17 Q28983	SWISSPROT	ZONADHESIN PRECURSOR
. 8000	46470		90 8		205 47 042036	FOGGGGW	NEUROFILAMENT TRIPLET H PROTEIN (200 KDA NEUROFILAMENT PROTEIN) (NEUROFILAMENT HEANY BOI YBEDTIDE) (NE.H)
0880	ı				12030	DAI PER	Mine and the self of the self of the self of the self of the self of the self of the self of the self of the self of the self of the self of the self of the self of the self of the self of the self of the self of the self of the self of the self of the self of the self of the self of the self of the self of the self of the self of the self of the self of the self of the self of the self of the self of the self of the self of the self of the self of the self of the self of the self of the self of the self of the self of the self of the self of the self of the self of the self of the self of the self of the self of the self of the self of the self of the self of the self of the self of the self of the self of the self of the self of the self of the self of the self of the self of the self of the self of the self of the self of the self of the self of the self of the self of the self of the self of the self of the self of the self of the self of the self of the self of the self of the self of the self of the self of the self of the self of the self of the self of the self of the self of the self of the self of the self of the self of the self of the self of the self of the self of the self of the self of the self of the self of the self of the self of the self of the self of the self of the self of the self of the self of the self of the self of the self of the self of the self of the self of the self of the self of the self of the self of the self of the self of the self of the self of the self of the self of the self of the self of the self of the self of the self of the self of the self of the self of the self of the self of the self of the self of the self of the self of the self of the self of the self of the self of the self of the self of the self of the self of the self of the self of the self of the self of the self of the self of the self of the self of the self of the self of the self of the self of the self of the self of the self of the self of the self of the self of the self of the self of the self
5482	- 1				2.0E-17 M2/685.1		Mus musculus uira nign suiru keraun gene, complete cos
5482	18681	31697	1.75		2.0E-17 M27685.1		Mus musculus ultra high culfur keratin gene, complete cots
6394	19563		1.92	2.0E-17	2.0E-17 AF055066.1	LN	Homo sapiens MHC class 1 region
6619	ı		1.39		2.0E-17 AL134881.1	EST_HUMAN	DKFZp762J0610_r1 762 (synonym: hmel2) Homo sepiens cDNA done DKFZp762J0610 5'
8008	•	34568	68.0		2.0E-17 AB037839.1		Homo sapiens mRNA for KIAA1418 protein, partial cds
8275		34875			2.0E-17 Q95156	SWISSPROT	OLFACTORY RECEPTOR-LIKE PROTEIN OLF3
8651	ı		1.05		2.0E-17 AA300640.1	EST_HUMAN	EST13504 Testis tumor Homo sapiens cDNA 5 end similar to similar to glycogenin
10073	23111	36715			2.0E-17 BE299888.1	EST_HUMAN	600944690F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:2960615 5'
10108	İ	38744		2.0E-17	2.0E-17 AL163247.2	LN.	Homo sapiens chromosome 21 segment HS210047
10108	L	36745	3.53	2.0E-17	2.0E-17 AL163247.2	LN	Homo sapiens chromosome 21 segment HS21C047
							Human CYP19 gene for aromatase cytochrome P-450, promoter region (containing two cis-acting
10466	23501	37114	5.02		2.0E-17 D13391.1		transcriptional regulatory elements)
10590		37232		2.0E-17	2.0E-17 P98063	SWISSPROT	BONE MORPHOGENETIC PROTEIN 1 PRECURSOR (BMP-1)
10590	23625				2.0E-17 P98063	SWISSPROT	BONE MORPHOGENETIC PROTEIN 1 PRECURSOR (BMP-1)
10618				l	2.0E-17 AI798902.1	EST_HUMAN	we94b04.x1 Sogres_NFL_T_GBC_S1 Hamo saplens cDNA clone IMAGE:23487193'
10618	23652				2.0E-17 AI798902.1	_	we94b04.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2348719 3'
769	$\mathbf{I}_{-}$	<u> </u>			1.0E-17 P08183	SWISSPROT	MULTIDRUG RESISTANCE PROTEIN 1 (P-GLYCOPROTEIN 1)
1745	14894		2.01	1.0E-17	.1.0E-17 AJZ71736.1	IN	Homo sapiens Xq pseudoautosomal region; segment 2/2
1807	14956	28050	4.83		1.0E-17 AL163207.2	INT	Homo sapiens chromosome 21 segment HS21C007
2184	15319	28445			1.0E-17 P02461	SWISSPROT	COLLAGEN ALPHA 1(III) CHAIN PRECURSOR
2412	15542				1.0E-17 U79410.1	LN LN	Homo saplens thrombospondin 2 (THBS2) gene, promoter region and exons 1A and 1B
							Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3
3657	_		1.03		1.0E-17 AF224669.1	. 7	(UBE2D3) genes, complete cds
4256	17401		9.42		1.0E-17 R09942.1	EST_HUMAN	y/30e07.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:128388 5'

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	Top) Hit Acession Database Top Hit Acession No. Source	1.0E-17 A185642.1 EST_HUMAN   qe65b05.x1 Soares_fetal_lung_NbHL19W Homo sapiens cDNA clone IMAGE:1743825.3	1.0E-17 A185642.1 EST_HUMAN   qe65b05.x1 Soares fetal lung_NbHL19W Homo sapiens cDNA clone IMAGE:1743825.3'	1.0E-17 Q16831 SWISSPROT   URIDINE PHOSPHORYLASE (UDRPASE)	1.0E-17 BE062744.1 EST_HUMAN QV0-BT0263-101299-072-d07 BT0263 Homo saplens cDNA	1.0E-17 AW998538.1   EST_HUMAN   QV3-BN0046-220300-129-c10 BN0046 Homo saplens cDNA	1.0E-17 Q28824 SWISSPROT MYOSIN LIGHT CHAIN KINASE, SMOOTH MUSCLE (ALCK) CONTAINS: TELOKIN]	9.0E-18 A1472167.1 EST_HUMAN   tj85403.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2148389 3"		7.0E-18 AW316976.1 EST_HUMAN RIBOSOMAL PROTEIN L4 (HUMAN);	2 OF THIRD PERCENT NOT COAP Part Home saplens cDNA clone IMAGE:2837071 3' similar to gb:1.20868 60S	EST HIMAN	Alvivid L	7.0E-18 AW316976.1 EST_HUMAN RIBOSOMAL PROTEIN L4 (HUMAN);	2 DE 18 AW316078 1 FEST HIMMAN RIPOSONAL PROTEIN LA PHIMMAN.	L	6.0E-18 P52181 SWISSPROT (TGASE C) (TGC)		28155 NT	LN.	EST_HUMAN	EST_HUMAN	6.0E-18/AL163246.2 NT Homo sapiens chromosome 21 segment HS21C046		6.0E-18   U8T929.1 NT Human accinitate hydratase (ACO2) gene, exon 4	fqm65g11.x1 Soares_placenta_8to9weeke_2NbHP8to9W Homo capiens cDNA clone IMAGE:1893668 3' 5.0E-18 Al280214.1 EST HUMAN jamilar to contains Alu repolitive element;	46665	5.0E-18 AF087913.1 NT Human endogenous retrovirus HERV-P-T47D	5.0E-18 BE143312.1 EST_HUMAN MR0-HT0161-221099-002-006 HT0161 Homo septens cDNA
-									4758977 NT			T				Γ		!	11428155INT								46665		
	Most Similar (Top) Hit BLAST E Value	1.0E-17 AI1	1.0E-17 AI1	1.0E-17 Q1	1.0E-17 BE	1.0E-17 AV	1.0E-17 Q2	9.0E-18 AI	8.0E-18	7.0E-18 AW	7 01 40	7 0E-18 AV	101.1	7.0E-18 AW	7 0F-18 AW	6.0E-18 X7	6.0E-18 P5		6.0E-18	6.0E-18 AL	6.0E-18 AIS	6.0E-18 AB	6.0E-18 AL	6.0E-18 X8	6.0E-18 U8	5.0E-18 AI2	5.0E-18	5.0E-18 AF	5.0E-18 BE
	Expression Signal	1.62	1.62	1.33	1.26	1.04	1.52	3.05	2.14	16.47	16.47	100	+	10.65	10.65	1.23	3.99		3.47	0.78	0.48	0.48	3.63	1.69	3.91	12.48	0.59	1.29	3.47
	ORF SEQ ID NO:					36836	හසෙ		30044	26599	OUSSC	l	1	26599	00996								38124		32068	27390			
	Exon SEQ ID NO:	19946	19946			23246	24700	22747	17045	13570	43670	L	•	13570	13570	1	18001		21525		22367	Ц	24460		25364	14334	17573		21996
	Probe SEQ ID NO:	6791	6791	7238	8792	10210	11703	9698	3886	359	350	7801		12826	12826	3367	4868	,,,,	8444	25	9291	9291	11399	11612	12534	1171	4433	5387	8917

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Top Hit Descriptor	Homo sapiens lymphocyte activation-associated protein (LOC51088), mRNA	Homo sapiens lymphocyte activation-associated protein (LOC51088), mRNA	MR1-SN0035-080400-001-g11 SN0035 Homo sapiens cDNA	AV650547 GLC Homo sapiens cDNA clone GLCCGA02 3'	ho36h04.x1 NCI_CGAP_Ut1 Homo sapiens cDNA clone IMAGE:3039511.3' similar to contains MER29.b3 MER29 repetitive element :	ho36h04.x1 NCI_CGAP_Ut1 Homo sapiens cDNA clone IMAGE:3039511 3' similar to contains MER29 b3	MER29 repetitive element;	nq2411.s1 NCI_CGAP_Co10 Home sapiens cDNA clone IMAGE:1144845 3' similar to gb:M26326 KERATIN, TYPE I CYTOSKELETAL 18 (HUMAN);	wi33h08.x1 NCI_CGAP_Co16 Homo sapiens cDNA done IMAGE:2392095 3'	N-ACETYLLACTOSAMINIDE BETA-1, 8-N-ACETYLGLUCOSAMINYLTRANSFERASE (N- ACETYLG LICOSAMINY TRANSFERASE) (LIBRANCHING ENZYME) (1GNT)		N-ACETYLACTOSAMINIDE BETA-1,6-N-ACETYLGLUCOSAMINYLTRANSFERASE (N- ACETYLGLUCOSAMINYLTRANSFERASE) (I-BRANCHING ENZYME) (IGNT)	ar93b06.x1 Barstead colon HPLRB7 Homo sapiens cDNA done IMAGE:2173139 3' similar to contains Alu	repetitive clement;	ou23e06.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1627138 3'	ou23e06.x1 Soares_NHT_GBC_S1 Homo sapiens cDNA clone IMAGE:1627138 3'	rx64a08.s1 NCI_CGAP_Alv1 Homo saplens cDNA clone IMAGE:1266998 similar to contains L1.t2 L1	repetitive element;	EST83633 Pitultary gland, subtracted (protactin/growth hormone) II Homo sapiens cDNA 5' end similar to	EST containing O family repeat	cb23h11.s1 NCI_CGAP_Kid5 Homo sapiens cDNA clone IMAGE:1324581 3' similar to SW:RS5_HUMAN	P46782 40S RIBOSOMAL PROTEIN S6.;	CM0-BT0690-210300-298-g07 BT0690 Homo saplens cDNA	Homo saplens chromosome 21 segment HS21C047	PM0-BN0081-100300-001-b08 BN0081 Horno saptens cDNA	601B84856F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4103652 5'	df31h12.y1 Morton Fetal Cochlea Homo saplens cDNA clone IMAGE:2485126 5	QV1-LT0036-150200-070-e07 LT0036 Homo sepiens cDNA	601114352F1 NIH_MGC_16 Homo sepiens cDNA clone IMAGE:3355044 5'	DYNEIN GAMMA CHAIN, FLAGELLAR OUTER ARM
Top Hit Database Source			EST_HUMAN	EST_HUMAN /	EST HUMAN	Т	EST_HUMAN (	EST HUMAN	EST HUMAN	TOGGSSIMS	1	SWISSPROT			EST_HUMAN	EST_HUMAN	Г	EST_HUMAN		EST_HUMAN	Г	EST HUMAN	EST_HUMAN	Г	EST_HUMAN	EST_HUMAN			П	SWISSPROT
Top Hit Acession No.	10242378 NT	10242378 NT	5.0E-18 AW867182.1	5.0E-18 AV650547.1	4 0E-18 BE044076 1		4.0E-18 BE044076.1	4.0E-18 AA621814.1	4.0E-18 AI738592.1	008400	200430	Q06430		4.0E-18 AI581586.1	4.0E-18 A1017565.1	4.0E-18 AI017565.1	j	4.0E-18 AA746811.1		4.0E-18 AA371807.1		3.0E-18 AA814196.1	3.0E-18 BE088634.1	3.0E-18 AL163247.2	3.0E-18 BE001671.1	3.0E-18 BF218650.1	3.0E-18 AW022015.1	2.0E-18 AW 836820.1	2.0E-18 BE256097.1	Q39575
Most Similar (Top) Hit BLAST E Value	5.0E-18	5.0E-18	5.0E-18	5.0E-18	4 05-18		4.0E-18	4.0E-18	4.0E-18	100000	4.0E-18	4.0E-18 Q06430		4.0E-18	4.0E-18	4.0E-18		4.0E-18		4.0E-18		3.0E-18	3.05-18	3.0E-18	3.0E-18	3.05-18	3.0E-18	2.0E-18	2.0E-18	2.0E-18 Q39575
Expression Signal	3.43	3.43	6.29	28.95	0.91		0.91	52.62	1.05	2	07.L	1.26		0.61	2.47	2.47		0.62		7.59		3.81	2.25	1.06	4.72	1.99	4.56	4.2	74.12	0.94
ORF SEQ ID NO:	37932	37833			26386	1	26387	27998		90500	00007	28537		30050	31691	31692				37964		27114		30225				26512		29374
SEQ ID NO:	24292	l _	25450	<u> </u>	13355	L	13355	14903	15081		15407	15407	l	17051	18678	18678	l	21112		24323		14048	14126	ı	1_	24238		13480	IJ	Ll
Probe SEQ ID NO:	11223	11223	12675	13063	127	1	127	1754	1938	700	22/4	2274		3892	5479	5479		8029		11254	!	872	953	4060	8969	11167	12832	261	1176	3193

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	Top Hit Descriptor	ak53a07.s1 Soares, testis. NHT Homo sepiens cDNA done IMAGE:1409652.3' similar to TR:014577 014577 BAC CLONE RG114A06 FROM 7031, COMPLETE SEQUENCE.	Human DNA, SINE repetitive element	Human DNA, SINE repetitive element	602021164F1 NCI_CGAP_Brn67 Homo saplens cDNA clone IMAGE:4156670 5	Human IFNAR gene for interferon alpha/bela receptor	Human IFNAR gene for interferon alpha/beta receptor	1.3-HT0619-220700-222-C12 HT0619 Homo sapiens cDNA	hi94g01.x1 Soares_NFL_T_GBC_S1 Homo saplens cDNA clone IMAGE:2979984 3' similar to contains MER19.t2 MER19 repetitive element;	aa89d11.r1 Stratagene fetal retina 937202 Homo saplens cDNA clone IMAGE:838486 5' similar to TR:061634 G61634 POLYPEPTIDE PR77 ;	HTM1-160F1 HTM1 Homo saplens cDNA	xf67e10.x1 NCI_CGAP_Gas4 Homo saplens cDNA clone IMAGE:2623146 3' similar to contains MER10.t2	MER10 repetitive element ;	xf67e10.x1 NCI_CGAP_Gas4 Homo sepiens cDNA_clone IMAGE:2623146 3' similar to contains MER10.t2 MER10 reportitive element :	ha33d06.x1 NCI_CGAP_Kld12 Hamo saplens cDNA clone IMAGE:2875499 3' similar to contains THR.b3	THR repetitive element :	xg47e09.x1 NC]_CGAP_Ut1 Homo sapiens cDNA done IMAGE:2630728 3' similar to cantains MER8.b2 MER8 repetitive element ;	601114352F1 NIH_MGC_16 Hamo saplens cDNA clone IMAGE:3355044 5'	ye43g05.r1 Soares fetal liver spieen 1NFLS Homo sapiens cDNA clone IMAGE:120536 5' similar to contains	L1 repetitive element ;	AV653405 GLC Homo sapiens cDNA clone GLCDKE11 3'	Homo sapiens mRNA for Na,K-ATPase alpha-subunit, complete cds	Homo sapiens mRNA for Na.KATPase alphe-subunit, complete cds	Homo saplens chromosome 21 segment HS21C080	αα69d09.xt Soares_senescent_fibroblasts_NbHSF Homo sepiens cDNA clone IMAGE:1680593 3' similar to contains L1.t1 L1 repetitive element ;	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RoRet gene, and sodium phosphate transporter (NPT3) gene, complete cds	Homo sapiens alvoican 3 (GPC3) dene, partial cds and flankha repeat regions
	Top Hit Database Source	EST_HUMAN O		T L	EST_HUMAN 6	IN	H L	EST_HUMAN II	EST HUMAN N	EST HUMAN T	Т		EST_HUMAN N	EST HUMAN	T	EST_HUMAN T	EST HUMAN N	Г	Г	HUMAN	EST_HUMAN A				EST_HUMAN c	) TN	
·	Top Hit Acession No.	2.0E-18 AA868610.1	D14547.1	D14547.1		2.0E-18 X60459.1	X60459.1	BF352940.1	0E-18 AW665853.1	AA457619.1	2.0E-18 BE439524.1		0E-18 AW151673.1	2 0F-18 AW151673.1		.0E-18 AW470791.1	AW151299.1	2.0E-18 BE256097.1		0E-18 T95406.1	.0E-18 AV653405.1	.0E-18 D00099.1	.0E-18 D00099.1	.0E-18 AL163280.2	.0E-18 AI148288.1	.0E-18 U91328.1	.0E-18 AF003529.1
	Most Similar (Top) Hit BLAST E Value	2.0E-18	2.0E-18	2.0E-18	2.0E-18	2.0E-18	2.0E-18	2.0E-18	2.0E-18	2.0E-18	2.0E-18		2.0E-18	2 0F-18		2.0E-18	2.0E-18	2.0E-18		1.0E-18	1.0E-18	1.0E-18	1.0E-18	1.0E-18	1.0E-18	1.0E-18	1.0E-18
	Expression Signal	4.2	3.51	3.51	<u>4</u> .	16.0	0.91	0.0	2.93	0.50	0.5		0.95	960		2.91	4.46	12.67		0.75	2.64	3.08	3.08	1.31	1.05	4.93	4.65
	ORF SEQ ID NO:		31886	31887		32820	32821	32938	32979	34141			36884	36885		37925	38716				31651	32174		33128	35254	36740	L
	Exon SEQ ID NO:	18724	18817	18817	19184	19467	19467	19577	19615	20665	١		23288	23288		24286	25014	14339		17675			18882	19746	21717	23141	1
	Probe SEQ ID NO:	5527	5623	5823	2999	6294	6294	6408	6448	7594	8341		10253	10253		11217	12031	12465		4537	5471	2688	5688	6584	8637	10103	12416

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					_		
Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Detabese Source	Top Hit Descriptor
559	13752	26780	6.1	6	0E-19 AA281961.1	EST_HUMAN	zt11406.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE;712811 5' similar to contains MER19.t2 MER19 repetitive element ;
98			3.91	9.0E-19	9.0E-19 AA281961.1	EST_HUMAN	zt11d06.r1 NCI_CGAP_GCB1 Homo sepiens cDNA clone IMAGE:712811 5' similar to contains MER19.t2 MER19 repetitive element;
8032	_		3.69	9.0E-19	9.0E-19 F08688.1	EST_HUMAN	HSC23F051 normalized infant brain cDNA Homo sapiens cDNA clone c-23f05
8886	1	L		9.0E-19	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
8886	21965	35502		L	AL163203.2	TN	Homo saplens chromosome 21 segment HS21C003
11392	1		3.15		.0E-19 AB032969.1	NT	Homo sapiens mRNA for KIAA1143 protein, partial cds
12171	13762	26780	19.34		AA281961.1	EST_HUMAN	zt11d06.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:712811 5' similar to contains MER19.t2 MER19 repetitive element ;
1073					8.0E-19 AW974902.1	EST_HUMAN	EST387007 MAGE resequences, MAGN Homo sepiens cDNA
8342	21423	34948	1.12	$\Box$		EST_HUMAN	MRO-HT0404-210200-001-g06 HT0404 Homo saplens cDNA
2319	15451	28583	1.74		4758139 NT	NT	Homo saplens DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 6 (RNA helicase, 54kD) (DDX6) mRNA
6585		L	2.11	7.0E-19	0E-19 AF092090.1	NT	Rattus norvegicus cp151 mRNA, partial cds
7452			0.94	_	.0E-19 P26444	SWISSPROT	BETA CRYSTALLIN A2
10216	l		0.54	7	.0E-19 AI344951.1	EST_HUMAN	tb01c08.x1 NCi_CGAP_Lu26 Homo sapiens cDNA clone IMAGE:2052302 3'
12316			1.72		.0E-19 AA705684.1	EST HUMAN	zi60b01.s1 Soares_fetal_liver_spicen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:435145 3'
3879	17038		1.16		6.0E-19 AW852930.1	EST HUMAN	PM0-CT0248-131099-001-g01 CT0248 Homo sapiens cDNA
4585	17722		1.56		P34986	SWISSPROT	OLFACTORY RECEPTOR 6 (M50)
4585	1_	30706	1.56		6.0E-19 P34986	SWISSPROT	OLFACTORY RECEPTOR 6 (M50)
4921	18051		1.2	6.0E-19	6.0E-19 AJ271735.1	NT	Homo sapiens Xq pseudoautocomal region; segment 1/2
5978	19163	32483	5.17	_	5.0E-19 Q00193	SWISSPROT	ZONA PELLUCIDA SPERM-BINDING PROTEIN B PRECURSOR (ZONA PELLUCIDA GLYCOPROTEIN   IZP-X) (RC55)
6346	1.				5.0E-19 AW663302.1	EST_HUMAN	hh77b06.y1 NCI_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2968787 5'
10639	1		1.18		5.0E-19 AJ297699.1	TN	Homo sapiens partial IL-12RB1 gene for IL-12 receptor beta1 chaln, exon 14
11829	•				5.0E-19 AW183725.1	EST_HUMAN	x/87602.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2664171 3' similar to contains element MSR1 repetitive element;
	ı						Human germline T-cell receptor beta chain TCRBV13S1, TCRBV6S8A2T, TCRBV5S6A3N2T,
							TCRBV1356A2T, TCRBV6S9P, TCRBV5S3A2T, TCRBV13S8P, TCRBV6S3A1N1T, TCRBV5S2,
						ŀ	TCRBV6S6A2T, TCRBV6S7P, TCRBV13S4, TCRBV6S2A1N1T, TCRBV5S4A2T, TCRBV6S4A1,
13083					5.0E-19 ∪66060.1	ž	I CKBVZSSIAZI, I CKBVIZY
568		i			4.0E-19 AB007970.1	Ę	Homo sapiens mKNA, chromosome 1 specific ranscript NAAUSU1
2747			1.15		4.0E-19 BF697362.1	EST_HUMAN	602130910F1 NIH_MGC_56 Homo saptens cDNA clone IMAGE:4287674 5

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		İ					
Probe SEQ ID NO:	SEQ ID	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Vælue	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
5512	18710	31725	1.2		4.0E-19 AF224669.1	. LN	Homo sepiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D3) genes, complete cds
3925	l	30114	1.02	3.0E-19 Q28997		SWISSPROT	BETA-2 ADRENERGIC RECEPTOR
3955	17113		1.02			SWISSPROT	BETA-2 ADRENERGIC RECEPTOR
4400	17543	30526	0.85			SWISSPROT	LIM-ONLY PROTEIN 8 (TRIPLE LIM DOMAIN PROTEIN 8)
4400	17543		0.85	3.0E-19		SWISSPROT	LIM-ONLY PROTEIN 6 (TRIPLE LIM DOMAIN PROTEIN 8)
4569	17707	98908	1.42			EST HUMAN	AV708136 ADC Homo sapiens cDNA clone ADCAMA11 5
5394	18596		0.69			NT	Homo sapiens NPD008 protein (NPD008) mRNA, complete cds
	l				)  -	ļ	Homo saplens similar to aldo-keto reductase family 1, member B11 (aldose reductase-like) (H. sapiens)
7543	1.	}	1.88		1432214	Z	(LOCSSZZZ), MHANA
9658		34614	1.00			NT	M.musculus mRNA for IPCR33 protein
12563	25385		16.36		3.0E-19 AF165520.1	TN	Homo sapiens phorbolin I protein (PBI) mRNA, complete cds
2627	<u></u>	28865	20.06			N <sub>T</sub>	Homo sapiens chromosome 21 segment HS21C001
							qp91e02.x1 NCI_CGAP_Kid5 Homo sapiens cDNA clone IMAGE:1915898 3' similar to TR:Q69386 Q69386
4568	17706		1.34			EST_HUMAN	POL/ENV GENE;
6179	19355	32703	0.81	2.0E-19	2.0E-19 AV731382.1	EST_HUMAN	AV731382 HTF Homo sapiens cDNA clone HTFAZC06 5'
7493	20568	34040	0.63		7657286 NT	NT	Mus musculus keratin-associated protein 9-1 (Krtap9-1), mRNA
8525	21606		10.24		2.0E-19 AA012854.1	EST_HUMAN	ze34c09,r1 Soares retina N2b4HR Homo saptens cDNA clone IMAGE:360880 5
10113	23151	L	0.64		2.0E-19 Q95155	SWISSPROT	OLFACTORY RECEPTOR-LIKE PROTEIN OLF2
<u>4</u>	L		1.86		1.0E-19 BE408611.1	EST_HUMAN	601304125F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3638310 5'
							yo79g07,r1 Scares adult brain NZb4HB55Y Homo sapiens cDNA clone IMAGE:184188 5' similar to contains
2233 2333	- (	28496	1.54	ļ	1.0E-19 H30/95.1	ES L HUMAN	MEKTO TERMINATE EMITTER (
2782	╛		2.4		038044.1	Z	Human gene for An-recupior, exon 7-9
2909	16087		6.72	1.0E-19	4758977 NT	LN	Homo sapiens protein tyrosine phosphatase, non-receptor type substrate 1 (P i PNS1) mKNA
							gj49b12.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1383631 3' similar to contains MER37.t2
3488	16655	29869	1.18		1.0E-19 AA834967.1	ESI HUMAN	MEK3 / repeutive element;
							wm91b08.x1 NCI_CGAP_Ut2 Homo sapiens cDNA clone IMAGE:2443287 3' similar to TR:Q16530 Q16530
5452	18652	31631	0.73		۱.	EST_HUMAN	PMS3 MRNA:
6199	19374	L	2.6		1.0E-19 U12186.1	NT	Oryciolagus cuniculus sodium/dicarboxylate cotransporter mRNA, partial cds
							nh22d03.s1 NCI_CGAP_Pr1 Home appiens cDNA clone IMAGE:853093 cimilar to contains L1.t1 L1
6337	26213		.0.63		1.0E-19 AA595527.1	EST_HUMAN	repetitive element;
7806	20862	34355	1.05	L	1.0E-19 U08813.1	ΙN	Oryctolagus cuniculus Na+/glucose cotransporter-related protein mRNA, complete cds
7806	1				1.0E-19 U08813.1	TN	Oryciolagus cuniculus Na+/glucose cotransporter-related protein mRNA, complete cds
7977	25856		0.75		1.0E-19 AF200719.1	TN	Homo saplens pituitary tumor fransforming gene protein (PTTG) gene, complete cds
	1			l			

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	contains														1	Í				은	뒫	1							
Top Hit Descriptor Rabbit phosphorylase kinase beta subunit mRNA, complete cds	ye72b02.rl Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:123243 5' similar to contains OFR repetitive element;	Human dystrophin (DMD) gene, exons 7, 8 and 9, and partial cds	RC0-ST0174-191099-031-b05 ST0174 Homo sapiens cDNA	yy31e09.r1 Soares melanocyte 2NbHM Homo saplens cDNA clone IMAGE:2728725'	601279682F1 NIH MGC 39 Homo sapiens cDNA clone IMAGE:3611493 5	Mus musculus keratin-associated protein 9-1 (Krtap9-1), mRNA	Mus musculus keratin-associated protein 9-1 (Krtap9-1), mRNA	ag86f09.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:18420893'	qg88f09.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1842089 3'	PM4-AN0096-050900-003-a04 AN0096 Homo sapiens cDNA	DKFZp547D092_r1 547 (synonym: hfbr1) Homo sapiens cDNA clone DKFZp547D092 5'	nI46c04.s1 NCI_CGAP_Pr4 Homo sapiens cDNA clone IMAGE:1043718 similar to contains MER29.b2 MER29 repetitive element ;	n146604.51 NCI_CGAP_Pr4 Hamo sapiens cDNA clone IMAGE:1043718 similar to contains MER29.b2	WEK 28 repetitive element;	Homo sapiens ribosomal protein L13a (RPL13A), mRNA	ALU SUBFAMILY J SEQUENCE CONTAMINATION WARNING ENTRY	601441231F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3916231 51	AV725123 HTC Homo saplens cDNA clone HTCBTA01 5'	AF075301 Human fetal liver cDNA library Homo sapiens cDNA clone HA0250	zh78d08.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE.418191 3' similar to contains MER30.t1 MER30 repetitive element ;	Zh78d08.st Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMACE:418191 3' similar to	MR3.HTn487-150200-113-n01 HTn487 Home samiens cDNA	Mus musculus MMAN-g mRNA, complete cds	Mus musculus MMAN-g mRNA, complete cds	HYPOTHETICAL PROTEIN DJ845024.1	Homo sapiens chromosome 21 segment HS21C047	HISTONE H2B C (H2B/C)	tz64g03.x1 NOL_CGAP_Ov35 Homo sapiens cDNA clone IMAGE:2293396 3'	QV3-DT0043-090200-080-c04 DT0043 Homo sapiens cDNA
Top Hit Database Source	EST_HUMAN	۲	EST_HUMAN	EST_HUMAN	EST HUMAN	ĽN	- 1:	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST HUMAN		ESI HUMAN	FN.	SWISSPROT	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	HODE	EST HIMAN	LN	TN	SWISSPROT	TN	SWISSPROT	EST_HUMAN	EST HUMAN
t Similar AST E Road false 1.0E-19 M64657.1	199920.1	U60822.1	1.0E-19 AW812259.1	1.0E-19 N44631.1	1.0E-19 BE616026.1	7657286 NT	7657286 NT	8.0E-20 AI221371.1	8.0E-20 AI221371.1	7.0E-20 BF326455.1	7.0E-20 AL138120.1	7.0E-20 AA557657.1		7.0E-20 AA55/657.1	6912633 NT	P39188	6.0E-20 BE622434.1	5.0E-20 AV725123.1	5.0E-20 AF075301.1	5.0E-20 W90525.1	E OF ON MONEOE 4	5.0E-20 We0323.1	5.0E-20 AB028174.1	5.0E-20 AB028174.1	608090	4.0E-20 AL163247.2	299880	4.0E-20 AI874352.1	4W937469.1
Most Similar (Top) Hit BLAST E Value 1.0E-19	1.0E-19 T99920.1	1.0E-19 U60822.1	1.0E-19	1.0E-19	1.0E-19	8.0E-20	8.0E-20	8.0E-20	8.0E-20	7.0E-20	7.0E-20	7.0E-20		7.0E-20	7.0E-20	6.0E-20 P39188	6.0E-20	5.0E-20	5.0E-20	5.0E-20	100	5.0E-20	5.0E-20	5.0E-20	5.0E-20 O60809	4.0E-20	4.0E-20 Q99880	4.0E-20	4.0E-20
Expression Signal	2.72	69.0	25.12	1.59	1.87	2.4	2.4	1.46	1.46	0.71	5.66	8.83	1	8.83	2.89	3.64	4.58	1.8	1.42	6.96	90	07.0	2 2	-	1.13	46.0	1.13	5.61	1.13
ORF SEQ ID NO: 35261				37042		33336					31474	35305	$\rfloor$	32308		29822	30511		33799	34733	707704	34808	35657			27889			37357
Exan SEQ ID NO: 21724	22018	22989		23435	- 1	- 1	- 1	20752	20752	16521	18580	21773		21773	24998	16808	17530	17853	20347	21213	24.24.0	21277	22114	22114	21087	14802	18957	21192	23750
Probe SEQ ID NO: 8644	8939	0566	10390	10400	11184	6784	6784	7687	7687	3349	7134	8693		883	12014	3645	4387	4718	7264	8131	5	200	9035	9035	9844	1649	5765	8110	10717

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	_	_			_,	_,						_		_	_,		<del></del> ;						_			··· 3		*1152 *184
Top Hit Descriptor	Human BXP21 gene	OLFACTORY RECEPTOR-LIKE PROTEIN 114	Zk36b12.s1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:484895 3' similar to	contains L1.0 L1 lebeuuve denian.	Human DNA, SINE repetitive element	601843561F1 NIH_MGC_54 Hamo sapiens cDNA clone IMAGE:4064343 51	RETROVIRUS-RELATED POL POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE ; ENDONUCLEASE]	601514180F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3915522 5'	x/24e10.x1 NCI_CGAP_U4 Homo sapiens cDNA clone IMAGE:2761098 3' similar to SW:RS5_MOUSE P97461 40S RIBOSOMAL PROTEIN S5. ;	ng69H09.sf NCI_CGAP_Lip2 Homo saplens cDNA done IMAGE:040097 similar to TR:G1224066 G1224066 ORF2: FUNCTION UNKNOWN.;	nge9fr09.s1 NCI_CGAP_Lip2 Homo saplens cDNA clone IMAGE:940097 similar to TR:G1224066	SIZZENOV CN. Z. FONOTION CHANGES.	x/24e10.x1 NCI_CGAP_U/4 Homo sapiens cDNA clone IMAGE:2781096 3' similar to SW:RS5_MOUSE P97461 40S RIBOSOMAL PROTEIN S5. ;	ZONADHESIN PRECURSOR	ZONADHESIN PRECURSOR	Homo sapiens malate dehydrogenase 1, NAD (soluble) (MDH1) mRNA	EST180326 Liver III Homo sepiens cDNA 5' end	Homo sapiens RGH1 gene, retrovirus-like element	Homo sapiens RGH1 gene, retrovírus-like element	CHR220310 Chromosome 22 exon Homo sapiens cDNA clone C22_391 5'	Z111d06.r1 NCI_CGAP_GCB1 Homo saplens cDNA clone IMAGE:712811 5' similar to contains MER19.t2	MER19 repetitive element;	hr84b06.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3135155 3' similar to contains L1.t2 L1	repetitive element;	AF049567 Human activated dendritic cell mRNA Homo sapiens cDNA clone GA05	Homo sapiens Autosomal Highly Conserved Protein (AHCP), mRNA	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced	nc60g08.r1 NCI_CGAP_Pr1 Homo saplens cDNA clone IMAGE:745694 similar to contains L1.t3 L1 repetitive element;
Top Hit Detabase Source	Ę	SWISSPROT	100	ESI HUMAN	NT	EST_HUMAN	SWISSPROT	EST HUMAN	EST_HUMAN	EST_HUMAN	MAN HOD	ES L'HOMAN	EST_HUMAN	SWISSPROT	SWISSPROT	NT	EST_HUMAN	FN	NT	EST_HUMAN		EST_HUMAN		EST_HUMAN	EST HUMAN	LN	LN	EST_HUMAN
Top Hit Acession No.						3.0E-20 BF185264.1	911369	22.1	1	0E-20 AA516335.1	A 546005 4	Z.UE-ZU AAS 16353.1	2.0E-20 AW303868.1	l		2.0E-20 5174538 NT	4A309467.1	J10083.1	J10083.1	155371.1		.0E-20 AA281961.1	•	.0E-20 BF115158.1	.0E-20 AF049567.1	11418491 NT	.0E-20 AF223391.1	.0E-20 AA420453.1
Most Similar (Top) Hit BLAST E Value	3.0E-20 (	3.0E-20 P23273		3.0E-20	3.0E-20	3.0E-20	3 0E-20 P11369	3.0E-20	2.0E-20	2.0E-20	5	Z.0E-20/	2.0E-20	2.0E-20	2.0E-20	2.0E-20	2.0E-20	2.0E-20	2.0E-20	2.0E-20		1.0E-20		1.0E-20	1.0E-20	1.0E-20	1.0E-20	1.0E-20
Expression Signal	1.22	1.29		1.08	269	0.47	1.59	609	5.65	2.49		7.48	5.32	5,15	5.15	6.0	76.0	2.65				6.61		1.02	0.74		2.03	
ORF SEQ ID NO:	28468	30455		30864		37168		32109		27355		2/320			31164		34915			31852		28327						ļ .
Exan SEQ ID NO:	15341	ı	l		22214	L	<u> </u>	25239	<u></u>	14300	l	14300	14030	18189	18189	18376	21391	22466	L	<u>L</u>		15995		17698		22439	24836	l
Probe SEQ ID NO:	2207	4325		4747	9135	10527	10900	12331	853	1135		1135	2878	5061	5061	5258	6069	9391	9391	12743		2070		4560	7034	9364	11847	12461

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Top Hit Descriptor	AJ003514 Selected chromosome 21 cDNA library Homo sapiens cDNA clone MP1p112-8J21	RC3-NN0068-090500-021-b03 NN0068 Homo saplens cDNA	bb30a02.y1 NIH_MGC_10 Homo sapiens cDNA done IMAGE.2984714 5' similar to SW.:NIAM_HUMAN 096169 NADH-UBIQUINONE OXIDOREDUCTASE ASHI SUBUNIT PRECURSOR ;	ob71f06.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1336835 3'	ATP SYNTHASE A CHAIN (PROTEIN 6)	LAMININ BETA-2 CHAIN PRECURSOR (S-LAMININ) (LAMININ CHAIN B3)	LAMININ BETA-2 CHAIN PRECURSOR (S-LAMININ) (LAMININ CHAIN B3)	Hamo sapiens chromosame 21 segment HS21 C100	zk67a06.r1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:487858 5'	Hamo sapiens chromosome 21 segment HS21C018	Homo sapiens dNT-2 gene for mitochondrial 5(3')-deoxyribonucleotidase (dNT-2 gene), exons 1-5	Human chromosomal protein HMG1 related gene	RC0-CT0301-271199-031-F03 CT0301 Homo saplens cDNA	zg73d03.s1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:398981 3' similar to	gb:M14338 VITAMIN K-DEPENDENT PROTEIN S PRECURSOR (HUMAN);contains THR.t3 OFR	repetitive element;	601304125F1 NIH_MGC_21 Homo sapiens cDNA done IMAGE:3638310 5	PM1-HT0454-080100-002-h09 HT0454 Homo sapiens cDNA	Homo sapiens protein tyrosine phosphatase, non-receptor type 21 (PTPN21), mRNA	om23g03 s1 Soarce_NFL_T_GBC_S1 Homo saplens cDNA clone IMAGE:1541908 3' similar to TR:002711	601649871F1 NIH MGC 74 Homo saplens cDNA clone IMAGE:3933880 57	Homo sapiens protein twostne phosphatase, non-receptor type 21 (PTPN21), mRNA	Homo seriens melanoma antiden, family C. 1 (MAGEC1), mRNA	hebse10.x1 NCI CGAP CML1 Homo sepiens cDNA clone IMAGE:2918164 3	783411 x1 NCI CGAP Pr28 Homo sapiens cDNA clone IMAGE:3303573 3' similar to contains OFR.t1	OFR repetitive element;	ZINC FINGER PROTEIN GL11 (GL1-1)	ZINC FINGER PROTEIN GLI1 (GLI-1)	z72c04.r1 Sogres_testis_NHT Homo saplens cDNA clone IMAGE:727878 5'	cos6eo8.ε1 NCI_CGAP_Kid5 Homo sapiens cDNA clone IMAGE:1573094 3' similar to TR:Q16530 Q16530 PMS3 MRNA ;contains OFR.t1 OFR repetitive element ;	
Top Hit Database Source	EST_HUMAN	EST_HUMAN	EST HUMAN	EST HUMAN	SWISSPROT	SWISSPROT	SWISSPROT	NT	EST_HUMAN	NT	N.	N.	EST_HUMAN			EST_HUMAN	EST_HUMAN	EST_HUMAN	LN TN	140	EST HIMAN	LNT	Į.	EST HIMAN		EST_HUMAN	SWISSPROT	SWISSPROT	EST_HUMAN	EST HUMAN	1
Top Hit Acession No.	9.0E-21 AJ003514.1	9.0E-21 AW898189.1	3.0E-21 AW674891.1	3.0E-21 AA809411.1	021330	P15800	715800		7.0E-21 AA046502.1	.0E-21 AL163218.2	7.0E-21 AJ277557.1	7.0E-21 D14718.1	7.0E-21 AW 856922.1			7.0E-21 AA723404.1	8.0E-21 BE408611.1	5.0E-21 BE162737.1	5902031 NT	7 7070004	5.0E-21 AMSZO184.1	5902031 NT	TN ASSAZA NT	5 0F-24 AW440864 1		5.0E-21 BE856505.1	091690	Q91690	5.0E-21 AA393574.1	4.0E-21 AA970713.1	
Most Similar (Top) Hit BLAST E Value	9.0E-21	9.0E-21	8.0E-21	8.0E-21	8.0E-21 O21330	7.0E-21 P15800	7.0E-21 P15800	7.0E-21	7.0E-21	7.0E-21	7.0E-21	7.0E-21	7.0E-21			7.0E-21	6.0E-21	6.0E-21	5.0E-21	10	3.0E-21	5.0F-21	5 OE-24	5 OE-24	17.00	5.0E-21	5.0E-21 Q91690	5.0E-21 Q91690	5.0E-21	4.0E-21	
Expression Signal	1.18	3.98	98.0	3.91	3.8	3.85	3.85	1.36	6.29	0.94	1.46	4.94	1.07			1.94	0.75	1.39	1.34		1.63	1 10	0 33	0.77	3	,	0.54	0.54	1.28	1.86	
ORF SEQ ID NO:				38510		28385		29958		33104	35203						ŀ		27181		1097		L			33734			L	28015	
Exon SEQ ID NO:	16155	25135	22090	24819	25250	15266	15266	16953	17512	19726	21663	21954	23354			24016	17369	22412	14120	1	13463	1	1	20247	2021	20291	1	23834	L	14921	ı
Probe SEQ ID NO:	2979	12174	8011	11830	12345	2130	2130	3792	4369	6564	8582	8875	10319			10934	4220	9336	947		4662	OUR	4000	200	7000	7157	10801	10801	12259	1772	

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Top Hit Descriptor		A-like protein gene, hereditary haemochromatosis unsporter (NPT3) gene, complete cds		ens cDNA clone IMAGE:629771 3'			kyribonucleotidase (dNT-2 gene), exons 1-5	kyribonucleotidase (dNT-2 gene), exons 1-5	103'	me IMAGE:4064945 5	scDNA	s dDNA		s cDNA	8	8	s cDNA			ts30f03.x1 NCI_CGAP_Pan1 Homo septens cDNA clone IMAGE:2230109 3' simiter to TR:Q99854 Q99854 HYPOTHETICAL 51.1 KD PROTEIN ;	iens cDNA done IMAGE:366910 5'	iens cDNA clone IMAGE:366910 5	omo sapiens cDNA clcne IMAGE:323667 5'		o oDNA	SE1005052 5'	ht09g01.x1 NCI_CGAP_Kld13 Homo saplens cDNA clone IMAGE:3146256 3' similar to contains MER29.b3 MER29 repetitive element ;	one IMAGE:3951008 5'
Ap doT	Rattus norvegicus mRNA for rTIM, complete cds	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RoRet gene, and sodium phosphate transporter (NPT3) gene, complete cds	Homo sapiens chromosome 21 segment HS21C002	zq15d06.s1 Stratagene fetal retina 937202 Homo sapiens cDNA clone IMAGE:629771 3'	Homo sapiens chromosome 21 segment HS21C001	Homo sapiens LGMD2B gene	Homo sapiens dNT-2 gene for mitochondrial 5(3)-deoxyribonucleotidase (dNT-2 gene), exons 1-5	Homo sepiens dNT-2 gene for mitochondrial 5(3)-deoxyribonucleotidase (dNT-2 gene), exons 1-5	AV661044 GLC Homo sepiens oDNA clone GLCGOA10 3'	601844465F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4064945 5	RC1-OT0083-100800-019-g08 OT0083 Homo saplens cDNA	CM1-NN0063-280400-203-h08 NN0063 Homo sapiens aDNA	Homo sapiens chromosome 21 segment HS21C013	QV3-HT0458-170200-090-912 HT0458 Hamo sapiens cDNA	Homo sapiens mRNA for KIAA0397 protein, partial cds	Homo saplens mRNA for KIAA0397 protein, partial cds	RC4-BT0311-141199-011-h06 BT0311 Homo saplens cDNA	ZONADHESIN PRECURSOR	ZONADHESIN PRECURSOR	ts30f03.x1 NOI_CGAP_Pan1 Homo seplens cDNA ce HYPOTHETICAL 51.1 KD PROTEIN;	2297a12.r1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA done IMAGE:366910 5	ze97a12.r1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:366910 5	228h02.r1 Soares_senescent_fibroblasts_NbHSF Homo sapiens cDNA clone IMAGE:323667 5	Homo sapiens hyperion gene, exons 1-50	QV0+HT0103-091199-050-911 HT0103 Homo sepiene oDNA	AU136779 PLACE1 Homo sapiens cDNA clone PLACE1005052 5	ht09g01.x1 NCI_CGAP_Kid13 Homo saplens cDNA MER29 repetitive element;	601880636F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:3951008 5
Top Hit Dettabase Source	LΝ	F	TN	EST_HUMAN	FN	NT	NT	LN	EST HUMAN	EST HUMAN	EST_HUMAN	EST HUMAN	LN	EST_HUMAN	<u>N</u>	LN	EST_HUMAN	SWISSPROT	SWISSPROT	EST HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	ΝΤ	EST HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN
Top Hit Acession No.	4.0E-21 AB019576.1	4.0E-21 U91328.1	4.0E-21 AL163202.2	3.0E-21 AA218891.1	3.0E-21 AL163201.2	3.0E-21 AJ007973.1	3.0E-21 AJ277557.1	3.0E-21 AJ277557.1	3.0E-21 AV661044.1	3.0E-21 BF184739.1	3.0E-21 BF361093.1	3.0E-21 AW897760.1	3.0E-21 AL163213.2	2.0E-21 BE163247.1	2.0E-21 AB007857.2	2.0E-21 AB007857.2	2.0E-21 BE064410.1	Q28983	Q28983	2.0E-21 AI624582.1	2.0E-21 AA027211.1	2.0E-21 AA027211.1	2.0E-21 W44493.1	2.0E-21 AJ010770.1	2.0E-21 BE141785.1	2.0E-21 AU136779.1	2.0E-21 BE350127.1	2.0E-21 BE973829.1
Most Similar (Top) Hit BLAST E Value	4.0E-21	4.0E-21	4.0E-21	3.0€-21	3.0E-21	3.0E-21	3.0E-21	3.0E-21	3.0E-21	3.0E-21	3.0E-21	3.0E-21	3.0E-21	2.0E-21	2.0E-21	2.0E-21	2.0E-21	2.0E-21 Q28983	2.0E-21 Q28983	2.0E-21	2.0E-21	2.0E-21	2.0E-21	2.0E-21	2.0E-21	2.0E-21	2.0E-21	2.0E-21
Expression Signal	2.61	0.82	0.61	1:1	1.51	6.41	0.92	0.92	0.9	2.74	7.52	0.92	3.58	24.5	0.61	0.61	3.03	2.59	2.59	1.56	0.8	0.8	0.74	0.58			2.04	
ORF SEQ ID NO:	33568	36614	36642		28611		31878	31879			33493					27190	L	28937		_	l							38335
Exan SEQ ID NO:	20147	23022	23048	1_	15479		18810	18810	19046	1	1	1	ı	ı				15821	ı	18796	18888	L	<u> </u>	L	ĺ	Ι.		H
Probe SEQ (D NO:	7011	6983	10010	1884	2348	3149	5616	5616	5856	6308	7215	9894	12879	150	958	858	1241	2703	2703	5601	5694	5694	6157	8467	8558	9023	11313	11599

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Probe SEQ ID NO:	Exen SEQ (D NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acesskon No	Top Hit Database Source	Top Hit Descriptor
11599	24652	38336	2.88	-	.0E-21 BE973829.1	EST_HUMAN	601680636F1 NIH_MGC_83 Home sapiens cDNA clane IMAGE:3951008 51
12572	ı		6.44		2.0E-21 AF176815.1	ΙN	Homo sapiens putative 8-hydroxyguanine DNA glycosylase gene, complete cds
	l_						n46c04.s1 NCI_CGAP_Pr4 Homo sapiens cDNA clone IMAGE:1043718 similar to contains MER29.b2
1284		27509		•	1.0E-21 AA557657.1	EST_HUMAN	MER29 repetitive element;
1434	l .		4.93	Ì	1.0E-21 AI601264.1	EST_HUMAN	ar88d12.x1 Barstead colon HPLRB7 Homo sapiens cDNA clone IMAGE:2152343 3'
9816	19776		2.73		.0E-21 AL079752.1	EST_HUMAN	DKFZp43410830_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp43410830 5
	l						og47e05.x1 Soares_tests_NHT Homo sapiens cDNA clone IMAGE:1838336 3' similar to gb:M64241 QM
7342	- [	]				ES HOMAIN	ROLEIN (IDONAL)
10448	- 1		0.47	1.0E-21		L	Homo sapiens chromosome 21 segment HS21C003
10448	23483	37093	74.0	1.05-21	1.0E-21 AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
10812	23845		1.31	1.05-21	820038	NT	Homo saplens SET domain and mariner transposase fusion gene (SETMAR) mRNA
13014	1		1.67	1.0E-21	.0E-21 AF046133.1	NŤ	Homo saplens chromosome Xp22 410-8
1530	1768	20854	86.0			HST HIMAN	E94a03.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2296204 3' similar to TR:015408 Q15408 NEUTRAL PROTEASE LARGE SUBUNIT :
8803						N	Homo saplens chromosome 21 segment HS21C001
888				Ĺ		NT	Homo saplens chromosome 21 segment HS21C001
11031		ļ			9.0E-22 AV761874.1	EST_HUMAN	AV761874 MDS Homo sapiens cDNA clone MDSCCG05 5'
12007	24992	38698	1.39		9.0E-22 AU140358.1	EST_HUMAN	AU140358 PLACE2 Homo sapiens cDNA clone PLACE2000394 5'
971			7.93		8.0E-22 BE144748.1	EST_HUMAN	GM0-HT0179-281099-076-h05 HT0179 Homo sapiens cDNA
8080	L		3.36	_		EST_HUMAN	zk67a06.r1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:487858 5'
682	乚	ļ			6.2	LN	Homo saplens chromosome 21 segment HS21C046
4398	17541	30522	3.27		7.0E-22 Q61838	SWISSPROT	ALPHA-2-MACROGLOBULIN PRECURSOR (ALPHA2M)
5150	18272	31241	0.91	Ĺ	7.0E-22 AB008681.1	NT	Homo sapiens gene for ectivin receptor type IIB, complete cds
8888	21967		1.24		7.0E-22 AF151054.1	LN	Homo sapiens HSPC220 mRNA, complete cds
9032	22111	35653			7.0E-22 M78590.1	EST_HUMAN	EST00738 Fetal brain, Stratagone (cat#936206) Homo sapiens cDNA clone HFBCF07
9802			2.05		7.0E-22 AF009660.1	IN	Homo saplens T cell receptor beta locus, TCRBV7S3A2 to TCRBV12S2 region
8436	21517		1.25	Ĺ	6.0E-22 AW029123.1	EST_HUMAN	wx05g07.x1 NCI_CGAP_Gas4 Homo sepiens cDNA clone IMAGE:2542812 3'
6646	L	33192	3.27		5.0E-22 AL163303.2	N	Homo sapiens chromosome 21 segment HS21C103
10525	23560	37167			5.0E-22 U60822.1	TN	Human dystrophin (DMD) gene, exons 7, 8 and 9, and partial cds
							naa27b06.x1 NCI_CGAP_Pr28 Homo sapions oDNA clone IMAGE:3255898 3' similar to contains Alu
12833	25555		1.63		5.0E-22 BF476511.1	EST_HUMAN	repetitive element;
3726	16887		77.0		4.0E-22 AJ271735.1	LN	Hamo sapiens Xq pseudoautosomal region; segment 1/2
8008	26224		2.81		4.0E-22 AL163202.2	NT	Homo sapiens chronosome 21 segment HS21C002
10961	1 1	37677			4.0E-22 BF218030.1	EST_HUMAN	601882813F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4095434 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acessian No.	Top Hit Database Source	Top Hit Descriptor
13021	25672		3.85		4.0E-22 AL163209.2	NT	Homo sapiens chromosome 21 segment HS210009
ě	74454		134		3 DE. 22 A 1460679 1	EST HIMAN	tm14h10.x1 NCI_CGAP_Co14 Homo sapiens cDNA done IMAGE:2156611 3' similar to gb:L19593 HIGH_AFFINITY INTERLEUKIN-8 RECEPTOR B (HUMAN):contains L1.ft L1 repetitive element:
3	5						wi66504 x1 NCI CGAP Brn25 Homo sapiens cDNA clone IMAGE:2429839 3' similer to SW:RL21 HUMAN
2636	15759	28873	1.33		3.0E-22 A(859038.1	EST_HUMAN	P46778 60S RIBOSOMAL PROTEIN L21.;
3763	16924		1.65		3.0E-22 D14718.1	NT	Human chromosomal protein HMG1 related gene
7697	18052	31038	3.18	-	0E-22 AIN90125 1	H TSE	db28c07.x1 Sogres_pregnant_uterus_NbHPU Homo sepiens cDNA clone IMAGE:1697580 3' similar to contains MFR12.t2 MER12 repetitive element:
77	10002	L		1		NG - 12	RETROVIRUS-RELATED POLYPROTEIN ICONTAINS: REVERSE TRANSCRIPTASE:
8011	21061	34573	0.8		3.0E-22 P11369	SWISSPROT	ENDONUCLEASE
8425	21506		1.11	3.0E-22	3.0E-22 BE156613.1	EST_HUMAN	QV0-HT0368-090200-099-f12 HT0368 Horno saplens oDNA
8430	l		1.88			EST_HUMAN	RC5-BT0707-150300-021-H10 BT0707 Homo sapiens cDNA
8555	1	L			3.0E-22 X60660.1	ΤN	R.rattus RY2G5 mRNA for a potential ligand-binding protein
8555	_		1.14			NT	R. rettus RY2G5 mRNA for a potential ligand-binding protein
2008	15148		4.04		1	EST_HUMAN	yx73d05.s1 Soares melanocyte 2NbHM Homo sapiens cDNA clone IMAGE:267369 3'
2590	15715				P24916	SWISSPROT	IMMEDIATE EARLY GENE 13 PROTEIN PRECURSOR
3507	16674	29684	3.98		8394043 NT	NT	Homo sapiens protein kinase, AMP-activated, gamma 3 non-catalytic subunit (PRKAG3), mRNA
4341	17484		1.41	2.0E-22	AW817794.1	EST_HUMAN	PM1-ST0262-261189-001-d12 ST0262 Homo sapiens cDNA
5973	25814	32476	1.47		2.0E-22 W39456.1	EST_HUMAN	zz20101.r1 Sogres_senescent_fibroblasts_NbHSF Homo sepiens cDNA clone IMAGE:322873 5' similar to gb:X72308 MONOCYTE CHEMOTACTIC PROTEIN 3 PRECURSOR (HUMAN);
6306	19478				2.0E-22 BF092116.1	EST_HUMAN	RC0-TN0079-150900-025-h12 TN0079 Homo sapiens cDNA
7000	2000	octoo	4 70		3.05.33 A1278523.4	NVWI IT LOSS	d/36h06.x1 Soares_NhHWPu_S1 Homo sapiens cDNA cione IMAGE:1878299 3' similar to contains MFR29 tx MFR29 repolitive element
10001	23039	}			2.0E-22 AA715315.1	EST HUMAN	m04h11.s1 NCI_CGAP_Pr22 Homo sapiens cDNA clone IMAGE:1219269 3'
10001	ı	36631	0.85		2.0E-22 AA715315.1	EST_HUMAN	nv04h11.s1 NCI_CGAP_Pr22 Home sapiens cDNA clone IMAGE:12192693'
12056	ı				2.0E-22 AW418960.1	EST_HUMAN	ha24f04,x1 NCI_CGAP_Kid12 Homo sapiens cDNA clone IMAGE:28746553'
12139	25656				2.0E-22 AL163280.2	NT	Homo saplens chromosome 21 segment HS21C080
1927	15070				.0E-22 AW 865517.1	EST_HUMAN	PM4-SN0020-010400-009-h02 SN0020 Homo sapiens cDNA
2651	15774	28887	2.36		.0E-22 U50871.1	LΝ	Human familial Alzhelmer's disease (STM2) gene, complete cds
3497	16664	29676	1.53		.0E-22 D14547.1	NT	Human DNA, SINE repetitive element
7920	20971	34478	1.09	Į.	.0E-22 BE084667.1	EST_HUMAN	MR0-BT0659-220200-002-h07 BT0659 Homo sapiens oDNA
10776	23809	37432	1.05		.0E-22 Al365435.1	EST HUMAN	qz09b07.x1 NCI_CGAP_CLL1 Homo sapiens cDNA clone IMAGE::2020961 3' simitar to contains MER29.b2   MER29 repetitive element ;
	١	l					

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<u> </u>											_				_	٨	_,		-,-		-,-				-,-		-,-	.~	
Top Hit Descriptor	qz09b07.x1 NCI_CGAP_CLL1 Homo sapiens cDNA clone IMAGE:2020981 3' sImilar to contains MER29.b2 MER29 repetitive element ;	II.2-UM0078-070400-061-F11 UM0076 Hamo sepiens cDNA	Gallus gallus Dach2 protein (Dach2) mRNA, complete cds	AV647246 GLC Homo saplens cDNA clone GLCAWCD7 3'	Homo sapiens Not56 (D. melenogaster)-like protein (NOT56L) mRNA	Rattus norvegicus RIM1B (Rim1B) mRNA, complete cds	Homo sapiens chromosome 21 segment HS21C049	Homo sapiens mannosidase, beta A, Iysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D3) genes, complete cds	Homo sapiens mannosidase, bata A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D3) genes, complete cds	gg59c03.x1 Scares_testis_NHT Homo sepiens cDNA clone IMAGE:1839480 3' similar to sw.w.nv.n Mni isE P27348 PROTEIN MOV-10	SVY NAV IO_MODGE F 25275 FIXOTENAV IO.	Homo sapiens chromosome Xq28 melanoma antigen family A2a (MAGEA2A), melanoma antigen family A12 (MAGEA12), melanoma antigen family A2b (MAGEA2B), melanoma antigen family A3 (MAGEA3), caltractin	(CALT), NAD(P)H dehydrogenase-like protein (NSDHL), and LI>	Pongo pygmaeus offactory receptor (PPY116) gene, partial cds	Pongo pygmaeus olfactory receptor (PPY116) gene, partial cds	Homo sapiens chromosome 21 segment HS210027	Homo sapiens chromosome 21 segment HS21C027	건강당08.r1 Scares_prognant_uterus_NbHPU Home sapiens cDNA clone IMAGE:503968 5' similar to	Contains MENZS LEMENZE l'apenine evenine in . Himan endocennis retroviral element HC2	rigini onagginine remaine de l'ament HC2		RC3-NN00666-270400-011-h01 NN0066 Home capters CLINA	Homo sapiens cytochrome P450 polypeptide 43 (CYP3A43) gene, partial cds; cytochrome P450 polypeptide A (CyD34A) and machinema D450 polypeptide 7 (CYP3A7) genes, complete cds; and cytochrome P450		polybehude a Contract, bases are the	Homo sapiens KIAA0851 gene (partial), X13 gene and L21rL1 gene	Human matrix Gla protein (MGP) gene, complete cds	TENASCIN-X PRECURSOR (TN-X) (HEXABRACHION-LIKE)	TENASCIN-X PRECURSOR (TN-X) (HEXABRACHION-LIKE)
Top Hit Database Source	EST_HUMAN	EST_HUMAN	LN	EST_HUMAN	NT	ΙN	NT	·	L	No.	ES L'HOMAIN		M	NT	TN	L	Ę		NEST HUMAN	2 12	2	EST_HUMAN		ļ	Z	NT	NT	SWISSPROT	SWISSPROT
Top Hit Acession No.	.0E-22 AI365435.1	.0E-23 AW802801.1	.0E-23 AF198349.1	.0E-23 AV647246.1	5031952 NT	3.0E-23 AF199333.1	3.0E-23 AL163249.2	3.0E-23 AF224669.1	3 0E-23 AF224889 1	1000430	5.0E-23 AIZUST30.1		5.0E-23 U82671.2	5.0E-23 AF179818.1	5.0E-23 AF179818.1	3.0E-23 AL 163227.2	3.0E-23 AL163227.2		3.0E-23 AA130165.1	27,0004.1	3.0E-23 Z/0564.1	3.0E-23 AW 897927.1		, 10,000	3.0E-23 AF280107.1	2.0E-23 AJ289880.1	2.0E-23 M55270.1	P22105	P22105
Most Similar (Top) Hit BLAST E Value	1.0E-22	9.0E-23	8.0E-23	7.0E-23	7.0E-23	6.0E-23	6.0E-23	6.0E-23	8 0E-23	100	0.0E-23		5.0E-23	5.0E-23	5.0E-23	3.0E-23	3.0E-23		3.0E-Z3	3.05-23	3.UE-23	3.0E-23		1	3.0E-23	2.0E-23	2.0E-23	2.0E-23 P22105	2.0E-23 P22105
Expression Signal	1.05	12.31	0.74	2.21	3.74	1.83	1.15	4.93	4 93	,	3.18		4.01	3.69	2.78	29.0	79.0		3.26	37.6	3.72	1.42		,	1.35	3.69	3.46	1	F
ORF SEQ ID NO:	37433		29833	ļ	38000		30507	32097		1	32058		31796								36131				ļ	26899			
Exon SEQ ID NO:	23839	1	1	16555	l	16686	17526	25211			25335		18757	Ľ		1_	L	1		- 1	- 1	23558					15988	1	
Probe SEQ ID NO:	10776	13078	3661	3385	11293	3520	4383	12283	10083	3	12483		5560	6369	7695	6570	6570		8022	2   S	9450	10523			11372	683	1166	2856	2856

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Top Hit Descriptor	qs73f11 x/ NGL CGAP_Pr28 Homo saplens cDNA clone IMAGE:1943757 3' similar to TR:Q13537 Q13537 MER37 TRANSPOSABLE ELEMENT, COMPLETE CONSENSUS SEQUENCE.;	ns cDNA	ofens cDNA clone IMAGE:205418 5'	plens cDNA clone IMAGE:205418 5'	Homo sapiens cytochrome P450 polypeptide 43 (CYP3A43) gene, partial cds; cytochrome P450 polypeptide 4 (CYP3A4) and cytochrome P450 polypeptide 7 (CYP3A7) genes, complete cds; and cytochrome P450			l3) gene, exon 1	3A2 to TCRBV12S2 region	ARC1000946 5			lone IMAGE:3608653 5'	zw82c06.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:782698 5' similar to contains PTR5.t2		lone IMAGE:3636254 5'	lone IMAGE:3636254 5'	ns cDNA	olens cDNA clone IMAGE:852758 3' similar to				e Z-line, alpha 2 (CAPZA2), mRNA	ns cDNA	tplens cDNA clone DKFZp434A2311 5'	xx17f03.x1 Soares_NFL_T_GBC_S1 Homo saplens cDNA clone IMAGE:2813405 3' similar to contains Alu	ive element;	(TSPY), complete cds		R1 on chromosome 21q22, segment 3/3	Homo sepiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
Н ф	qs73f11.x1 NCI_CGAP_P/28 Homo saplens dDNA clone IMAGE:1943757 3' simil MER37 TRANSPOSABLE ELEMENT, COMPLETE CONSENSUS SEQUENCE.	MR3-HT0487-150200-113-g01 HT0487 Homo sapiens cDNA	yr16a02.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE::205418 5'	yr16a02.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:205418 5'	Homo sapiens cytochrome P450 polypeptide 43 (CY 4 (CYP3A4) and cytochrome P450 polypeptide 7 (C	polypeptide 5 (CYP3A5) gene, partial cds	Homo sapiens chromosome 21 segment HS21C103	Human alcohol dehydrogenase gamma subunit (ADH3) gene, exon 1	Homo saplens T cell receptor beta locus, TCRBV7S3A2 to TCRBV12S2 region	AU133931 OVARC1 Homo saplens cDNA clone OVARC1000946 5	Homo sapiens chromosome 21 segment HS21C052	Homo saplens chromosome 21 segment HS21C010	601236455F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3608653 5	zw82c06.r1 Soares_testia_NHT Homo sapiens cDN	PTR5 repetitive element;	601301762F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3636254 5	601301762F1 NIH_MGC_21 Homo sapiens cDNA clane IMAGE:3636254 5	QV0-NN1020-170400-195-a11 NN1020 Homo saplens cDNA	ab75a08.s1 Stratagene fetal retina 937202 Homo saplens cDNA clone IMAGE:852758 3' similar to	TR:E19822 E19822 CA PROTEIN.;	OLFACTORY RECEPTOR-LIKE PROTEIN IS	OLFACTORY RECEPTOR-LIKE PROTEIN IS	Hamo sapiens capping protein (actin filament) muscle Z-line, alpha 2 (CAPZA2), mRNA	QV0-DT0047-170200-122-a06 DT0047 Homo sapiens cDNA	DKFZp434A2311_r1 434 (synonym: htes3) Homo saplens cDNA clone DKFZp434A2311 5	xv17f03.x1 Soares_NFL_T_GBC_S1 Homo saplent	repetitive element contains MER19.t2 MER19 repetitive element	Macaca fuscata mRNA for Tectic-Specific Protein Y (TSPY), complete cds	Homo sapiens chromosome 21 segment HS21C049	Homo saplens 959 kb contig between AML1 and CBR1 on chromosome 21q22, segment 3/3	Homo sapiens calcium channel alpha1E subunit (C. spiced
Top Hit Database Source	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN		뉟	Ā	N	FZ	EST_HUMAN	N	F	EST HUMAN		EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN		EST HUMAN	SWISSPROT	SWISSPROT	INT	EST HUMAN	EST HUMAN		EST HUMAN	LN	LN LN	Į.	LN
Top Hit Acession No.	2.0E-23 AI201458.1	2.0E-23 BE165980.1	159931.1	159931.1		4F280107.1	AL163303.2	2.0E-23 M32658.1	4F009660.1	AU133931.1	0E-23 AL163252.2	0E-23 AL163210.2	.0E-23 BE378471.1		.0E-23 AA448097.1	.0E-23 BE409843.1	.0E-23 BE409643.1	.0E-23 AW901816.1		9.0E-24 AA663213.1	P23269	8.0E-24 P23269	11422027 NT	AW937954.1	AL039498.1		7.0E-24 AW303317.1	6.0E-24 AB001421.1	AL163249.2	5.0E-24 AJ229043.1	5.0E-24 AF223391.1
Most Similar (Top) Hit BLAST E Value	2.0E-23	2.0E-23	2.0E-23	2.0E-23		2.0E-23	2.0E-23	2.0E-23	2.0E-23	2.0E-23	1.0E-23	1.0E-23	1.0E-23		1.0E-23	1.0E-23	1.0E-23	1.0E-23		9.0E-24	8.0E-24	8.0E-24	8.0E-24	7.0E-24	7.0E-24		7.0E-24	6.0E-24	6.0E-24	5.0E-24	5.0E-24
Expression Signal	1.11	3.53	4.43	4.43		5.28	0.95	6.7	3.68	2.3	1.57	5.42	3.27		4.61	2.19	2.19	1.35		1.67	1.12	1.12	0.95	0.94	16.79		1.61	2.21			1.27
ORF SEQ ID NO:			30246	30247		_	35665				30769				35169	37625	37628				30888		33121							30241	
Exon SEQ ID NO:	16624	16970	17240	17240	1	21140	22123	25199		Ĺ	Ĺ	18018	Ĺ		21632	23392	23992	1		13758	17906	17906	19740	17133	ı	۱.,	23961	<u> </u>		L	ì
Probe SEQ ID NO:	3457	3810	4085	4085		8057	9044	12265	12844	12983	4650	4888	6861		8551	10909	10909	13082		299	4771	4771	6578	3976	5281		10876	724	861	4078	7935

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Probe SEQ ID NO:	SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
4371	17514		6.0	4.0E-24	4.0E-24 BF369469.1	EST_HUMAN	RCO-GN0090-250900-022-h09 GN0090 Homo sapiens cDNA
6052	19234	32559	2.77	4.0E-24	4.0E-24 AA594178.1	EST_HUMAN	nn31h05.s1 NCI_CGAP_Gas1 Homo sapiens cDNA done IMAGE:1085529 3' simitar to SW:POL_MLVRK P31795 POL POLYPROTEIN ;
8880	1	ļ		4.0E-24	4.0E-24 AW813711.1	EST_HUMAN	RC3-ST0197-130100-014-f06 ST0197 Homo sepiens cDNA
11454	1		2.05	4.0E-24	4.0E-24 BE544822.1	EST_HUMAN	601078812F1 NIH_MGC_12 Homo saplens cDNA clone IMAGE:3464498 5'
12669				4.0E-24	4.0E-24 AB029016.1	ĻΝ	Homo sapiens mRNA for KIAA1093 protein, partial cds
7229	20134	33551	0.73	3.0E-24	3.0E-24 U66061.1	NT	Human germline T-cell receptor beta chain TCRBV17S1A1T, TCRBV2S1, TCRBV10S1P, TCRBV2BS1P, TCRBV19S1P, TCRBV19S1P, TCRBV19S1P, TCRBV19S1P, TCRBV3AS1, TCRBV14S1, TCRBV3S1, TCRBV4S1A1T, TRY4, TRY5, TRY6, TRY7, TRY8, TCRBD1, TCRBJ1S1, TCRBJ1S2,
7229	20134	33552	0.73	3.0E-24	3.0E-24 U66061.1	F	Human germline T-cell receptor beta chain TCRBV17S1A1T, TCRBV2S1, TCRBV10S1P, TCRBV29S1P, TCRBV19S1P, TCRBV19S1P, TCRBV19S1P, TCRBV19S1P, TCRBV19S1, TCRBV19S1, TCRBV19S1, TCRBV19S1, TCRBV4S1A1T, TRY4, TRY6, TRY6, TRY7, TRY8, TCRBD1, TCRBJ1S1, TCRBJ1S2.>
8618	21698		2.94	3.0E-24	3.0E-24 AW614871.1	EST_HUMAN	hh68c08.x1 NC_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2967960 3' similar to contains MER29.b2 MER29 repetitive element ;
8673	21753		1.24	3.0E-24	3.0E-24 AW982076.1	EST HUMAN	EST374149 MAGE resequences, MAGG Homo sapiens cDNA
9665	ı	36198		3.0E-24	3.0E-24 AL1632522	NT	Homo saplens chromosome 21 segment HS21 C052
12756	ı	L	1.34	3.0E-24	3.0E-24 BF127762.1	EST_HUMAN	601810449F1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4053396 5'
2422	15551	L		2.0E-24	2.0E-24 AA167539.1	EST_HUMAN	zp11f09.r1 Stratagene fetal retina 937202 Homo sapiens cDNA clone IMAGE:609161 51
3800	ı		0.82	2.0E-24		EST_HUMAN	RC3-NN0068-090500-021-b03 NN0068 Homo sapiens cDNA
7515	26219		0.63	2.0E-24		NT	Homo sapiens chromosome 21 segment HS210009
7643	20712			2.0E-24	2.0E-24 AF086824.1	LN	Mus musculus morrac-interacting citron kinase (Crik) mRNA, complete ods
7648	20717			2.0E-24	2.0E-24 AJ003536.1	EST_HUMAN	AJ003536 Selected chromosome 21 cDNA library Homo sapiens cDNA clone MPlp112-5H13
8938	22017	35559	3.81	2.0E-24	2.0E-24 AL119158.1	EST_HUMAN	DKFZp761L1712_r1 761 (synonym: hamy2) Homo saplens cDNA clone DKFZp761L1712 5
							yr92b09.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:212729 5 similar to contains
8977			0.0		2.0E-24 H69214.1	EST_HUMAN	MER28 repetitive element;
10058	23096	36698	1.06	2.0E-24	2.0E-24 AI521759.1	EST_HUMAN	ti77a09.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2138008 3'
10058	23096	36699	1.06	2.0E-24	2.0E-24 AI521759.1	EST_HUMAN	ti77a09.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2138008 3
12580			21.43	2.0E-24	2.0E-24 M28877.1	NT	Human O family dispersed repeat element
1731	14881	27972	4.81	1.0E-24	7706340 NT	N	Homo sapiens CGI-127 protein (LOC51645), mRNA
2738			1.65	1.0E-24	1.0E-24 AW820194.1	EST_HUMAN	QV0-ST0294-100400-185-c10 ST0294 Homo saplens cDNA
3085		29278	0.72	1.0E-24	1.0E-24 D86423.1	Į.	Mus musculus mRNA for HGT keratin, partial cds
4385	17528		1.93	1.0E-24	1.0E-24 AF143313.1	LN.	Homo saplens PTEN (PTEN) gene, exon 2

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Top Hit Descriptor	Mus musculus keratin complex 1, gene C29 (Krt1-c29), mRNA	Homo sapiens chromosome 21 segment HS21C103	MR0-HT0168-271199-005-d09 HT0166 Homo sapiens cDNA	CM0-NN1010-130300-281-d07 NN1010 Homo sapiens cDNA	Homo sapiens putative secreted protein (SIG11), mRNA	ne92e10.s1 NCI_CGAP_Kid1 Homo sepiens cDNA clone IMAGE:911754 similar to contains MER1.b2 MER1 repetitive element;	ne08e09.s1 NCI_CGAP_Co3 Homo sepiens cDNA done IMAGE:880408 3' similar to contains THR.b2 THR repositive element	n/25h06.s1 NCI_CGAP_Pr1 Hamo sapiens cDNA clone IMAGE:914843 similar to SW:R14A_YEAST P36105 PROBABLE 60S RIBOSOMAL PROTEIN L14EA.	zh65h07.r1 Soares_fatal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:416989 5'	Mus musculus otogelin (Otog), mRNA	IL3-CT0219-161199-031-D04 CT0219 Homo sapiens cDNA	EST391217 MAGE resequences, MAGP Homo sapiens cDNA	ye56h04,r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:121783 5'	PM3-OT0093-280200-001-907 OT0093 Homo saplens cDNA	QV3-HT0543-140400-149-e11 HT0543 Homo sapiens cDNA	EST97317 Thymus I Homo saplens cDNA 5' end similar to EST containing O family repeat	RC5-BT0377-131289-031-F02 BT0377 Homo sapiens cDNA	Hamo sapiens hypothetical protein FLJ20344 (FLJ20344), mRNA	Homo sapiens hypothetical protein FLJ20344 (FLJ20344), mRNA	KALLISTATIN PRECURSOR (KALLIKREIN INHIBITOR) (PROTEASE INHIBITOR 4)	Homo sapiens chromosome 21 segment HS21C010	nf30h10.s1 NCI_CGAP_Pr1 Homo saplens cDNA clone IMAGE:915331 similar to contains L1.t1 L1	reproduct State Residuals (hotel like 4 (TR) 4) and NA	CIVILIO SERVETS MENSACIONI (DELE PINITA) I (1 DE 1) III MANA MANA MANA MANA MANA MANA MANA		40S RIBOSOMAL PROTEIN S16	40S RIBOSOMAL PROTEIN S16	40S RIBOSOMAL PROTEIN S16	AL449573 Homo sapiens Testis (Stavrides GS) Homo septens cDNA	DKFZp434H0313_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434H0313 5'	Human endogenous retrovirus, complete genome
Top Hit Database Source	LN	N	EST_HUMAN	EST_HUMAN	TN	EST HUMAN			Τ	NT	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST HUMAN	EST_HUMAN	EST_HUMAN	TN	NT	SWISSPROT			NICHOLD IN	TANAL TANAL	ESI TOMAIN	SWISSPROT	SWISSPROT	SWISSPROT	EST_HUMAN	EST_HUMAN	N
Top Hit Acession No.	7106336 NT	.0E-24 AL163303.2	.0E-24 BE144526.1	.0E-24 AW901164.1	TV06707 NT	.0E-25 AA483944.1	OE-25 & & 488646 1	0E-25 AA583540.1	6.0E-25 W87623.1	7305360 NT	5.0E-25 AW850271.1	5.0E-25 AW979107.1	198107.1	4.0E-25 AW887671.1	4.0E-25 BE170957.1	4.0E-25 AA383873.1	3.0E-25 BE068922.1	8923321 NT	8923321 NT	29622	.0E-25 AL163210.2	A 620040 4	3.0E-20 AA37 90 13.1	2.05-20	35555710.1	P17008	21 7008	217008	2.0E-25 AL449573.1	.0E-25 AL040229.1	9635487 NT
Most Similar (Top) Hit BLAST E Value	1.0E-24	1.0E-24	1.0E-24	1.0E-24	9.0E-25	7.0E-25	7.05-25	7.0E-25	6.0E-25	6.0E-25	5.0E-25	5.0E-25	4.0E-25 T98107.1	4.0E-25	4.0E-25	4.0E-25	3.0E-25	3.0E-25	3.0E-25	3.0E-25 P29622	3.0E-25	20 20 0	3.0E-20/	2.05-20	Z.UE-20	2.0E-25 P17008	2.0E-25 P17008	2.0E-25 P17008	2.0E-25	1.0E-25	1.0E-25
Expression Signal	1.13	4.85	5.07	2.29	1.37	2.7	2 4	3.64	5.04	11.72	1.61	3.12	2.66	2.81	4.06	0.83	1.02	3.12	3.12	7.0	5.42		7	6.4	56.7	3.71	1.61	1.61	2.13	0.81	2.07
ORF SEQ ID NO:		34272		34732	,	31206				34458	27920	38333	27716			36779	28516	29581	29582	31119		jung	Ì			28848	30436			26617	
Exon SEQ ID NO:	1	i	20959			18239	1	1	l_	L	<u> </u>		14631	16656	17578	23182	l	16566	16566	18144	21613		-	14333	- 1	_	17450	17450	23006		14434
Probe SEQ ID NO:	6531	7720	7907	8130	11999	5111	0412	12003	7131	7899	1683	11596	1478	3489	4436	10144	2256	3396	3396	5015	8532	1000	/97	13/8	2382	2893	4307	4307	2962	375	1277

Page 259 of 550 Table 4 Single Exon Probes Expressed in Placenta

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Top Hit Descriptor	PM4-HT0454-080100-002-h09 HT0454 Homo sapiens cDNA	Homo sapiens HSPC059 protein (HSPC059), mRNA	Homo sapiens HSPC059 protein (HSPC059), mRNA	zq45b06.s1 Stratagene hNT neuron (#937233) Homo sapiens cDNA clone IMAGE:632627 3' similar to	contains Alu repetitive element;	nn54h11.s1 NCI_CGAP_Kid6 Homo sapiens cDNA clone IMAGE:1087749 3	z/36g04.s1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:384822 3' similar to contains PTR5,t3 PTR5 repetitive element ;	R.rattus RY2G5 mRNA for a potential ligand-binding protein	Rrattus RY2G5 mRNA for a potential ligand-binding protein	Homo sapiens MAGE-B2 (MAGE-B2), MAGE-B3 (MAGE-B3), MAGE-B4 (MAGE-B4), and MAGE-B1 MAGE-B1) genes, complete cds	Human DNA, SINE repetitive element	Human DNA, SINE repetitive element	Homo sapiens chromosome 21 segment HS21 C018	QV-BT087-301298-006 BT087 Homo sapiens cDNA	Hama sapiens chromosome 21 segment HS21C086	Human DNA, SINE repetitive element	Homo sapiens X-linked anhidrolitic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat.	Hisapiens DNA for endogenous retroviral like element	hd02e12.x1 Soares_NFL_T_GBC_S1 Homo saplens cDNA clone IMAGE.2908366 3'	Homo sapiens chromosome 21 segment HS21C002	zn30d08.r1 Stratagene neurospitholium NT2RAMI 937234 Homo sapiens cDNA clone IMAGE:548943 6' simitar to gb:M14338 VITAMIN K-DEPENDENT PROTEIN S PRECURSOR (HUMAN);	EST386629 MAGE reseguences, MAGC Homo sapiens cDNA	Homo sapiens chromosome 9 duplication of the T cell receptor beta locus and trypsinogen gene families	zq52h04.r1 Stratagene neuroepithelium (#937231) Homo sapiens cDNA clone IMAGE:645271 5'	Homo capiens chromosome 21 segment HS210002	Homo saplens chromosome 21 cegment HS21C002	Homo sapiens chromosome 21 segment HS21C010	as38h08.x1 Barstaad aorta HPLRB6 Homo sapiens cDNA done IMAGE:2319519 3' similar to WP:F49C12.11 CE03371;
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Most Similar (Top) Hit BLAST E Value	1.0E-25	1.0E-25	1.0E-25		1.0E-25/	1.0E-25	1.0E-25	1.0E-25	1.0E-25	1.0E-25	1.0E-25	1.0E-25	9.0E-26	9.0E-26	9.0E-26	8.0E-26	1	7.0E-20	7.0E-26	7.0E-26	7.0E-26	7.0E-26	6.0E-26	6.0E-26	6.05-26	6.0E-26	6.0E-26	
Expression Signal	2.71	1.16	1.16		0.95	2.95	3.56	1.32	1.32	3.41	1.62	1.62	1.94	2.35	5.33	1.51	i u	10.01	192	0.84	6.85	5.49	3.83	0.69	0.62	0.62	2.15	0.89
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	Exon ORF SEQ Expression (Top) Hit Top Hit Acession Signal BLAST E No. Source	Exon         ORF SEQ         Expression         Top) Hit Top Hit Acession No.         Top Hit Acession ID No.         Top Hit Acession ID No.         Top Hit Acession ID No.         Database Source         Database Source         Source         Source         Value         Value         Value         Value         Value         Value         Value         EST_HUMAN         PM1-HT0454-080100-002-h09 HT0454 Hom	Exon         ORF SEQ         Expression         (Top) Hit Acession No.         Top Hit Acession Signal         Top Hit Acession (Top) Hit Acession No.         Top Hit Acession Signal Signal No.         Top Hit Acession No.         Top Hit Acession No.         Database Source Signal No.         Source Signal No.         No.         Source Signal No.         No.         Source Signal No.         No.         No.         No.         No.         No.         No.         No.         No.         No.         No.  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AA709079.1         EST_HUMAN           24281         36389         1.32         1.0E-25         AA709079.1         INT           25209         38369         1.32         1.0E-25         AA5060.1         NT           26209         38369         1.62         1.0E-25         D14547.1         NT           26209         38369         1.62         1.0E-25         D4547.1         NT           26209         38369         1.62         1.0E-25         D4547.1         NT           26209         38369         1.62         1.0E-25         D4547.1	Exon NO:         ORF SEQ ID NO:         Expression Signal         Top Hit Acession Value         Top Hit Acession Value         Top Hit Acession No:         Top Hit Acession Signal         Top Hit Acession Value         Top Hit Acession Signal         Top Hit Acession Value         Top Hit Acession Signal         Top Hit Acession Value         Top Hit Acession Signal         Top Hit Acession Value         Top Hit Acession Signal         Top Hit Acession 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Top Hit Descriptor	as38h08.x1 Barstead aorta HPLRB6 Homo sapiens cDNA clone IMAGE:2319519 3' similar to WP:F49C12.11 CE03371;	Homo sapiens upstream binding transcription factor, RNA polymerase I (UBTF), mRNA	601191345F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3535210 5'	Homa saplens chromosome 21 segment HS21 C046	Human DNA, SINE repetitive element	DKFZp434l066_r1 434 (synonym; htes3) Homo sapiens cDNA clone DKFZp434l066 5'	zn30d08.rl Stratagene neuroepithelium NT2RAMI 937234 Homo sepiens cDNA clone IMAGE.548943 5' similar to gb.1M14338 VITAMIN K-DEPENDENT PROTEIN S PRECURSOR (HUMAN);	2630ff0.r1 Stratagene colon (#937204) Homo saciens cDNA clone IMAGE:588427 5' similar to TR:G695374 G695374 THYROID RECEPTOR INTERACTOR;	2030f10.r1 Stratagene cdon (#837204) Homo sapiens cDNA clone IMAGE:588427 5' similar to TR:C695374 Gees374 THYROID RECEPTOR INTERACTOR:	601864963F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4083278 5'	QV2-PT0012-040400-124-e05 PT0012 Homo sapiens cDNA	QV2-PT0012-040400-124-e05 PT0012 Homo saplens cDNA	nn37405.s1 NCI_CGAP_GC5 Homo sepiens cDNA clone IMAGE:1088057 3' sImilar to contains OFR.t1 OFR repetitive element;	Homo sepiens chromosome 21 segment HS21C082	DKFZp566L171_s1 566 (synonym: hfkd2) Homo saplens cDNA clone DKFZp566L1713'	M.musculus mRNA for astrocytic phosphoprotein, PEA-15	Homo saplens DNA for amylold precursor protein, complete cds	to89a01.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2185416 3' similar to contains Alu	repetitive element, contains element with the recommendation of the recommendation of the recommendation of the recommendation of the recommendation of the recommendation of the recommendation of the recommendation of the recommendation of the recommendation of the recommendation of the recommendation of the recommendation of the recommendation of the recommendation of the recommendation of the recommendation of the recommendation of the recommendation of the recommendation of the recommendation of 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hfkd2) Homo sapiens cDNA clone DKFZp566C2146 5'	CHR220032 Chromosome 22 exon Homo sapiens cDNA clone C22_45 5'	UI-HF-BM0-edw-d-10-0-UI.r1 NIH_MGC_38 Homo sepiens cDNA clone IMAGE:3063210 5'
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Most Similar (Top) Hit BLAST E Value	5.0E-26	4.0E-26	4.0E-26	4.0E-26	3.0E-26 D14547.1	3.0E-26	3.0E-26	3.0E-26	305-26	3.0E-26	3.0E-26	3.0E-26	3.0E-26	2.0E-26	2.0E-26/	2.0E-26	2.0E-26	200	2.05-201	2.05-20,0	Z-20.2	2.0E-26	1.0E-26	1.0E-26	1.0E-26	1.0E-26	,	1.0E-26	1.0E-26
Expression Signal	0.89	3.29		1.38	1.25	,   	3.34	1.41	1.41	6.09	1.97	1.97	7.79	6.84	3.07	5.22	8.1	000	2.30	7.00	0/:	2.33	8.96	1.42	6.28	2.89	1.96	2.77	1.16
ORF SEQ ID NO:	27427		37613		28038			30035	30036	33521		38551	38591	26915		29499			27700				26398						
SEQ ID NO:	14366	22667			14946	15200	15228	17037	17037	1	ı	l		13882	15060	18477	24070			10/27	0/707	26088	13365			20208	24203		25763
Probe SEQ ID NO:	1204	9612	10897	11604	1797	2059	2088	3878	3878	7051	11867	11867	11902	669	1917	3303	10991		200	10/11	12388	12604	139	2105	2751	6980	11131	12655	13175
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Top Hit Descriptor	RC6-FN0138-110800-022-A02 FN0138 Homo sapiens cDNA	Homo sepiens MAGE-82 (MAGE-82), MAGE-83 (MAGE-83), MAGE-84 (MAGE-84), and MAGE-81 MAGE-81) nepes complete cris	THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CO	naausou/xi nci_cushrtz8 Homo septens cunva ctone tiwage:3233944 3 similar to contains unr.tt OFR repetitive element:	ASOCIAL A NO. COAD 1 and Hand aminor a DNA alone 1844 CE: 340 845 9, similar to contains THD NO	WASCULXTINCT COAPTILITY FIORIO SABISTIS COINA GIORE INALGE: 2400130 3 SITTIBLE LO COTRATAS LITTLES TARRESTED T THR readshive element:	Home caliane chamber 21 seamont HS21C027	and the second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second s	Buornooxi Schrieder Reta Danie Septemb Construction of the Construction of the Construction of Burnooxide (Charles of Burnooxide)	au87h08.x1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE.2783295 3' similær to gb:K00558	TUBULIN ALPHA-1 CHAIN (HUMAN);	PM2-SN0018-220300-002-807 SN0018 Homo sepiens cDNA	ADP, ATP CARRIER PROTEIN, LIVER ISOFORM T2 (ADP/ATP TRANSLOCASE 3) (ADENINE	NUCLEOTIDE TRANSLOCATOR 3) (ANT 3)	Homo sapiens WRN (WRN) gene, complete cds	AV732214 HTF Homo sapiens cDNA clone HTFBCB06 5'	MR4-BT0398-250800-204-d06 BT0398 Homo saplens cDNA	J1751F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA clone J1751 5' similar to	REPETITIVE ELEMENT L1	CM1-CT0316-091299-063-d07 CT0315 Homo saplens cDNA	CM1-CT0315-091299-063-d07 CT0315 Homo sapiens cDNA	Human endogenous retroviral element HC2	hi51h12.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2975879 3' sImilar to TR:O76040	O76040 ORF2: FUNCTION UNKNOWN.;	Human mRNA for KIAA0231 gene, partial cds	Homo sapiens Xq pseudoautosomal region; segment 1/2	Human nucleolar protein (B23) mRNA, complete cds	Homo saplens MAGE-B2 (MAGE-B2), MAGE-B3 (MAGE-B3), MAGE-B4 (MAGE-B4), and MAGE-B1	(MAGE-B1) genes, complete cds	Homo sapiens chromosome 21 segment HS21C103	602121491F1 NIH_MGC_56 Hamo saplens cDNA clone IMAGE:4278527 5'	602121491F1 NIH_MGC_56 Homo sapiens cDNA clane IMAGE:4278527 5	Mus musculus sperm tail associated protein (Stap), mRNA
Top Hit Database Source	EST_HUMAN	i i		EST HIMAN	T	NAMI LI TAR	T		EST_HUMAN	Г	EST HUMAN	EST_HUMAN	Π	ISSPROT	IN TN	EST_HUMAN /	EST HUMAN				HUMAN	Г		LHUMAN	NT TN	NT	TN		NT	INT		T_HUMAN	
Top Hit Acession No.	.0E-27 BF371227.1	05.27   103.163 1	1.00106.1	0E-27 RE44556 1		0E.07 AI834482 4	0.0E 27 A 460077 0	2. 122501.2	.0E-27 AW162737.1		8.0E-27 AW 162737.1	8.0E-27 AW864776.1		P12236	8.0E-27 AF181897.1	8.0E-27 AV732214.1	8.0E-27 BE926560.1		1.0E-27 N84970.1	3.0E-27 AW857579.1	3.0E-27 AW857579.1	Z70664.1		.0E-27 AW629172.1	7.0E-27 D86984.1	.0E-27 AJ271735.1	5.0E-27 M26697.1		6.0E-27 U93163.1	5.0E-27 AL163303.2	5.0E-27 BF686614.1	5.0E-27 BF666614.1	9910569 NT
Most Similar (Top) Hit BLAST E Value	9.0E-27	120 30 0		0 OF.27		0.00.07	2000	0.01-27	8.0E-27		8.0E-27	8.0E-27		8.0E-27 P12236	8.0E-27	8.0E-27	8.0E-27		8.0E-27	8.0E-27	8.0E-27	7.0E-27		7	7.0E-27	7.0E-27	6.0E-27			5.0E-27	5.0E-27		4.0E-27
Expression Signal	0.87	20.3	20.02	u.	3	20,	100	1.0	23.84		23.84	1.82			0.75		2.65		2.49	1.63	1.63	1.77		2.19	26.0	3.7	3.21		1.55	0.73	3.21		1.65
ORF SEQ ID NO:						26240			27678		27679					32308				36048	38049						37679		38781		37081		33444
SEQ ID NO:	20816	02760	П	2511B	1	42240		3	14801	L	14001	15369			16602	19002	18543			22484	ı	1		18322	22137	24067	1_						20035
Probe SEQ ID NO:	7277	Sign	See	12443	2	,		5	1448		1448	2236		3254	3434	5812	7117		7192	9410	9410	701		5201	8906	10988	10964		12094	7954	10442	10442	6883
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. Top Hit Descriptor	Homo sapiens chromosome 21 segment HS21C009	Rattus norvegicus putative four repeat ion channel mRNA, complete cds	QV0-OT0033-070300-162-b10 OT0033 Homo sapiens cDNA	H.sapiens DNA for endogenous retroviral like element	Homo sapiens chromosome 21 segment HS21C079	R.raitus RYA3 mRNA for a potential ligand-binding protein	PM0-BT0527-090100-001-d11 BT0527 Homo sapiens cDNA	7844C08 Chromosome 7 Fetal Brain cDNA Library Homo sapiens cDNA clone 7B44C08	601458531F1 NIH_MGC_66 Homo sapiens cDNA clane IMAGE:3862086 5	Homo sapiens alpha NAC mRNA, complete cds	nk01b10.s1 NCI_CGAP_P11 Homo sapiens cDNA clone IMAGE:1000699 similar to gb:M17886 60S ACIDIC RIBOSOMAL PROTEIN P1 (HUMAN);	hi51h12.x1 Scares_NPL_T_GBC_S1 Homo sepiens cDNA clone IMAGE:2975879 3' similar to TR:076040 078040 ORF2: FUNCTION UNKNOWN. ;	Homo sapiens jun dimertzation protein gene, partial cds; cfos gene, complete cds; and unknown gene	Home sapiens jun dimerization protein gene, partial cds; cfos gene, complete cds; and unknown gene	y35e01.11 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:150840 5' similar to	SP:HMGC_MOUSE Q02591 HOMEOBOX PROTEIN;	wi28g07.x1 NCI_CGAP_Ut1 Homo sapiens cDNA clone IMAGE:2426268 3'	rabogho5.s1 NCI_CGAP_Thy1 Homo sapiens cDNA done IMAGE:943737 similar to contains L1.t3 L1	R. rattus RYA3 mRNA for a potential ligand-binding protein	EST00738 Fetal brain, Stratagene (cat#936206) Homo sapiens cDNA done HFBCF07	EST00738 Fetal brain, Stratagene (cat#936206) Homo sapiens cDNA clone HFBCF07	AU121685 MAMMA1 Hamo sapiens cDNA clone MAMMA1000746 5'	nk01b10.c1 NCI_CGAP_Pr11 Home sapiens cDNA clone IMAGE:1000699 similar to gb:M17886 60S	ACIDIC RIBOSOMAL PROTEIN P1 (HUMAN);	Homo sapiens putative MTAP (MTAP) mRNA, partial cds, alternativaly spliced	Homo saptens chromosome 21 segment HS21C046	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes,	complete cas)	Homo sapiens Retina-derived POU-domain factor-1 (RPI-1), mKNA
Top Hit Database Source	TN	NT	EST_HUMAN	NT	NT	NT	EST_HUMAN	EST_HUMAN	EST_HUMAN	뉟	EST_HUMAN	EST HUMAN	F	Z		EST_HUMAN	EST_HUMAN	TOT LIMAN	LO L	EST HUMAN	EST_HUMAN	EST HUMAN		EST_HUMAN	TN	LN		z	LN S
Top Hit Acession No.	4.0E-27 AL163209.2	4.DE-27 AF078779.1	4.0E-27 AW880859.1	4.0E-27 X89211.1	4.0E-27 AL163279.2	3.0E-27 X60658.1	3.0E-27 BE071924.1	3.0E-27 AA077705.1	3.0E-27 BF035327.1	2.0E-27 AF054187.1	2.0E-27 AA565345.1	2.0E-27 AW629172.1	2.0E-27 AF111167.2	2 0E-27 AF111167 2		2.0E-27 H02655.1	2.0E-27 AI866347.1	205 27 00661527 4	2.0E-27 X60658 1	2.0E-27 M78590.1	2.0E-27 M78590.1	2.0E-27 AU121685.1		2.0E-27 AA565345.1	2.0E-27 AF216650.1	1.0E-27 AL163246.2		ABOZOSS	6005855 NT
Most Similar (Top) Hit BLAST E Value	4.0E-27	4.DE-27	4.0E-27	4.0E-27	4.0E-27	3.0E-27	3.0E-27	3.0E-27	3.0E-27	2.0E-27	2.0E-27	2.0E-27				2.0E-27	2.0E-27	2000	2.0E-27	2.0E-27	2.0E-27	2.0E-27		2.0E-27	2.0E-27	1.0E-27			1.0E-27
Expression Signal	0.98	1.31	0.61	2.62	1.17	7.1	1.55	6.81	3.49	9.28	24.24	13.34	1.45	1 45		0.79	1.17	C	0.83	1.45	1.45	3.61		6.43	1.64	2.34		4.97	6.51
ORF SEQ ID NO:			36577	38592			l	31641	ļ				29489			33373		L	36625						38791				33222
Exon SEQ ID NO:	21207	l	22984	ı	26080	15239	17529	18662	22771	13280	15087		1			19967	21364	l	1	1_	23276	L	<u> </u>	15087	26087	13645	<u> </u>		19833
Probe SEQ ID NO:	8125	8172	9945	11903	13213	2089	4386	5462	9505	42	1944	3178	3296	320F		6814	8282	8	9409	10241	10241	11197		11777	12107	449		1021	6674

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Single Exon Probes Expressed in Pracerita	Top Hit Descriptor	HSPD20461 HM3 Homo sapiens cDNA clone s4000095C10	HSPD20461 HM3 Homo sepiens cDNA clone s4000085C10	Homo sapiens mRNA for KIAA0454 protein, partial cds	RC6-BT0627-140200-011-E06 BT0627 Homo sapiens cDNA	Humen mRNA for KIAA0250 gene, partial cds	Bos taurus latrophilin 3 splice variant bbah mRNA, complete cds	hw/17c11.x1 NCI_CGAP_Lu24 Homo sapiens cDNA done IMAGE:3183188 3' similar to TR:Q07314 Q07314 SECRETED NEUREXIN III-ALPHA-C PRECURSOR. [3] TR:Q07280 TR:Q07313;	AU 126260 NT2RP1 Homo sapiens cDNA clone NT2RP 1000443 5'	zp18g12.s1 Stratagene fetal retina 937202 Homo saplens cDNA clone IMAGE:609862.3'	CM2-TN0140-070900-372-g01 TN0140 Homo saplens cDNA	au83h08.xf Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:27829113' similar to	AT 14.0000 COUNTY INFORMATION OF THE CONTROL OF THE INCOME.	HOUTSTON I WAR I THOUGH SQUEETS COUNTY WHITE I VENT I SOUNDER SOUNDER SOUNDER SALVEN WITHOUTS AN INTERNATIONAL STATE OF THE SALVEN SALVEN WITHOUTS AND THE SALVEN SALVEN SALVEN WITHOUTS AND THE SALVEN SALVEN SALVEN SALVEN SALVEN SALVEN SALVEN SALVEN SALVEN SALVEN SALVEN SALVEN SALVEN SALVEN SALVEN SALVEN SALVEN SALVEN SALVEN SALVEN SALVEN SALVEN SALVEN SALVEN SALVEN SALVEN SALVEN SALVEN SALVEN SALVEN SALVEN SALVEN SALVEN SALVEN SALVEN SALVEN SALVEN SALVEN SALVEN SALVEN SALVEN SALVEN SALVEN SALVEN SALVEN SALVEN SALVEN SALVEN SALVEN SALVEN SALVEN SALVEN SALVEN SALVEN SALVEN SALVEN SALVEN SALVEN SALVEN SALVEN SALVEN SALVEN SALVEN SALVEN SALVEN SALVEN SALVEN SALVEN SALVEN SALVEN SALVEN SALVEN SALVEN SALVEN SALVEN SALVEN SALVEN SALVEN SALVEN SALVEN SALVEN SALVEN SALVEN SALVEN SALVEN SALVEN SALVEN SALVEN SALVEN SALVEN SALVEN SALVEN SALVEN SALVEN SALVEN SALVEN SALVEN SALVEN SALVEN SALVEN SALVEN SALVEN SALVEN SALVEN SALVEN SALVEN SALVEN SALVEN SALVEN SALVEN SALVEN SALVEN SALVEN SALVEN SALVEN 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deplete and the deplete and the deplete and the deplete and the deplete and the deplete and the depl	AV73548 CB Homo sepiens cDNA clone CBFAKA12 5	Homo sapiens zinc finger protein ZNF191 (ZNF191) gene, complete cds	ea60e03.71 NCI_CGAP_CGB1 Homo sepiens cDNA clone IMAGE:825340 5' similar to contains Alu repositive element:	Mod 18-07 vt NCI CGAD Pand Home saniers c DNA clone INA GF-2455692 3' similar to contains THB b1	THR repetitive element;	y/89f10.r1 Soares placenta No2HP Homo sapiens cDNA clone IMAGE:146443 5'	xn33c09.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE::2895504 3' similar to SW:GG95_HUMAN Q08379 GOLGIN-95. ;	601300703F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3635305 5	qf66f10.x1 Sogres_tests_NHT Homo sapiens cDNA clone IMAGE:1755019 3' similar to gb:M19503 LINE-1 REVERSE TRANSCRIPTASE HOMOLOG (HUMAN);	Homo sapiens chromosome 9 duplication of the T cell receptor beta locus and trypsinogen gene families	Felic catus GAPDH mRNA for glyceraldehyde-3-phosphate dehydrogenase, complete cds	qf89f10.x1 Soares_lestis_NHT Homo sapiens cDNA clone IMAGE:1755019 3' similar to gb:M19503 LINE-1 REVERSE TRANSCRIPTASE HOMOLOG (HUMAN);	RC3-CT0254-240400-210-f12 CT0264 Homo saplens cDNA	RC0-CT0379-070100-031-h01 CT0379 Homo sapiens cDNA
e Exon Pione	Top Hit Database Source	EST_HUMAN	EST_HUMAN	M	<b>EST_HUMAN</b>	LN.	IN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	MAAN ILI TOO	TOT TOTAL	EST TOWAR	ı۱	EST_HUMAN	N	ENT LIMAN	NONO! - ION	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST HUMAN	ž	N L	EST_HUMAN	EST_HUMAN	EST_HUMAN
טוונט	Top Hit Acession No.	1.0E-27 F30158.1	1.0E-27 F30158.1	1.0E-27 AB007923.1	1.0E-27 BE079780.1	1.0E-27 D87449.1	1.0E-27 AF111093.1	9.0E-28 BE348399.1	9.0E-28 AU126260.1	9.0E-28 AA174078.1	9.0E-28 BF377859.1	0 OE 00 NM 457574 4	1.1.707CL VA	7.0E-28 AU142/50.1	111009/1411	7.0E-28 AV735348.1	6.0E-28 AF016052.1	8 OE 20 A A E O 4 E E 2 1	1.00400	5.0E-28 Al921003.1	5.0E-28 R79762.1	4.0E-28 AW 195066.1	4.0E-28 BE409100.1	4.0E-28 AI198941.1	4.0E-28 AF029308.1	4.0E-28 AB038241.1	4.0E-28 AI198941.1	4.0E-28 AW854244.1	4.0E-28 AW862350.1
	Most Similar (Top) Hit BLAST E Value	1.0E-27	1.0E-27	1.0E-27	1.0E-27	1.0E-27	1.0E-27	9.0E-28	9.0E-28	9.0E-28	9.0E-28	20	0.05-20	7.05-78	/.ue-28	7.0E-28	6.0E-28	00 10	0.05-20	5.0E-28	5.0E-28	4.0E-28	4.0E-28	4.0E-28	4.0E-28	4.0E-28	4.0E-28	4.0E-28	4.0E-28
	Expression Signal	1.65	1.65	1.16	1.69	2.65	3.05	2.26	2.17	0.47	3.04	06.53	13.38	11.0	60.	5.04	1.28	8	76:0	2.75	38.94	1.46	1.34	3,56	4.19	14.89	4.34	1.7	1.62
	ORF SEQ ID NO:	33566	33567	35430		36551	İ		١	37243			207.20	27430	38192						30269	28926			l _		34030		
	Exon SEQ ID NO:	20146	l	21888		22963	24990	13368	13535	23636	25173	1	1	- 1	74377	25141	22198		11007	13542	17270	15809	16352	Į.	1.		<u> </u>	1	26069
	Probe SEQ ID NO:	7010	7010	8803	9186	8923	12005	4	321	10601	12224	4.000	COC71	1208	1403	12181	9119	12000	2007	328	4116	2689	3177	7483	11105	11255	11278	12622	12773

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Top Hit Descriptor	Homo sapiens metalloprotease-Ike, disintegrin-like, cystelne-rich protein 2 epsilon (ADAM22) mRNA, complete ods	Homo sapiens T cell receptor beta locus, TCRBV7S3A2 to TCRBV12S2 region	MR3-HT0713-280500-013-f09 HT0713 Homo sapiens cDNA	Homo sapiens MHC class 1 region	wj98f07x1 NCI_CGAP_Lym12 Homo sapiens cDNA clone IMAGE:2410885 3' similar to contains Alu	repetitive element; contains element rick repetitive element;	KCZ-B 1004z-Z10Z0C-115-105 B 1004Z nomo sapens	Homo sapiens low density ilpoprotein-related protein 2 (LRP2), mRNA	Homo saplens fow density lipoprotein-related protein 2 (LRP2), mRNA	RC1-BT0254-220300-019-c05 BT0254 Homo saplens cDNA	Homo sapiens ITGB4 gene for integrin beta 4 subunit, exons 3-41	qo35b06.x1 NCI_CGAP_Lu6 Homo sapiens oDNA clone IMAGE:1910483 3' similar to contains L1.b2 L1	repetitive element;	Homo saplens chronosome 21 segment HS21C009	hr76c03.x1 NCI_CGAP_Kld11 Homo sapiens cDNA done IMAGE:3134404 3' similar to contains LOR1.b1	LOK1 repetitive element :	601814186F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4048751 5	Sus scrofa domestica submaxillary apomucin mRNA, complete cds	EST384394 MAGE resequences, MAGL Homo sapiens cDNA	Homo sapiens mannosidase, beta A, Iysosomai (MANBA) gene, and ublquitin-conjugating enzyme E2D 3	(UBE2D3) genes, complete cds	1,79c09.r1 Soares Infant brain 1NIB Homo sapiens cDNA clone IMAGE:44300 5	Human gene for Ah-receptor, exon 7-9	QV1-BT0821-120900-360-b03 BT0821 Homo saplens cDNA	Human zinc finger protein ZNF131 mRNA, partial cds	Homo sapiens similar to ribosomal protein L12 (H. sapiens) (LOC63091), mRNA	Homo sapiens hypothetical protein FLJ10968 (FLJ10968), mRNA	EST179615 HCC cell line (matastasis to liver in mouse) II Homo sapiens cDNA 5' end similar to similar to	retrovital LTR	Homo sapiens gamma-glutamyltransferase-like activity 1 (GGTLA1), mRNA	Homo sapiens gamma-glutamyltransferase-like activity 1 (GGTLA1), mRNA	251c01.r1 Soares retina N2b4HR Homo sepiens cDNA clone IMAGE:380448 5	Homo saplens chromosome 21 segment HS21C047
Top Hit Database Source	Į.	IN	T_HUMAN	N	Г	╗	ESI HOMAN	NT	IN	EST_HUMAN	FZ		EST_HUMAN	NT		EST_HUMAN	EST_HUMAN	INT	EST_HUMAN			EST HUMAN		EST_HUMAN	NT	N	Į.		EST_HUMAN	F	TN	EST_HUMAN	NT
Top Hit Acessian No.	3.0E-28 AF165382.1	3.0E-28 AF009660.1				3.0E-28 AI831991.1	3.0E-28 BE082801.1	11430460	11430460 NT	2.0E-28 BE062167.1	711107.3		2.0E-28 AI348634.1	2.0E-28 AL163209.2				.0E-28 AF005273.1	2.0E-28 AW972305.1		.1	2.0E-28 H06376.1	.0E-28 D38044.1	.0E-28 BF333236.1	.0E-28 U09410.1	11429885 NT	8922793 NT		.0E-28 AA308744.1	4758431 NT	4758431 NT		.0E-28 AL163247.2
Most Similar (Top) Hit BLAST E Value	3.0E-28	3.0E-28	3.0E-28	3.0E-28		١	ļ				2.0E-28 Y11107.3		2.0E-28	2.0E-28		2.0E-28	2.0E-28	2.0E-28	2.0E-28					-	-	ľ	ľ		_	1.0E-28	1.0E-28	١	
Expression Signal	2.29	46.0	2.28	2.09		3.77	3.29	1.22	1.22	12.79	9.24			18.0		1.48	3	0.93	2.23		2.52	1.74			0.95	1,95	3.03		4.75	5.91		99'.	4.56
ORF SEQ ID NO:				37878						26354				2963		32968		34837			38603		27744	28560					36099		36721		
Exon SEQ ID NO:	14468	Ľ	22106		ľ	-1	- 1		ı	13326	14353	l	i	16614			19627	١.	١.		24900	25424	14661	1	ı	L	1		22535		_	li	lł
Probe SEQ ID NO:	1312	5227	9027	11176		12653	12803	12865	12865	9	1191		2546	3446		6437	6460	8234	9783		11913	12631	1508	2294	4691	8044	8208		9478	10080	10080	12186	13013

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Top Hit Descriptor	hi76g06.xf Scares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:29782663'	HYPOTHETICAL GENE 50 PROTEIN	EST378521 MAGE resequences, MAGI Hamo sapiens cDNA	Reftus norvegicus mRNA for 45 kDa secretory protein, partial	wp69b01.x1 NCI_CGAP_Bm25 Homo sapiens cDNA clone INAGE:2466985 3' sImitar to TR:015475 015475 UNNAMED HERV-H PROTEIN ;contains LTR7.b1 LTR7 repetitive element;	RC3-UT0062-210800-021-c05 UT0062 Homo sapiens cDNA	602184092F1 NIH_MGC_42 Homo sapiens cDNA clone IMAGE:4300079 6'	Hamo septens chromosome 21 segment HS210003	RC3-010091-170300-011-c12 OT0091 Hamo saplens cDNA	601451827F1 NIH_MGC_65 Homo saplens cDNA clone IMAGE:3855726 5	cn15c02.x1 Normal Human Trabecular Bone Cells Homo expient cDNA clone NHTBC_cn15c02 random	QV1-HT0471-280300-121-805 HT0471 Homo sapiens cDNA	wd35g06.x1 Sceres_NFL_T_GBC_S1 Home saplens cDNA clone IMAGE:2330170 3' similar to contains	MEKZ9 IZ MEKZ9 repetitive element;	wd35g06.x/i Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2330170 3' simitar to contains MER29.t2 MER29 repetitive element;	Human 90 kD heat shock protein gene, complete cds	Homo saplens PTS gene for 5-pyruvoyltetrahydropterin synthase, complete cds	QV1-BT0821-120900-360-b03 BT0821 Homo saplens cDNA	601152657F1 NIH_MGC_19 Hamo sapiens cDNA clone IMAGE:3508527 5	Human gene for Ah-receptor, exon 7-9	xv17f03.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2813405 3' similar to contains Alu repetitive element; contains MER19.t2 MER19 repetitive element;	Homo sapiens chromosome 21 segment HS21C046	htt0g01.x1 NCI_CGAP_Kid13 Homo saplens cDNA clone IMAGE:3146256 3' similar to contains MER29.b3 MER29 repetitive element;	#62b01.r1 Soares_tests_NHT Homo sapiens cDNA clone IMAGE:726889 5' similar to TR:G1335769	G1335769 GAG-POL POLYPROTEIN.;	Human Hst IM15 mRNA for Hst Im15, complete cds	Human HsLIM15 mRNA for HsLim15, complete cds	Homo sapiens envelope protein RIC-6 (env) gene, complete cds	Homo sapiens envelope protein RIC-6 (env) gene, complete cds
Top Hit Database Source	EST_HUMAN	SWISSPROT	EST_HUMAN	LN	EST_HUMAN	EST_HUMAN	EST_HUMAN	NT	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN		EST HUMAN	EST_HUMAN	F	TN	EST HUMAN	EST_HUMAN	N	EST HUMAN	N	EST HUMAN	1	<b>EST_HUMAN</b>	TN	TN	INT	TN
Top Hit Acession	9.0E-29 AW663987.1	200130	.0E-29 AW966447.1	.0E-29 AJ132352.1	6.0E-29 Al936748.1	6.0E-29 BE940436.1	6.0E-29 BF568097.1	5.0E-29 AL163203.2	5.0E-29 AW887541.1	5.0E-29 BE61 2449.1	4.0E-29 Al752387.1	4.0E-29 BE164930.1		4.0E-29 AI678101.1	J.0E-29 AI678101.1		1.1	3.0E-29 BF333236.1	3.0E-29 BE314018.1	.0E-29 D38044.1	.0E-29 AW303317.1	.0E-29 AL163246.2	0E-29 BE350127 1		3.0E-29 AA403053.1	3.0E-29 D63882.1	3.0E-29 D63882.1	2.0E-29 AF084869.1	2.0E-29 AF084869.1
Most Similar (Top) Hit BLAST E Value	9.0E-29	8.0E-29 Q00130	7.0E-29	7.0E-29	6.0E-29	6.0E-29	6.0E-29	5.0E-29	5.0E-29	5.0E-29	4.0E-29	4.0E-29		4.0E-29	4.0E-29	4.0E-29 J04988.1	3.0E-29	3.0E-29	3.0E-29	3.0E-29	3.0E-29	<u>۳</u>					ľ	Ľ	
Expression Signal	1.8	2.57	1.98	9.03	6.9	5.19	2.1	2.39	8.35	1.49	2.28	7.06		0.64	0.54	3.59	1.31	1.1	0.83	3.23	122	1.49	8			1.36	8	0.98	
ORF SEQ ID NO:	31543		27870		26817					- 				34870		35563				l	ļ				38278		-	26727	
Exon SEQ ID NO:	26122	1	L	25779		1	1	1	22008	L_		19312		21354	21354	L	1	1	1	1		L	l	_l_	24602	١.		L	L
Probe SEQ ID NO:	13135	12752	1632	13197	909	12495	12587	5113	8929	12795	3304	6133		8272	8272	8944	4536	4855	6053	8931	050	9731	10484	5	11546	12385	13092	505	505

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Top Hit Descriptor	wr65d10.x1 NCI_CGAP_Ut1 Homo sapiens cDNA clone IMAGE:2492563 3' similar to TR:O15546 O15546 HERV-E ENVELOPE GLYCOPROTEIN ;	wr65d10.x1 NCI_CGAP_Ut1 Homo sapiens cDNA clone IMAGE:2492563 3' similar to TR:015546 015546 HERV-E ENVELOPE GLYCOPROTEIN ;	H.sapiens mRNA for laminin-5, alpha3b chain	H.sapiens mRNA for laminin-5, alpha3b chain	Homo sapiens chromosome 21 segment HS21C068	os71e04.x1 NCL_CGAPGC2 Homo sapiens cDNA clone IMAGE:1610814 3' similar to contains L1.t2 L1 repetitive element;	wf27g07.x1 Sogres_NFL_T_GBC_S1 Homo saplens cDNA clone IMAGE:2356860 3' simitar to contains element MER8 repetitive element ;	wf27g07.x1 Soeres_NFL_T_GBC_S1 Homo sepiens cDNA clone IMAGE:2356860 3' similær to contains releases the repetitive element:	GOLDON MILE OF LAND CONTROL STREET OF HOME STREET AND ACTION IMAGE: 3846648 5	Homo sapiens DNA-binding protein (LOC36242), mRNA	Homo saplens DNA-binding protein (LOC56242). mRNA	Homo sapiens chromosome 21 segment HS210048	Homo sapiens chromosome 21 segment HS21C048	Homo sapiens chromosome 21 segment HS21C048	Hamo sapiens chromosame 21 segment HS21C048	Homo sapiens splicing factor similar to dnaJ (SPF31), mRNA	RC1-HN0003-220300-021-b04 HN0003 Homo sapiens cDNA	R.ratus RYA3 mRNA for a potential ligand-binding protein	rz20c07.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1288332 3' similar to contains MER4.b1 MER4 repetitive element;	Homo sapiens zinc/iron regulated transporter-like (ZIRTL), mRNA	HSC23F051 normalized infant brain cDNA Homo sapiens cDNA clone c-23f05	EST97317 Thymus I Homo sapiens cDINA 5' end similar to EST containing O family repeat	PT2.1_13_B11.r tumor2 Homo saplens cDNA 3'	PM4-BT0724-150400-004-d11 BT0724 Homo saplens cDNA	Human mRNA for integrin alpha subunit, complete cds	QV0-BN0147-290400-214-f12 BN0147 Homo sapiens cDNA	QV0-BN0147-290400-214-12 BN0147 Homo saplens cDNA	Homo sapiens CTCL tumor antigen se20-10 mRNA, partial cds
Top Hit Database Source	EST_HUMAN	T_HUMAN		LN T	LN	EST_HUMAN	EST_HUMAN		Т	NOW CHI					LΝ		T HUMAN	N⊤	EST HUMAN		EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	N	EST_HUMAN	T HUMAN	Į,
Top Hit Acession No.	0E-29 Al963604.1	A1963604.1	X84900.1	2.0E-29 X84900.1	0E-29 AL163268.2	2.0E-29 Al082459.1	2.0E-29 AI806418.1	A 1006419 4	AIOUC410.1	10567821 NT	10567824 NT	2.0E-29 AL163248.2	AL163248.2	AL163248.2	AL163248.2	11425108 NT			9.0E-30 AA781215.1	11422745 NT	F08688.1	8.0E-30 AA383873.1	A1557072.1	BE091133.1	D25303.1	6.0E-30 BE008026.1	6.0E-30 BE008026.1	AF177227.1
Most Similar (Top) Hit BLAST E Value	2.0E-29	2.0E-29	2.0E-29	2.0E-29	2.0E-29	2.0E-29	2.0E-29	200	2.0E-20	2 OF-20	2 OE-30	2.0E-29	2.0E-29	2.0E-29	2.0E-29	2.0E-29	1.0E-29	1.0E-29	9.0E-30	9.0E-30	8.0E-30	8.0E-30	8.0E-30	7.0E-30	6.0E-30	6.0E-30	6.0E-30	6.0E-30
Expression	7.8	7.8	2.31	2.31	2.65	0.78	1.49	2	1.46	- 6	80	2.76	2.76	3.65	3.65	1.67	8.27	2.81	3.53	4.55	10.5	226	2.79	1.07	1.57	3.15	1.02	0.76
ORF SEQ ID NO:	27794	27795	28024	28025	30516	32446		2000	32835	35308	25300	36327	36328	37084				37503	33261			35076			١_		29450	
Exon SEQ ID NO:	14716	14718	14931	L	17537	19132	1	1	19481	21856	21858		L.	L			22071	23883			<u>L</u>	١.	1	L	14963	1_		23793
Probe SEQ ID NO:	1563	1563	1782	1782	4394	5946	6089	7700	75//	8777	77778	9708	9708	10444	10444	11767	8992	10850	6712	12266	6449	8465	8882	1645	1814	3259	4881	10760

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Top Hit Descriptor	Human lambda-immunoglobulin constant region complex (germline)	tg92g03.x1 NOLCGAP_CL1 Homo saplens cDNA clone IMAGE:2116276 3' similar to contains Alu repetitive element;	Human aconitate hydratase (ACO2) gene, exon 7	Homo sapiens chromosome 21 segment HS21C078	Homo saplens chromosome 21 segment HS21C010	Homo saplens chromosome 21 segment HS21C010	QV3-DT0043-090200-080-c06 DT0043 Homo saplens cDNA	QV3-DT0043-090200-080-c06 DT0043 Homo saplens cDNA	CM1-ST0181-091199-035-f08 ST0181 Hamo sepiens cDNA	qq93c05.x1 Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA,cione IMAGE:1938920 3 similar to contains MER29.b2 MER29 repetitive element;	Hamo sapiens telomerase reverse transcriptase (TERT) gene, exons 1-6	Rattus norvegicus putative four repeat Ion channel mRNA, complete cds	Rattus norvegicus putative four repeat ion channel mRNA, complete cds	ht09g01.x1 NCI_CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3146256 3' similar to contains MER29.b3	WIENZE SEPONDE GENERAL	TRANSCRIPTION FACTOR AP-2	CM0-CT0307-310100-188-hd3 C10307 Homo sapiens CUNA	HSC23F051 normalized intent brain dDNA Homo saptens cDNA clone c-23r05	RC5-HT0582-110400-013-H08 HT0582 Homo sapiens cDNA	IL2-NT0101-280700-116-E04 NT0101 Homo saplens cDNA	Homo sapiens Y-linked zinc finger protein (ZFY) gene, complete cds	UI-H-BI1-afo-c-12-0-UI.s1 NCI_CGAP_Sub3 Homo saplens cDNA clone IMAGE:2/22558 3		П	C18639 Human placenta cDNA (TFullwara) Homo sapiens cDNA clone GEN-5/0001 5	7-637-612.x1 NCI_CGAP_Lu24 Homo sapiens cDNA cions IMAGE:3284692.3' similar to SW:DHSA_HUMAN P31040 SUCCINATE DEHYDROGENASE [UBIQUINONE] FLAYOPROTEIN SUBUNIT PRECURSOR;		П	ES1383657 MAGE resequences, MAGE Homo sapiens cuiva
Top Hit Database Source	TN	EST_HUMAN	Ν	LN L	ΝΤ	IN	EST HUMAN	EST_HUMAN	EST_HUMAN	EST HUMAN	Ę	¥	TN	100	ESI HUMAIN	SWISSPROT	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST HUMAN	TN	EST_HUMAN	EST HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN		EST_HUMAN	EST HUMAN
Top Hit Acession No.	6.0E-30 X51755.1	6.0E-30 Al399992.1	5.0E-30 U87931.1	5.0E-30 AL163278.2	5.0E-30 AL163210.2	5.0E-30 AL163210.2	4.0E-30 AW937471.1	4.0E-30 AW937471.1	4.0E-30 AW812488.1	3.DE-30 Al338551.1	3.0E-30 AF128893.1	3.0E-30 AF078779.1	3.0E-30 AF078779.1		3.0E-30 BE350127.1	P34056	2.0E-30 AW857315.1	2.0E-30 F08688.1	2.0E-30 BE175877.1	2.0E-30 BE765232.1	2.0E-30 AF114156.1	2.0E-30 AW 206581.1	2.0E-30 BE298945.1	2.0E-30 BE298945.1	2.0E-30 C18939.1	2.0E-30 BE670617.1		2.0E-30 BE670617.1	AW971568.1
Most Similar (Top) Hit BLAST E Value	6.0E-30	5.0E-30	5.0E-30	5.0E-30	5.0E-30	5.0E-30	4.0E-30	4.0E-30	4.0E-30	3.0E-30	3.0E-30	3.0E-30	3.0E-30		3.0E-30	3.0E-30 P34056	2.0E-30	2.0E-30		2.0E-30				2.0E-30			ĺ	[	
Expression Signal	1.75	43.22	5.79	2.12	2.76	2.76	2.38	2.38	1.65	4.56	1,15	0.53	0.45		0.74	1.52	1.42	2.53	5.5	9.93	6.83	1.95	2.02	2.02	4.69	1.7.1		1.71	3.78
ORF SEQ ID NO:		30274	L			38149		28471			30013				Ī	38211	26908		27745						35349	35452			36828
Exon SEQ ID NO:	18485	17276	25928	L		L				14338	┸	1		1		24541	13875	14273	L	15895	16162	L.	18030	18030	21814	21915	l		23238
Probe SEQ ID NO:	13161	4121	5353	11126	11423	11423	2210	2210	9106	1175	3853	8138	8683		10649	11482	692	1108	1509	2772	2986	3889	4900	4900	8734	8836		8836	10201

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Table 4
Single Exon Probes Expressed in Placenta

						_	7	<u>.</u>	7	_			7	4	L	_	$\neg$		Πİ	<u>.</u>	٦	$\neg$	_		Ť	Ĩ	<u></u>	<u></u>	ΞĨ
Top Hit Descriptor	ha33d06.x1 NCI_CGAP_Kid12 Homo sepiens cDNA clone IMAGE:2875499 3' similær to contains THR.b3 THR repetitive element ;	C18939 Human placenta cDNA (TFujiwara) Homo sapiens cDNA clone GEN-570C01 5'	hd30b04.x1 Soares_NFL_T_GBC_S1 Homo sepiens cDNA clone IMAGE:2910991 3' similar to contains  MER1.t3 MER1 tapetitive element;	Homo sapiens chromosome 21 segment HS21 C003	ac77b08.s1 Stratagene lung (#937210) Homo sapiens cDNA clone IMAGE:868599 3'	602022560F1 NCI_CGAP_Brn67 Homo sapiens cDNA done IMAGE:4157891 5'	EST186868 HCC cell line (matastasis to liver in mouse) II Homo sapiens cDNA 5' end	601809932F1 NIH_MGC_18 Homo sapiens cDNA clone IMAGE:4040694 5	MR0-BT0249-091299-101-g01 BT0249 Homo saplens cDNA	EST11698 Uterus Homo sapiens cDNA 5' end	CHR220532 Chromosome 22 excn Homo capiens cDNA clone C22_728 5	yc65e06.r1 Stratagene liver (#937224) Homo sapiens cDNA clone IMAGE:85570 5'	yc65e06.r1 Stratagene liver (#937224) Homo saplens cDNA clone IMAGE:85570 5'	y99b08.rf Sogres infent brain 1NIB Homo sapiens cDNA clone IMAGE:30566 5' similar to gb:X12953 RAS- RELATED PROTEIN RAB-2 (HUMAN):	v/99b08.rl Spares infant brain 1NIB Homo sapiens cDNA clone IMAGE:30566 5' similar to qb;X12953 RAS-	RELATED PROTEIN RAB-2 (HUMAN);	HSC05F032 normalized Infant brain cDNA Homo sapiens cDNA clone c-05f03 3'	Rattus norvegicus putative four repeat ion channel mRNA, complete cds	Mus musculus syndecan 4 (Sdc4), mRNA	Homo sapiens hypothetical protein FLJ20420 (FLJ20420), mRNA	Homo sapiens chromosome 21 segment HS21 C008	EST84555 Colon adenocarcinoma IV Homo sapiens cDNA 5' end	hw05a11.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3182012.3'	[hw05a11.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3182012.3'	Homo sapiens V1-vascular vascpressin receptor AVPR1A gene, promoter region and partial cds	Homo sapiens V1-vascular vasopressin receptor AVPR1A gene, promoter region and partial cds	601304125F1 NIH_MGC_21 Homo sepiens cDNA clane IMAGE:3638310 5'	Homo septens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spilced	Homo sapiens MHC class 1 region
Top Hit Database Source	EST_HUMAN	EST HUMAN	EST HUMAN	NT	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST HUMAN		EST_HUMAN	EST_HUMAN	NT	LΝ	LN	ΝΤ	EST HUMAN	EST_HUMAN	<b>EST_HUMAN</b>	IN	IN	EST HUMAN	LN	NT
Top Hit Acesslon No.	E-30 AW 470791.1	DE-30 C18939.1	E-30 AW 468897.1			1.0E-30 BF347728.1	DE-30 AA315045.1	DE-30 BF183230.1	DE-30 BE061586.1	DE-30 AA299211.1	0E-30 H55593.1	E-31 T73025.1	DE-31 T73025.1	DE-31 R18214 1		0E-31 R18214.1	9.0E-31 Z38293.1	9.0E-31 AF078779.1	6755441 NT	TN 6853389 NT	0E-31 AL163208.2	0E-31 AA372637.1	0E-31 BE326517.1	0E-31 BE326517.1	0E-31 AF208541.1	0E-31 AF208541.1	.0E-31 BE408611.1	6.0E-31 AF223391.1	6.0E-31 AF055066.1
Most Similar (Top) Hit BLAST E Value	2.0E-30	1.05-30	1.0E-30	1.0E-30	1.0E-30	1.0E-30	1.0E-30	1.0E-30	1.0E-30	1.0E-30	1.0E-30		9.0E-31	9 OF-31		9.0E-31	9.0E-31	9.0E-31	9.0E-31	8.0E-31	8.0E-31	7.0E-31	7.0E-31	7.0E-31	4	7.	7		
Expression Signal	6.31	10.87	1.62	5.15	11.56	2.15	0.91	1.96	0.49	1.57	5.31	0.8	0.8	88.0		0.88	1.99	0.65	1.29	2.52	7.93	1.59	2.1	2.1	1.02	1.02	1.03	3.42	1.39
ORF SEQ ID NO:	36924	26548	26769					34460	34780			30020		36135		35136		35445		27325			28962	28963	_	35213			
Exon SEQ ID NO:	23322	13514	13744	13916	15418	15658	16296	20953	21268	26117	26025	17022	17022	24600		21600	21904	21908	25776	14267	15611	13911	15850	15850	21676	21676	_	16930	1 1
Probe SEQ ID NO:	10287	782	55.1	734	2286	2533	3120	7901	8176	12786	12937	3862	3862	8510	3	8519	8825	8827	13193	1102	2484	728	2733	2733	8595	8595	94686	3769	8347

Page 269 of 550 Table 4 Single Exon Probes Expressed in Placenta

		1	٦	٦	٦	Т		٦			Т	Т	T	Т	Т	T	7		П	٦	٦	П	٦	٦	Т		П		7
Top Hit Descriptor	ht09g01.x1 NCI_CGAP_Kld13 Homo sapiens cDNA clone IMAGE:3146256 3' similar to contains MER29.b3 MER29 repetitive element ;	AU119105 HEMBA1 Homo sapiens cDNA clone HEMBA1005050 5'	RC5-BT0377-091289-031-D12 BT0377 Homo sapiens cDNA	601433087F1 NIH_MGC_72 Homo saplens cDNA clone IMAGE:3918524 5'	Ното sapiens type I DNA topotsomerase gene, exch 8	Homo sapiens type I DNA topolsomerase gene, exon 8	7ko6f04.x1 NC_CGAP_GC6 Homo sapiens cDNA clone IMAGE:3443479 3' similar to TR:Q13537 Q13537 SIMILAR TO POGO ELEMENT ; contains L1.t1 L1 repetitive element ;	Homo sapiens Xq pseudoautosomal region; segment 1/2	POLYPEPTIDE N-ACETYLGALACTOSAMINYLTRANSFERASE (PROTEIN-UDP	ACETYLGALACTOSAMINYLIRANSFERASE) (UDP-GALNAC:POLYPEPTIDE, N- ACETYLGALACTOSAMINYLTRANSFERASE) (GALNAC-T1)	Homo saniene chromosome 21 segment HS21C080	I many deposits of the commence of the commence of the commence of the commence of the commence of the commence of the commence of the commence of the commence of the commence of the commence of the commence of the commence of the commence of the commence of the commence of the commence of the commence of the commence of the commence of the commence of the commence of the commence of the commence of the commence of the commence of the commence of the commence of the commence of the commence of the commence of the commence of the commence of the commence of the commence of the commence of the commence of the commence of the commence of the commence of the commence of the commence of the commence of the commence of the commence of the commence of the commence of the commence of the commence of the commence of the commence of the commence of the commence of the commence of the commence of the commence of the commence of the commence of the commence of the commence of the commence of the commence of the commence of the commence of the commence of the commence of the commence of the commence of the commence of the commence of the commence of the commence of the commence of the commence of the commence of the commence of the commence of the commence of the commence of the commence of the commence of the commence of the commence of the commence of the commence of the commence of the commence of the commence of the commence of the commence of the commence of the commence of the commence of the commence of the commence of the commence of the commence of the commence of the commence of the commence of the commence of the commence of the commence of the commence of the commence of the commence of the commence of the commence of the commence of the commence of the commence of the commence of the commence of the commence of the commence of the commence of the commence of the commence of the commence of the commence of the commence of the commence of the commence of the commence of the commence of the commence of the commenc	Homo saparis SE I donain and manner daisposase rusioni garie (SE IVIVA)	Rettus norvegicus GTP-binding protein REM2 (Rem2) mRNA, complete cds	Homo sapiens KIAA0569 gene product (KIAA0569), mRNA	Homo sapiens gene for ectivin receptor type IIB, complete cds	Homo sapiens SEC63, endoplesmic reticulum translocon component (S. cerevistae) like (SEC63L), mRNA	Homo sapiens NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 8 (19KD, ASHI) (NDUFB8) mRNA	Homo sapiens hypothetical protein FLJ10842 (FLJ10842), mRNA	Homo sapiens chranosame 21 segment HS21006	Horse mRNA for ferritin L-chain, complete cds	zu06d04.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:731047 5	40S RIBOSOMAL PROTEIN \$15 (RIG PROTEIN)	601458531F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3862086 5	QV2-LT0051-280300-111-f03 LT0051 Homo sapiens cDNA	tg44g05.x1 Soares_NFL_T_GBC_S1 Homo capiens cDNA clone IMAGE:21116723'	DKFZp761G1513_r1 761 (synonym: hamy2) Homo sapiens cDNA clone DKFZp761G1513 5	aa8811.s1 Stratagene fetal retina 937202 Homo sapiens cDNA clone IMAGE:838413 3' similar to contains THR:t2 THR repetitive element;	UI-H-BI3-akb-f-09-0-UI,s1 NCI_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2733833 3'
Top Hit Database Source	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	TN	NT	EST_HUMAN	TN		TOGGGGIMIO	- CA - CA - CA - CA - CA - CA - CA - CA	- I	12	Ę	NT	F	LΝ	NT.	Ā	١	L <sub>N</sub>	EST_HUMAN	SWISSPROT	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN
Top Hit Acessian No.	6.0E-31 BE350127.1	6.0E-31 AU119105.1	6.0E-31 AW372868.1	6.0E-31 BE894488.1	/60694.1	M60694.1	6.0E-31 BF056540.1	4.0E-31 AJ271735.1		740473	10473	4.0E-31 AL 1032CU.Z	5730038 NT	4.0E-31 AF084464.1	11430273 NT	4.0E-31 AB008681.1	6005871 NT	4826853 NT	11420329 NT	3.0E-31 AL 163208.2	514523.1	3.0E-31 AA421242.1	211174	3.0E-31 BF035327.1	2.0E-31 AW 838171.1	2.0E-31 Al39338B.1	2.0E-31 AL119245.1	2.0E-31 AA458824.1	2.0E-31 AW444496.1
Most Similar (Top) Hit BLAST E Value	6.0E-31	6.0E-31	6.0E-31	6.0E-31	5.0E-31 M60694.1	5.0E-31 M50694.1	6.0E-31	4.0E-31		4 05 34 040473	4.0E-31	4.0E-31	4.0E-31	4.0E-31	4.0E-31	4.0E-31	3.0E-31	3.0E-31		1	3.0E-31 D14523.1		3.0E-31 P11174				2.0E-31	2.0E-31	
Expression Signal	0.75	1.43	3.7	2.54	3.39	3.39	1.29	3.02		*	1000	Z.US	1.57	0.48	1.55		1.75	8.04			2.59	0.65	2.03	3.47	1.58	1.05	2.22	4.63	
ORF SEQ ID NO:	35146	37689				26451					0/0/7			37402			28897	34041			36397			Ì	28211				Ш
SEQ ID	21607	24055	<u>L</u>		1_	13420	21720	ı	1_		ł	1	15963	23787	25526	25609	15782	20509		1		L	L	24482	L	1	L	<u> </u>	Ш
Probe SEQ ID NO:	8528	10978	12327	12459	197	197	9640	609		,	1942	1881	2849	10754	12787	12924	2660	7494	7663	8355	97.79	10822	10867	11421	1967	2288	2416	2511	5389

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SEO   CREATE SEO   Cypresol   Crop   Tit   Crop   Tit   Crop   Tit   Crop   Tit   Crop   Tit   Crop   Tit   Crop   Tit   Crop   Tit   Crop   Tit   Crop   Tit   Crop   Tit   Crop   Tit   Crop   Tit   Crop   Tit   Crop   Tit   Crop   Tit   Crop   Tit   Crop   Tit   Crop   Tit   Crop   Tit   Crop   Tit   Crop   Tit   Crop   Tit   Crop   Tit   Crop   Tit   Crop   Tit   Crop   Tit   Crop   Tit   Crop   Tit   Crop   Tit   Crop   Tit   Crop   Tit   Crop   Tit   Crop   Tit   Crop   Tit   Crop   Tit   Crop   Tit   Crop   Tit   Crop   Tit   Crop   Tit   Crop   Tit   Crop   Tit   Crop   Tit   Crop   Tit   Crop   Tit   Crop   Tit   Crop   Tit   Crop   Tit   Crop   Tit   Crop   Tit   Crop   Tit   Crop   Tit   Crop   Tit   Crop   Tit   Crop   Tit   Crop   Tit   Crop   Tit   Crop   Tit   Crop   Tit   Crop   Tit   Crop   Tit   Crop   Tit   Crop   Tit   Crop   Tit   Crop   Tit   Crop   Tit   Crop   Tit   Crop   Tit   Crop   Tit   Crop   Tit   Crop   Tit   Crop   Tit   Crop   Tit   Crop   Tit   Crop   Tit   Crop   Tit   Crop   Tit   Crop   Tit   Crop   Tit   Crop   Tit   Crop   Tit   Crop   Tit   Crop   Tit   Crop   Tit   Crop   Tit   Crop   Tit   Crop   Tit   Crop   Tit   Crop   Tit   Crop   Tit   Crop   Tit   Crop   Tit   Crop   Tit   Crop   Tit   Crop   Tit   Crop   Tit   Tit   Crop   Tit   Crop   Tit   Crop   Tit   Crop   Tit   Tit   Tit   Crop   Tit   Tit   Tit   Tit   Tit   Tit   Tit   Tit   Tit   Tit   Tit   Tit   Tit   Tit   Tit   Tit   Tit   Tit   Tit   Tit   Tit   Tit   Tit   Tit   Tit   Tit   Tit   Tit   Tit   Tit   Tit   Tit   Tit   Tit   Tit   Tit   Tit   Tit   Tit   Tit   Tit   Tit   Tit   Tit   Tit   Tit   Tit   Tit   Tit   Tit   Tit   Tit   Tit   Tit   Tit   Tit   Tit   Tit   Tit   Tit   Tit   Tit   Tit   Tit   Tit   Tit   Tit   Tit   Tit   Tit   Tit   Tit   Tit   Tit   Tit   Tit   Tit   Tit   Tit   Tit   Tit   Tit   Tit   Tit   Tit   Tit   Tit   Tit   Tit   Tit   Tit   Tit   Tit   Tit   Tit   Tit   Tit   Tit   Tit   Tit   Tit   Tit   Tit   Tit   Tit   Tit   Tit   Tit   Tit   Tit   Tit   Tit   Tit   Tit   Tit																	_		_	<del>- :</del>				_	_	-		<u> </u>			<del></del>
Exon NO:         CRF SEQ SIgnal         Expression Fignal         Most Similar (Top) Hit Plane         Top Hit Accession Plane         Top Hit Accession Plane         Top Hit Accession Source         Top Hit Accession Plane         Top Hit Accession Source         Top Hit Accession Source         Top Hit Accession Source         Top Hit Accession Source         Top Hit Accession Source         Top Hit Accession Source         Top Hit Accession Source         Top Hit Accession Source         Top Hit Accession Source         Top Hit Accession Source         Top Hit Accession Source         Top Hit Accession Source         Top Hit Accession Source         Top Hit Accession Source         Top Hit Accession Accession Accession Accession Accession Accession Accession Accession Accession Accession Accession Accession Accession Accession Accession Accession Accession Accession Accession Accession Accession Accession Accession Accession Accession Accession Accession Accession Accession Accession Accession Accession Accession Accession Accession Accession Accession Accession Accession Accession Accession Accession Accession Accession Accession Accession Accession Accession Accession Accession Accession Accession Accession Accession Accession Accession Accession Accession Accession Accession Accession Accession Accession Accession Accession Accession Accession Accession Accession Accession Accession Accession Accession Accession Accession Accession Accession Accession Accession Accession Accession Accession Accession Accession Accession Accession Accession Accession Accession Accession Accession Accession Accession Accession Accession Accession Accession Accession Accession Accession Accession Accession Accession Accession Accession Accession Accession Accession Accession Accession Accession Accession Acc	Top Hit Descriptor	oh37c03.s1 NCI_CGAP_Kid6 Homo sapiens cDNA clone IMAGE:1459972 3' simiter to contains L1.f3 L1 repetitive element;	Homo sapiens PRO1181 mRNA, complete cds	Homo sepiens chromosome 21 segment HS21C046	Homo sapiens AT-binding transcription factor 1 (ATBF1), mRNA	Homo sapiens AT-binding transcription factor 1 (ATBF1), mRNA	RC4-BT0311-141199-011-h06 BT0311 Homo sapiens cDNA	Homo sapiens FLI-1 gene, partial	AV731500 HTF Homo sepiens cDNA clone HTFAKC07 5'	Homo sepiens myeloid/lymphoid or mixed-lineage leukemia (trithorax (Drosophila) homolog); translocated to, 4, (MLLT4) mRNA	Homo sapiens myeloid/lymphoid or mixed-lineage leukemia (trithorax (Drosophila) homolog); translocated to, 4	(ML 14) mRNA	AV758634 BM Homo sapiens cDNA clone BMFBBH12 5	AV759834 BM Homo sapiens cDNA clone BMFBBH12 5	295a07.st Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:448500 3' similar to	contains I HK.t3 I HK repetitive element	601156285F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3139701 5	Homo sapiens myeloid/lymphold or mbed-lineage leukemia (trithorax (Drosophila) homolog); translocated to, 4 (MLLT4) mRNA	Homo sapiens myeloid/lymphoid or mixed-lineage leukemia (mithorax (Drosophila) homolog); translocated to, 4	(MLLT4) mRNA	601156285F1 NIH_MGC_21 Hamo sapiens cDNA clane IMAGE:3139701 5	Human cell 12-lipoxygenase mRNA, complete cds	H.sapiens mRNA for myosin	H.sapiens mRNA for myosin	zn66c08.r1 Strategene HeLa cell s3 937216 Homo capiens cDNA clone IMAGE: 363130 5	zn66c08.r1 Stratagene HeLa cell s3 937216 Homo sapiens cDNA clone IMAGE:563150 5	AV736449 CB Homo sapiens cDNA clone CBFBIA08 5	AV736449 CB Homo sapiens cDNA clone CBFBIA08 5	601573207F1 NIH_MGC_9 Home saplens cDNA clane IMAGE:3834433 5	Homo saplens chromosome 11open reading frame 9 (C110RF9), mRNA	nw21g02.s1 NCI_CGAP_GCB0 Homo sapiens cDNA clone IMAGE:1241138 3' similar to contains. I HK:t3   THR repetitive element;
Exon SEQ ID NO:         CORF SEQ Signal Signal SEQ ID NO:         Most Similar Crop) Hit Top Hit Acession Value         Most Similar No:         Most Similar No:         Most Similar No:         Most Similar No:         Most Similar No:         Most Similar No:         Most Similar No:         Most Similar No:         Most Similar No:         Most Similar No:         Most Similar No:         Most Similar No:         Most Similar No:         Most Similar No:         Most Similar No:         Most Similar No:         Most Similar No:         Most Similar No:         Most Similar No:         Most Similar No:         Most Similar No:         Most Similar No:         Most Similar No:         Most Similar No:         Most Similar No:         Most Similar No:         Most Similar No:         Most Similar No:         Most Similar No:         Most Similar No:         Most Similar No:         Most Similar No:         Most Similar No:         Most Similar No:         Most Similar No:         Most Similar No:         Most Similar No:         Most Similar No:         Most Similar No:         Most Similar No:         Most Similar No:         Most Similar No:         Most Similar No:         Most No:         Most No:         Most No:         Most No:         Most No:         Most No:         Most No:         Most No:         Most No:         Most No:         Most No:         Most No:         Most No:         Most No:         Most No:         Most No: <t< td=""><td>Top Hit Database Source</td><td>EST_HUMAN</td><td>NT</td><td>TN</td><td>NT</td><td>NT</td><td></td><td>LN</td><td>EST_HUMAN</td><td>LN</td><td></td><td>. 1</td><td></td><td>EST_HUMAN</td><td></td><td>EST_HUMAN</td><td>EST_HUMAN</td><td>LN</td><td></td><td>L</td><td>EST_HUMAN</td><td>TN</td><td>TN</td><td>NT</td><td>EST_HUMAN</td><td>EST_HUMAN</td><td>EST_HUMAN</td><td>EST_HUMAN</td><td>EST_HUMAN</td><td>TN</td><td>EST_HUMAN</td></t<>	Top Hit Database Source	EST_HUMAN	NT	TN	NT	NT		LN	EST_HUMAN	LN		. 1		EST_HUMAN		EST_HUMAN	EST_HUMAN	LN		L	EST_HUMAN	TN	TN	NT	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	TN	EST_HUMAN
Exon SEQ ID NO:         CAF SEQ Signal Signal SEQ ID NO:         Expression Signal SEQ ID NO:         Most Similar Value Auge           ADD NO:         2516 Signal SEQ ID NO:         2516 Signal Auge         Auges           14725         27282         10.42         5.0E-32/ID No:           20835         34327         3.4         4.0E-32/ID No:           20835         34327         3.4         4.0E-32/ID No:           20835         34327         3.4         4.0E-32/ID No:           20835         34327         3.4         4.0E-32/ID No:           20835         34327         3.4         4.0E-32/ID No:           20835         34327         3.4         4.0E-32/ID No:           20835         34327         3.4         4.0E-32/ID No:           22649         36222         3.1         3.0E-32/ID No:           22649         36222         3.1         3.0E-32/ID No:           22649         36222         3.1         3.0E-32/ID No:           25949         36222         3.1         3.0E-32/ID No:           25949         36222         3.1         3.0E-32/ID No:           25949         36222         3.1         3.0E-32/ID No:           25941         3.2	Top Hit Acession No.	AA864653.1	4F116827.1	4L163246.2	11432574	11432574	3E064410.1	117293.1	AV731500.1	5174574		5174574	4V758634.1	AV758634.1		AA777621.1	BE279086.1	5174574		5174574	BE279086.1	M35418.1	Z38133.1	Z38133.1	AA114294.1	AA114294.1	AV736449.1	AV736449.1	BE743299.1	11439789	AA720574.1
Evan SEQ ID NO:         Expression Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signa	<del></del>	6.0E-32	5.0E-32	4.0E-32	4.0E-32	4.0E-32	4.0E-32	3.0E-32	3.0E-32	3.0E-32		3.0E-32	3.0E-32	3.0E-32		3.0E-32	3.0E-32	3.0E-32		3.0E-32	3.0E-32	2.0E-32	2.0E-32	2.0E-32	2.05-32	2.0E-32	2.0E-32	2.0E-32	1.0E-32	1.0E-32	
Evan SEQ ID ID ID ID ID ID ID ID ID ID ID ID ID		25	10.42	1.64	3.4	3.4	0.93	2.64	15.82	0.75		0.75	3.1	3.1		3.43	7.95	4.85				0.89	5.55	5:55	3.34	3.34	1.28	1.28	1.25		
	ORF SEQ ID NO:								27721					١	1				L			32907						L			l i
Probe SEQ ID NO: 1059 964 7779 7779 7779 8554 468 1484 12843 112843 13020 6608 8608 8608 8608 8608 8608 8608 8	Exon SEQ ID NO:	26181	14225	14127	_	1	١_	13663	14637	1	l		ı	1	ı			ł	1_		L		<u>L</u> _	Ι.	_	L	L		L	L	ł I
	Probe SEQ ID NO:	12869	1059	954	7779	9/1/	8554	468	1484	2973		2573	9594	9594		11166	12433	12843		12843	13020	6382	6608	808	8473	8473	13154	13154	3163	7200	8795

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			-				
Probe SEQ ID NO:	SEQ D O O O	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Databæse Source	Top Hit Descriptor
3570	16735		4.8		9.0E-33 BE327112.1	EST_HUMAN	nw07e05.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE.3182216 3' similar to TR:O88539 O88539 WW DOMAIN BINDING PROTEIN 11.;
1	1		,	100		Ŀ	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively
0000	20067	35607	3.17	9.0E-33	9.0E-33 AF 223391.1	EST HIMAN	Spiroza 60202164F1 NCI CGAP Bri67 Homo sepiens cDNA clone IMAGE:4156670 5
11038	24117	1000		9.0E-33		LN	Homo sabiens chromosome 21 segment HS21 C080
8	13300	26320		7.0E-33	1736	LZ.	Homo sapiens short-chain elcohol dehydrogenase family member (HEP27) mRNA
62	13300	26321		7.0E-33	5031736 NT	N	Homo sapiens short-chain alcohol dehydrogenase family member (HEP27) mRNA
							to12b09.x1 NCI_CGAP_Ut2 Homo sapiens cDNA clone IMAGE:2178809 3' similar to contains OFR.t1 OFR
2228	15362	28491	3.04		7.0E-33 AI590115.1	EST_HUMAN	repetitive element;
2714	15832		7.95		7.0E-33 AV730056.1	EST_HUMAN	AV730056 HTF Homo sapiens cDNA clone HTFAVE06 5'
3314	16487		15		7.0E-33 AW971307.1	EST_HUMAN	EST383396 MAGE resequences, MAGL Homo sapiens cDNA
							Human hLRP mRNA for leukocyte common antigen-related peptide (protein-tyrosine phosphate) (EC
9147	- 1		0.87			LN	3.1.3.48)
11067		37777	1.88		7.0E-33 BF347229.1	EST_HUMAN	602021164F1 NCI_CGAP_Brn67 Homo saplens cDNA done IMAGE:4158670 5
11526	24582	38258	1.59		7.0E-33 AW971568.1	EST_HUMAN	EST383657 MAGE resequences, MAGL Homo sapiens cDNA
	ļ						not6h01.s1 NCI_CGAP_Phe1 Homo sapiens cDNA done IMAGE:1100881 3' similar to contains £1.t1 £1
12413		32082				LHUMAN	repetitive element:
3830	16990		0.93		6.0E-33 AL 163285.2	NT	Homo saplens chromosome 21 segment HS21 0085
6192	19368	32717	0.91	6.0E-33	6.0E-33 F30631.1	EST HUMAN	HSPD21201 HM3 Homo sapiens cDNA clane e4000107H06
6192	19368	L	0.91	6.0E-33	6.0E-33 F30631.1	EST_HUMAN	HSPD21201 HM3 Homo seplens cDNA clone s4000107H06
8778	21857	35400	1.86		6.0E-33 J04038.1	IN	Human glyceraidehyde-3-phosphate dehydrogenase (GAPDH) gene, complete cds
8899	21978	35517	3.12	6.0E-33	11429198 NT	ΤN	Homo sapiens similar to RAD23 (S. cerevisiae) homolog B (H. sapiens) (LOC63277), mRNA
10214	23250	36839	2.03	6.0E-33	TN 60999 NT	LN	Mus musculus SRY-box containing gene 6 (Sox6), mRNA
10214	L				FN 6095549	TN	Mus musculus SRY-box containing gene 8 (Sox8), mRNA
1818			1.8		5.0E-33 BF373515.1	EST_HUMAN	QV1-FT0169-100700-271-a02 FT0169 Homo sapiens cDNA
1831	15074		1.32		11141884 NT	LN	Homo sapiens solute carrier family 5 (choline transporter), member 7 (SLC5A7), mRNA
1947	15090	28190	1.63			LN	Homo sapiens spermidine synthase (SRM) mRNA
1947	15090		1.63	5.0E-33	4507208 NT	TN	Homo sapiens spermidine synthase (SRM) mRNA
2346	15477		26.2		5.0E-33 AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C085
4169	17319	30312	99.0		5.0E-33 AB014599.1	NT	Homo saplens mRNA for KIAA0699 protein, partial cds
10454	١.	37097			5.0E-33 AW 264679.1		xq33f11.x1 NCI_CGAP_Lu28 Homo sapiens cDNA clone IMAGE:2752461 3'
10454	23489	37098	0.82		5.0E-33 AW 264679.1	EST_HUMAN	xq33f11.x1 NCI_CGAP_Lu28 Homo saplens cDNA clone IMAGE:2752481 3'

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	protein, Angelman			E:844317 5' similar to			27271493	8 5' similar to HUMAN);			nilar to contains MER29.b3	nilar to contains MER29.b3			imilar to TR:Q13579	705204 3' similar to	705204 3' similar to		1 0000	E:844388 5 similar to				AGE:1675973 3' similar to IN);	2 and flanking repeat		
Top Hit Descriptor	Homo sapiens ubiquitin protein ligase E3A (human papiloma virus E6-assoclated protein, Angelman syndromo) (UBE3A), mRNA	Homo sapiens chromosome 21 segment HS21C007	Homo sapiens RAB1, member RAS oncogene family (RAB1) mRNA	ab51b11.r1 Stratagene lung carcinoma 937218 Homo sapiens cDNA clone IMAGE:844317 5' similar to	contains Alu repetitive element; contains MER28.b2 MER28 repetitive element;	Homo sapiens chromosome 21 segment HS21C010	UI-H-BI2-ahlc-03-0-UI.s1 NCI_CGAP_Sub4 Homo sapiens cDNA clone IMAGE:2727149 3	271a08.r1 Stratagene colon (#937204) Homo sepiens cDNA clone IMAGE:510038 5' slmilar to gb:X12671_rna1 HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN A1 (HUMAN);	Homo sapiens polymerase (DNA directed), alpha (POLA), mRNA	Homo sapiens polymerase (DNA directed), alpha (POLA), mRNA	httpgt01.x1 NCI_CGAP_Kid13 Homo saplens cDNA clone IMAGE:3146256 3' similar to contains MER29.b3 MER29 repetitive element;	ht09g01.x1 NCI_CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3146256 3' stmilar to contains MER29.b3	MER29 repetitive element;	AV647851 GLC Homo sapiens cDNA clone GLCBCF093'	ak32b12.s1 Soares_tests_NHT Homo sapiens cDNA clone IMAGE:1407647 3' similar to TR:Q13579 Q13579 MARINER TRANSPOSASE;	qb67g03.x1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:1705204 3' slmilar to contains OFR.t1 OFR repatitive element;	qb67g03.x1 Soares_fetal_heart_NbHH19W Homo capiens cDNA clone IMAGE:1705204.3' similar to	contains OFK.tl OFK repetitive element;	MR0-H 10405-100300-202-008 H 10405 Hamo sapiens curv	ab51g11.r1 Stratagene lung carcinoma 937218 Homo sepiens cDNA clone IMAGE:344338 5 similar to gb:X00734_cds1 TUBULIN BETA-5 CHAIN (HUMAN);	Homo saplens hypothetical protein SIRP-b2 (SIRP-b2), mRNA	Homo sapiens hypothetical protein SIRP-b2 (SIRP-b2), mRNA	q196d01.x1 Soares NHHMPu_S1 Homo sapiens cDNA clone IMAGE:1880161 31	oz21d03.x1 Soares_fetal_liver_spleen_1NFLS_31 Homo sapiens cDNA clone IMAGE:1675973 3' similar to gb:M29536 TRANSLATIONAL INITIATION FACTOR 2 BETA SUBUNIT (HUMAN);	Homo saplens X-linked anhidroitic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat	regions	Homo sapiens protein kinase C beta-II type (PRKCB1) mRNA, complete cds
Top Hit Database Source	NT	N	E		EST_HUMAN	IN	EST_HUMAN	EST HUMAN	L LZ	F	EST HUMAN	E I	EST_HUMAN	EST_HUMAN	EST HUMAN	EST HUMAN	t .	EST HUMAN	EST_HUMAN	EST HUMAN	N	L	<b>EST HUMAN</b>	EST HUMAN		Ę	LN.
Top Hit Acession No.	11433063 NT	4.0E-33 AL163207.2	4758987 NT		1		.0E-33 AW293349.1	0E-33 AA053053.1	33994	8393994 NT	0E-33 BE350127.1		3.0E-33 BE350127.1	3.0E-33 AV647851.1	0E-33 AA861510.1	0E-33 A1160189.1		2.0E-33 AI160189.1	2.0E-33 BE159039.1	AA626683.1	11421332 NT	2.0E-33 11421332 NT	AI277492.1	0E-33 A1052256.1		.0E-33 AF003528.1	.0E-33 M13975.1
Most Similar (Top) Hit BLAST E Value	5.0E-33	4.0E-33	4.0E-33		4.0E-33	4.0E-33	4.0E-33	4	4	4.0E-33	3.05-33		3.0E-33	3.0E-33	3.0E-33			1			L	L	Ì	l		1	
Expression Signal	1.45	2.25	3.37		1.16	4.78	2.38	24.75	0.79	0.79	5.62		5.83	1.16	0.87	1 67		5.53	4.53	8.64			1.39	2.15		1.61	98.0
ORF SEQ ID NO:			28454			05882	30722	34734	33060	33061	l				37298					31199							34113
Exon SEQ ID NO:	25165	l				15734	17743	18717	1	L	l		14278	16064	23689	1	1	- 1	17677	18228	ı	L	l	<u> </u>	↓_	13247	20637
Probe SEQ ID NO:	12212	1152	2194		2491	2610	4806	5519	6522	6522	1113		1114	2522	10655	<b>\$</b>	1	107	4539	5100	520	5204	6553	9301		6	7565

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Top Hit Descriptor	Human dystrophin (DMD) gene, exons 7, 8 and 9, and partial cds	QV3-BN0047-230200-102-b03 BN0047 Homo sapiens cDNA	Human dystrophin (DMD) gene, exons 7, 8 and 9, and partial cds	RC5-NN1055-260400-021-G03 NN1055 Homo sapiens cDNA	Homo septens X-linked anhidrotite ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions	AV727809 HTC Homo saplens cDNA clone HTCCNC12 5	Homo sapiens Xq pseudoautosomal region; segment 1/2	Homo sapiens hypothetical protein FLJ10900 (FLJ10900), mRNA	QV2-BT0258-071299-019-g07 BT0258 Homo sapiens cDNA	MR4-BT0399-200100-001-h03 BT0399 Homo saplens cDNA	yd15e05.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:108320 5'	yd15e05.r1 Soares fetal liver epleen 1NFLS Homo sapienc cDNA clone IMAGE:108320 5'	ly14c10.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:148722 5'	Human G2 protein mRNA, partial cds	Human G2 protein mRNA, partial cds	PM0-BN0065-100300-001-c08 BN0065 Homo sapiens cDNA	Mus musculus DAB/2J halr-specific (hack-1) gene	Homo sapiens Npw38-binding protein Npw8P (LOC51729), mRNA	Human splicing factor SRp55-1 (SRp-55) mRNA, complete cds	Rattus norvegicus putative four repeat ion channel mRNA, complete cds	Homo sapiens mRNA for KIAA1435 protein, partial cds	Homo sapiens chromosome 21 segment HS21C009	IE94c08 x1 NCI_CGAP_Pr28 Homo septens cDNA clone IMAGE:2249194 3'	Homo sapiens splicing factor 3a, subunit 3, 80kD (SF3A3), mRNA	ak35c01.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1407936 31	601874950F1 NIH_MGC_54 Homo sepiens cDNA clone IMAGE:4102213 5'	Human Ig germline H-chain D-region genes, partial cds	601458531F1 NIH MGC 66 Homo sapiens oDNA clone IMAGE:3862086 5	wd35g06.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2330170 3' similar to contains MER29 to MER29 to MER29 and the seperitive element;	wd35g06.xt Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2330170 3' sImilar to contains MER29.t2 MER29 repetitive element;	PLEXIN 4 PRECURSOR (TRANSMEMBRANE PROTEIN SEX)
Top Hit Database Source	TN	EST_HUMAN	FN	EST_HUMAN	F	FST HUMAN	NT	N	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	LN	TN	EST_HUMAN	ΝΤ	LN⊤	LN	N	NT	LN	EST_HUMAN	LN .	EST_HUMAN	EST_HUMAN	F	EST_HUMAN	EST HUMAN	EST HUMAN	SWISSPROT
Top Hit Acession No.	Je0822.1	1.0E-33 AW996818.1	J60822.1	1.0E-33 AW904491.1	1 0E 33 4 E003528 1	1 0E-33 AV727809 1	9.0E-34 AJ271735.1	8922751 NT	8.0E-34 BE062570.1	8.0E-34 BE069882.1	T70845.1	T70845.1	7.0E-34 H12866.1	6.0E-34 U10991.1	6.0E-34 U10991.1	6.0E-34 AW998611.1	6.0E-34 U03686.1	TN06500/1	5.0E-34 U30883.1	5.0E-34 AF078779.1	5.0E-34 AB037856.1	5.0E-34 AL163209.2	4.0E-34 AI804667.1	5803168 NT	4.0E-34 AA861773.1	4.0E-34 BF209778.1	3.0E-34 M37277.1	3.0E-34 BF035327.1	2.0E-34.AI678101.1	2.0E-34 AI878101.1	P51805
Most Similar (Top) Hit BLAST E Value	1.0E-33 U60822.1	1.0E-33	1.0E-33 U60822.1	1.0E-33	101	1 OF 33	9.0E-34	8.0E-34	8.0E-34	8.0E-34	7.0E-34 T70845.1	7.0E-34 T70845.1	7.0E-34	6.0E-34	8.0E-34	6.0E-34	6.0E-34	5.0E-34	5.0E-34	5.0E-34	5.0E-34	5.0E-34	4.0E-34	4.0E-34	4.0E-34	4.0E-34	3.0E-34	3.0E-34	2.0E-34	ļ	1
Expression Signal	1.4	1.56	2.44	1.25	5.7	2 10	4.77	0.98	1.93	29.0	2.5	0.54	3.85	1.74	1.74	1.58	222	3.15	5.24	1.17	2.02	1.93	2.09	6.0	0.62	0.83	0.66	2.96	0.75		
ORF SEQ ID NO:						31070		28501				27714		26711	26712				31257				28309			35857	32890		35774	·	
SEQ ID NO:	26229	1		l.	10047		L	1_	17757		14829	L	25334	13677	13677	l	25216	15072	18295	22148	23974	ı	15195	1	19166	22315	19531	L	22230	1	
Probe SEQ ID NO:	10227	11602	11962	12768		12087	13179	2240	4620	7974	1476	10204	12482	483	483	5247	12290	1929	5173	8067	10890	11532	2054	3241	5981	9238	6361	11420	9452	9452	11431

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Top Hit Descriptor	H.saptens mRNA for novel T-cell activation protein	Human mRNA for KIAA0366 gene, partial cds	Homo sapiens mRNA for KIAA1365 protein, partial cds	Homo sapiens carbamy phosphate synthetase I mRNA, complete cds	H.sapiens immunoglobulin kappa light chain variable region L14	Homo sapiens mRNA for KIAA0406 protein, partial cds	Homo sapiens Ring1 and YY1 binding protein (RYBP), mRNA	Homo saplens cit/2 kinase (CLX2), propint, cotet, glucocoarebrosidase (GBA), and metarin genes, complete	cas, mataxin pseudogare and glucoca edical dasa pseuvogare, end un onicosponanto ( 11 1555) gene, parvar cds	601431984F1 NIH_MGC_72 Homo saplens cDNA clone IMAGE:3917229 5'	qg38c05.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1837448 3' similar to	SW.Y249_HUMAN Q92539 HYPOTHETICAL PROTEIN KIAA0249.;	gg38c05.x1 Soares_testis_NHT Homo sapiens cDNA cione IMAGE:1837448 3' similar to SW:Y249_HUMAN Q92539 HYPOTHETICAL PROTEIN KIAA0249.;	zh84f12.r1 Soares, fetal liver, spleen, 1NFLS_S1 Homo sapiens cDNA clone IMAGE:428015 51	601109719F1 NIH_MGC_16 Homo saplens cDNA clone IMAGE:3350405 5'	yu98a07.r1 Scares fetal liver spleen 1NFLS Homo saciens cDNA clone IMAGE:241236 5' similar to contains	PTK5 repetitive element	ht09g01.x1 NCI_CGAP_KId13 Homo sapiens cDNA done IMAGE:3146256 3' shrilar to contains MER29.b3 MER29 repetitive element :	DKFZp434L148_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434L148 5'	Homo sapiens Y-linked zinc finger protein (ZFY) gene, complete cds	601125260F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3345063 5'	Homo saplens phospholipid scramblase 1 gene, complete cds	7n25a09.x1 NCI_CGAP_Lu24 Home sapiens cDNA clone IMAGE:3565361 3' similar to TR:Q9QZH7	Q9QZH7 F-BOX PROTEIN FBL2.;	7h25a09.x1 NCI_CGAP_Lu24 Homo sapiens dDNA done IMAGE:3565351 3 similar to 1 Ktu9u2h7 0902H7 F-80X PROTEIN FBL2 :	Homo saplens calctum channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively	spliced	w/03e/05.x1 NCI_CGAP_GC8 Homo sapiens cDNA clone IMAGE:2480432 3' similar to SW:POL1_HUMAN P10286 RETROVIRUS-RELATED POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE ;
Top Hit Database Source	Ł		IN	Ł	NT	NT			Ż	EST HUMAN		EST_HUMAN	EST HUMAN	Г	Т		EST_HUMAN	EST HUMAN	Т	Г	EST_HUMAN	П		EST_HUMAN	FAT HIMAN	Τ	NT	EST_HUMAN
Top Hit Acession No.	E-35 X94232.1	4.1	E-35 AB037786.1	E-35 AF154830.1	IE-35 X63392.1	E-35 AB007866.2	6912639 NT		0E-35 AF023268,1			E-35 A1208765.1	F.35 Al208765 1		Γ		0E-35 H91193.1	0E-35 BE350197 1	4 0F-35 AL046598.1	4.0E-35 AF114156.1	BE268182.1	3.0E-35 AF224492.1		0E-35 BF433100.1	0E-35 BE433100 1	1001001	0E-35 AF223391.1	0E-35 AW 003083.1
Most Similar (Top) Hit BLAST E Value	6.0E-35	6.0E-35/	6,0E-35	5.0E-35	5.0E-35	5.0E-35	5.0E-35		5.0E-35	5.0E-35	!	5.0E-35	5.0F-35	5 OF 35	4.0E-35		4.0E-35	4 05-35	4 0F-35	4.0E-35		1		3.0E-35	305.35		69	φ)
Expression Signal	0.57	0.61	2.97	0.61	2.25	0.99	2.87		1.72	4.25		2.17	216	2 54	20.46		11.21	1 67			S			23.43	. 23.43	200	1.45	1.5
ORF SEQ ID NO:	35525		36743			١			30653			35015	35018	L	27703	ļ	28114			38786				31634	24695			37022
SEQ ID NO:	21985	22907	23145	13373	14895	15958	16250		17667	ı	ı	21486	24.486	L	14619		15008	20732			l_	<u> </u>		18656	29201		22738	. 23413
Probe SEQ ID NO:	9088	2986	10107	148	1746	2844	3074		4579	8378		8405	. 8405	11451	1465		1862	7250	8715	12098	1610	2408		5456	6450	5	9689	10378
				_			_			_		_		_	_		_						_	_				

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100g01.x1 NCI\_CGAP\_KId13 Homo saplens cDNA clone IMAGE:3146256 3' similar to contains MER29.b3 TCBAP2E4328 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA Homo sapien 'OBAP2E4328 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA Homo sapie yddago'i rf Scares fefal liver spleen 1NFLS Homo saplens cDNA clone IMAGE:115762 5' similar to SP-A44282 A44282 RETROVIRUS-RELATED POL POLYPROTEIN - HUMAN; Homo saplens hypothetical protein (LOC51233), mRNA (6632F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA clone K6932 5' similar to K6832F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA clone K6832 5' similar to REPETITIVE ELEMENT hi86s12.x1 Soares, NFL\_T\_GBC\_S1 Homo sapiens cDNA clone IMAGE:2979168 3' similar to SW:TR12\_HUMAN Q14669 THYROID RECEPTOR INTERACTING PROTEIN 12; spleen 1NFLS Homo saplens cDNA clone IMAGE:274079 5 frinfo16 Regional genomic DNA specific cDNA library Homo sepiens cDNA done CR12-1 frinfo16 Regional genomic DNA specific cDNA library Homo sepiens cDNA clone CR12-1 601496774F1 NIH\_MGC\_70 Homo septens cDNA clone IMAGE:3898699 5' Homo septens chromosome 21 segment HS21C010 601496774F1 NIH\_MGC\_70 Homo sapiens cDNA clone IMAGE:3898699 5 rop Hit Descriptor CM2-MT0125-280700-297-G02 MT0125 Homo saplens cDNA CM2-MT0125-280700-297-G02 MT0125 Homo saplens cDNA QV0-BT0701-210400-199-b04 BT0701 Homo saplens cDNA Homo saplens Grb2-associated binder 2 (KIAA0571), mRNA Homo sapiens Grb2-associated binder 2 (KIAA0571), mRNA Homo sapiens mRNA for KIAA0895 protein, partial cds Homo sapiens Grb2-associated binder 2 (KIAA0571), mRNA Homo sapiens Grb2-associated binder 2 (KIAA0571), mRNA IL2-ST0162-131099-006-412 ST0162 Homo sapiens cDNA IL2-ST0162-131099-006-d12 ST0162 Homo sepiens cDNA first 6 Regional genomic DNA specific cDNA library A971F Heart Homo sapiens cDNA clone A971 cDNA clone TCBAP4328 yq19a12.rl Soares fetal liver H.sapiens PROS-27 mRN MER29 repetitive element **CDNA clone TCBAP4328** REPETITIVE ELEMENT EST\_HUMAN EST\_HUMAN EST\_HUMAN EST\_HUMAN EST\_HUMAN EST\_HUMAN EST\_HUMAN HUMAN EST\_HUMAN EST\_HUMAN EST HUMAN EST HUMAN EST\_HUMAN EST\_HUMAN EST\_HUMAN EST HUMAN EST\_HUMAN EST\_HUMAN Top Hilt Database Source È 7705994 NT z 6912459 NT 6912459 BE904978.1 6912459 Top Hit Acession 2.0E.35 H49239.1 2.0E.35 BF332417.1 2.0E.35 BE832636.1 2.0E.35 BE832636.1 2.0E.35 X59417.1 2.0E.35 6912 1.0E-35 AW389473.1 1.0E-35 BE350127.1 2.0E-35 AW665005.1 2.0E-35 AB020702.1 2.0E-35 AL163210.2 2.0E-35 BE904978.1 BE247575.1 2.0E-35|BE247676.1 AA631949. AA631949. 2.0E-35 AB018413.1 Š 1.0E-35 T87947.1 2.0E-35 N88965.1 N88965.1 T11909. 2.0E-35 1.0E-35/ 2.0E-35 2.0E-35 (Top) Hit BLAST E Most Similar Value 1.74 5.76 35.82 0.6 1.22 133 1.33 35.82 1,34 0.85 .93 0.6 1.13 1.08 0.85 1.08 3.01 4.56 Expression Signal 26372 26296 29050 28847 ORF SEQ ID NO: 37749 29570 27001 27436 33786 26372 29570 30184 30185 29571 32111 29571 15940 17176 16005 13952 13952 14107 15730 14376 15865 16556 25247 16005 16556 16556 SEO ID 15424 17178 18894 ö 1681 13056 2826 932 1215 4792 5700 12342 3386 3386 3647 11036 12157 12342 Probe SEQ ID 111 4019 4019 7253 2507

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Top Hit Descriptor	ht09g01.x1 NCI_CGAP_Kld13 Homo sapiens cDNA clone IMAGE:3146256 3' similar to contains MER29.b3 MER29 repetitive element;	Homo saplens transcription elongation factor B (SIII), polypeptide 1-like (TCEB1L) mRNA	AV650422 GLC Homo sapiens cDNA clone GLCCEF06 3'	AV650422 GLC Hamo saplens cDNA clone GLCCEF06 3'	Mus musculus activin receptor Interacting protein 1 (Arip1-pending), mRNA	Mus musculus activin receptor Interacting protein 1 (Arip1-pending), mRNA	Homo saplens chromatin assembly factor 1, subunit B (p60) (CHAF1B), mRNA	MR1-ST0111-111189-011-d07 ST0111 Homo sapiens cDNA	MR1-ST0111-111199-011-d07 ST0111 Homo sapiens cDNA	Homo sapiens mRNA for KIAA1279 protein, partial cds	Homo sapiens KIAA0645 gene product (KIAA0645), mRNA	AU158595 PLACE3 Homo sapiens cDNA clone PLACE3000382 3'	AU158595 PLACE3 Homo saplens cDNA clone PLACE3000382 3'	naa08d06.x1 NCI_CGAP_Pr28 Home saplens cDNA clone IMAGE:3254051 3' similar to TR:O31341 O31341 BETA-GALACTOSIDASE	naa08d06.x1 NCI_CGAP_Pr28 Homo saplens cDNA clone IMAGE:3254051 3' similar to TR:031341	031341 BETA-GALACTOSIDASE;	Homo sapiens mRNA for KIAA1057 protein, partial cds	Homo saplens mRNA for KIAA1057 protein, partial cds	promma-7.001.r bytumor Homo sapiens cDNA 5'	Homo sapiens fibulin 1 (FBLN1), mRNA	Homo sapiens casen kinase 1, epsilon (CSNK1E), mRNA	601584833F1 NIH_MGC_7 Homo saplens cDNA clone IMAGE:3938985 5	B.bovis BBSc mRNA for scinderin	EST54988 Hippocampus II Homo sapiens cDNA 5' end similar to similar to endogenous retrovirus 9, 5' LTR	CM1-CT0315-091299-063-407 CT0315 Homo sapiens cDNA	Homo saplens C-terminal binding protein 2 (CTBP2) mRNA	ADHESIVE PLAQUE MATRIX PROTEIN PRECURSOR (FOOT PROTEIN 1) (MGFP1) (MGFP-1)	ADHESIVE PLAQUE MATRIX PROTEIN PRECURSOR (FOOT PROTEIN 1) (MGFP1) (MGFP-1)	Human carcinoembryonic antigen gene family member 12 (CGM12) gene, exons L and LIN	Human carcinoembryonic antigen gene family member 12 (CGM12) gene, exons L and L/N	Homo sapiens glutathione transferase A4 gene, exon 1
Top Hit Database Source	EST_HUMAN		HUMAN	HUMAN				EST_HUMAN	EST_HUMAN			HUMAN	EST_HUMAN /		T	EST_HUMAN	LN	INT	EST_HUMAN			T_HUMAN	IN	EST HUMAN	T		SWISSPROT	SSPROT			NT
Top Hit Acession No.	.0E-35 BE350127.1	6006030 NT	.0E-35 AV650422.1	.0E-35 AV650422.1	7656905 NT	7656905 NT	11526236 NT	.0E-35 AW808665.1	.0E-35 AW 808665.1	.0E-35 AB033105.1	11418002 NT	.0E-35 AU158595.1	.0E-35 AU158595.1	0E-35 BE589594 1		.0E-35 BF589594.1	.0E-35 AB028980.1	.0E-35 AB028980.1	.0E-35 AI525119.1	11418274 NT	11418110 NT	2.1	8.0E-36 X78479.1	8.0E-36 AA348480.1		4557498 NT	.0E-36 Q27409	.0E-36 Q27409		ı	.0E-36 AF052051.1
Most Similar (Top) Hit BLAST E Value	1.0E-35	1.0E-35	1.0E-35	1.0E-35	1.0E-35	1.0E-35	1.0E-35	1.0E-35	1.0E-35	1.0E-35	1.0E-35	1.0E-35	1.0E-35	1 0E-35		1.0E-35	1.0E-35	1.0E-35	1.0E-35	1.0E-35	1.0E-35	1.0E-35	8.0E-36	8.0E-36	7.0E-36	7.0E-36	7.0E-38	7.0E-36	7.0E-36	7.0E-36	7.0E-36
Expression Signal	1.34	1.87	1.67	1.67	4.82	4.82	1.48	0.74	0.74	0.99	16.0	246	2.46	0 72		0.72	1.49	1.49	2.04	6.35	1.26	2.49	29:0	0.76	1.53	5.25	1.09	1.09	6.31	6.31	27,38
ORF SEQ ID NO:	29051	29397	29418	29419	30661	30662	31896	31475	31476	34196	34373	36383	36384	37462		37463	38743	38744					32650	36070			31360	31361	34389		32040
Exon SEQ ID NO:	15940	16386	16406	16406	17680	17680	18821	18561	18561	20720	20874	25861	25861	23838		23838	25036	25036	1	26077	25284	25539	19310	22504	1	L	18392	18392	20887		25388
Probe SEQ ID NO:	2826	3212	3232	3232	4542	4542	5627	7135	7135	7652	7819	9742	9742	10805		10805	12055	12055	12062	12188	12405	12806	6131	9430	2997	3188	6273	5273	7832	7832	12570

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Top Hit Descriptor	Homo sapiens ninjurin 2 (NINJ2), mRNA	Homo sapiens TCL6 game, exon 12	UI-H-BW1-anv-c-12-0-UI.st NCI_CGAP_Sub7 Homo sapiens cDNA clane IMAGE:3083542.3'	thg3b06.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sepiens cDNA clone IMAGE:2126195.3' similar to gp:M11949 PANCREATIC SECRETORY TRYPSIN INHIBITOR PRECURSOR (HUMAN);	hod6h02.x1 NCI_CGAP_Co14 Homo sapiens cDNA clone IMAGE:3036627 3' similar to SW:IMA2_HUMAN P52292 IMPORTIN ALPHA-2 SUBUNIT ;	Homo saplens syncytin precursor, mRNA, complete cds	C16927 Clontech human aorta polyA+ mRNA (#6572) Homo sapiens cDNA clone GEN-535C11 5	tt95c09.xt NCI_CGAP_CLL1 Homo sapiens cDNA clone IMAGE:2107024 3' similar to contains MER9.b2 MER9 repetitive element ;	Homo sapiens Xq pseudoautosomal region; segment 1/2	601285567F1 NIH_MGC_44 Homo sapiens cDNA done IMAGE:3607289 5	Hamo sapiens chramosome 21 segment HS21C009	Homo sapiens API5-like 1 (API5L1), mRNA	Homo sapiens API5-like 1 (API5L1), mRNA	Homo sepiens N-ethylmaleimide-sensitive factor (NSF), mRNA	Homo sapiens Xq pseudoautosomal region; segment 1/2	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA	PM3-BN0176-100400-001-g04 BN0176 Homo septens cDNA	601298574F1 NIH_MGC_19 Homo saplens cDNA clone IMAGE:3628386 5	2820020.5prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2820020 5	601282266F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3604168 5	601282266F1 NIH_MGC_44 Homo sepiens cUNA clone IMAGE:3504168 5	Homo saplens chromosome 21 segment HS21C004	y/19f05.r1 Soares placenta Nb2HP Homo Sapiens cDNA clone IMAGE:139/13 b	Homo sapiens a disintegrin and metalloproteinase domain 22 (ADAM22), trancript variant 3, mKNA	Human platelet Glycoprotein IIb (GPIIb) gene, exons 2-29	Homo sapiens DNA for amylold precursor protein, complete cds	Homo capiens DNA for amyloid precursor protein, complete cds	zu69c10.r1 Soares_testis_NHT Homo sapiens cDNA done IMAGE:743250 5	Homo sapiens nuckear factor of activated T-cells, cytoplasmic 2 (NFATC2), mKNA	AV753629 TP Homo sapiens cDNA done TPGABH01 5	Homo sapiens neurexin II-alpha gene, partial cds
Top Hit Database Source	FZ	LN	EST_HUMAN	EST_HUMAN	EST_HUMAN	LN	EST_HUMAN	EST HUMAN	L	EST_HUMAN	TN	NT	NT	NT	NT	NT	EST HUMAN		EST_HUMAN	EST_HUMAN	EST_HUMAN	NT	EST_HUMAN	IN	NT	LN	TN	EST HUMAN	l I	EST_HUMAN	LN.
Top Hit Acession No.	7706622 NT	6.0E-36 AB035346.1	.0E-36 BF515101.1	.0E-36 AI435169.1	6.0E-36 AW 780143.1	6.0E-36 AF208161.1	516927.1	6.0E-36 A1380499.1	5.0E-36 AJ271735.1	5.0E-36 BE388436.1	5.0E-36 AL163209.2	5729729 NT	5729729 NT	11079227 NT	5.0E-36 AJ271735.1	11417862 NT	4.0E-36 BE010038.1	4.0E-36 BE382574.1	4.0E-36 AW247772.1	4.0E-36 BE389299.1	4.0E-36 BE389299.1	4.0E-36 AL163204.2	4.0E-36 R64023.1	11497041 NT	4.0E-36 M33320.1	4.0E-36 D87675.1	4.0E-36 D87675.1	4.0E-36 AA400370.1	11420516 NT	4.0E-36 AV753629.1	3.0E-36 AF099810.1
Most Similar (Top) Hit BLAST E Value	6.0E-36	6.0E-36	6.0E-36	6.0E-36	6.0E-36	6.0E-36/	6.0E-36 C16927.1	6.0E-36	5.0E-36/	5.0E-36	5.0E-36	5.0E-36	5.0E-36	5.0E-36	5.0E-36	5.0E-36	4.0E-36	4.0E-36	4.0E-36	4.0E-36	4.0E-36	4.0E-36	4.0E-36	4.0E-36	4.0E-36	4.0E-36	4.0E-36	4.0E-36	4.0E-36	4.0E-36	3.0E-36
Expression Signal	1.92	5.59	0.59	7.17	3.03	4.62	0.63	3.49	15.16	21.08	3.24	1.31	1.31	0.59	6.11	2.36	1.57	1.36	41.4	1.1	1.1	0.69	96.0	2.49	1.78	1.45	1.45	3.13	1.91		
ORF SEQ ID NO:	28315		29894	1	l	35471	ł	38521		29033	29863	Ĺ	31029		L	32095	27473							32704	34388		L	37941			26934
Exen SEQ ID NO:	15201	l_	1		1	1		24830		L	16861	18039	18039	1	l_			14829	15429	16603	16603	18008	19024	19356	<u>L</u>	L	١.		25328	<u></u>	13896
Probe SEQ ID NO:	2060	2490	3729	5446	7258	8853	10430	11841	4	2809	3700	4909	4909	7966	12155	12458	1252	1677	2297	3435	3435	4877	5833	6180	7831	8752	8752	11235	12475	12520	714

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Top Hit Descriptor	Homo sapiens KIAA0952 protein (KIAA0952), mRNA	Mus musculus junctophilin 1 (Jp1-pending), mRNA	601458531F1 NIH_MGC_68 Homo sapiens cDNA clone IMACE:3862086 5'	601106343F1 NIH_MGC_16 Homo saplens cDNA clone IMAGE:3342706 5'	QV0-OT0030-240300-174-h04 OT0030 Homo sapiens cDNA	Mus musculus p47-phox gene, complete cds	EST06648 Infant Brain, Bento Scares Homo sapiens aDNA clone HIBBJ28 5' end	yc44a07.r1 Stratagene liver (#937224) Homo sapiens cDNA clone IMAGE:83508 5'	UI-H-BW1-amu-a-11-0-UI.s1 NCI_CGAP_Sub7 Homo sapiens cDNA clone IMAGE:3071132 3'	Homo saplens ubiquitin specific protease 13 (isopeptidase T-3) (USP13) mRNA	Homo sapiens ubiquitin specific protease 13 (isopeptidase T-3) (USP13) mRNA	601300938F1 NIH_MGC_21 Hamo sapiens cDNA done IMAGE:3635480 5'	RC1-HT0217-131199-021-h07 HT0217 Homo sapiens cDNA	RC1-HT0217-131199-021-h07 HT0217 Homo saplens cDNA	602136493F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4272886 5'	Homo sapiens human endogenous retrovirus W proC6-19 protease (pro) gene, partial cds	DKFZp434G022_r1 434 (synonym: htes3) Homo saplens cDNA clone DKFZp434G022 5'	Homo sapiens zinc finger protein 147 (estrogen-responsive finger protein) (ZNF147) mRNA	w637c12.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2307862 3' similar to contains Alu	repailive element,	yg36g10.r1 Soares infant brain 1NIB Homo sapiens cDNA done IMAGE:34529 5' similar to SP:CAHP_HUMAN P35219 CARBONIC ANHYDRASE-RELATED PROTEIN ;	yg36g10.r1 Soares infant brain 1NIB Homo sapiens cDNA done IMAGE:34529 5' similar to SP-CAHP HIMAN P35249 CARBONIC ANHYDRASE RELATED PROTEIN :	DKFZp7614229 r1 761 (symonym: hamy2) Homo sapiens cDNA done DKFZp761A229 5'	2051a12.r1 Stratagene endothellal cell 937223 Homo sepiens cDNA clone IMAGE:590398 5	2051a12.r1 Stratagene endothelial cell 937223 Homo sapiens cDNA clone IMAGE:590398 51	nc60e08.r1 NCI_CGAP_Pr1 Homo saplens cDNA clone IMAGE:745670	nc60e08.r1 NCI_CGAP_Pr1 Homo sapiens cDNA clone IMAGE:745670	AU141688 THYRO1 Homo sepiens cDNA clone THYRO1001033 5	AU141688 THYRO1 Homo sapiens cDNA clone THYRO1001033 5	xe82b07.x1 NCI_CGAP_Bm35 Hama sapiens cDNA clone IMAGE:2614357 3'	QV3-NN1023-010600-199-h01 NN1023 Homo sapiens cDNA	RC3-CT0279-040500-017-a10 CT0279 Home sapiens cDNA
Top Hit Database Source	LZ.	N	EST HUMAN	EST_HUMAN	EST_HUMAN	NT	EST_HUMAN	EST HUMAN	EST_HUMAN	TN	NT	EST_HUMAN	EST_HUMAN	EST HUMAN	EST HUMAN	ΤN	EST_HUMAN	LN.	MANULL TOTAL	ES L HOMAIN	EST_HUMAN	H H	EST HUMAN	EST HUMAN	EST HUMAN	EST_HUMAN	EST HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST HUMAN
Top Hit Acession Na	7662401 NT	10181139 NT	3.0E-36 BF035327.1	2.0E-36 BE259267.1	2.0E-36 AW880376.1	2.0E-36 AF267747.1			2.0E-36 BF512794.1	. 4507848 NT	4507848 NT	.0E-36 BE409310.1	.0E-36 BE146523.1	.0E-36 BE146523.1		.0E-36 AF156962.1	.0E-36 AL04446.1	4827064 NT	7 7 7 7 7 7 7	UE-36 AI86 / /14.1	.0E-36 R25012.1	0E.38 B25012 1	1.0E-36 AL120542.1	1.0E-36 AA148034.1	1.0E-36 AA148034.1	1.0E-36 AA420467.1	1.0E-36 AA420467.1	1.0E-36 AU141688.1	1.0E-36 AU141688.1	1.0E-36 AW 103658.1	1.0E-36 BF364169.1	1.0E-36 AW855868.1
Most Similar (Top) Hit BLASTE Value	3.0E-36	3.0E-36	3.0E-36	2.0E-36	2.0E-36	2.0E-36	2.0E-36 T08756.1	2.0E-36 T69629.1	2.0E-36	2.0E-36	2.0E-36	1.0E-36	1.0E-36	1.0E-36	1.0E-36	1.0E-36/	1.0E-36	1.0E-36	Lo	1.05-30	1.0E-38	1 05,38	1 0E-36 /	1.0E-36/	1.0E-36/	1.0E-36/	1.0E-36	1.0E-36	1.0E-36	1.0E-36	1.0E-36	1.0E-36/
Expression Signal	1.19	7.5	1.84	2.5	10.78	2.68	3.75	13.94	0.94	0.74	0.74	1.74	1.71	1.71	1.83	3.33	0.64	1.23		4.27	9.1	-	0.72	4.06	4.06	0.76	0.76	89.0	0.68	3.33		
ORF SEQ ID NO:	28630	30743	38086	29427	31174	31848	32471	33254	36212		Ĺ	L	ĺ				32344	32523			33055	32056		Ì.					34978	35850	l	37176
Exan SEQ ID NO:	15504	17761	24420	16412	18202	18798	19156	19864	22643	22687	22687	14083	15346	l	1	16594	ı	19203	ł	19484	19684	70907	1	21229	21229	┖	L.,	1	21454	22307		23569
Probe SEQ ID NO:	2373	4624	11368	3238	5074	5603	5970	9029	9588	9749	9749	806	2212	2212	2275	3425	5847	6020		6312	6219	8 1 2	6820	8147	8147	8243	8243	8373	8373	9229	10320	10534

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Top Hit Descriptor	RC3-CT0279-040500-017-a10 CT0279 Homo saplans cDNA	CM3-NN0061-140400-147-h12 NN0061 Homo sapiens cDNA	UI-HF-BN0-ale-c-03-0-UI.r1 NIH_MGC_30 Homo sapiens cDNA clone IMAGE:3079277 5	Homo sapiens PP3227 protein (PP3227), mRNA	Homo sapiens Ran GTPase activating protein 1 (RANGAP1), mRNA	Homo sapiens chromosome 21 segment HS21C013	Homo sapiens Sad1 unc-84 domain protein 2 (SUN2) mRNA, partial ods	ws80b07.x1 NCI_CGAP_Co3 Homo sapians cDNA clone IMAGE:2504245 3'	ws80b07.x1 NCI_CGAP_Co3 Home sapiens cDNA clone IMAGE:2504245 3'	73D4 Human retina cDNA Tsp509I-cleaved sublibrary Homo sapiens cDNA not directional	Homo sapiens chlmerin (chimaerin) 2 (CHN2) mRNA	CM0-UT0003-050800-503-d09 UT0003 Homo sapiens cDNA	ht06g01 x1 NCI_CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3146256 3' stmilar to contains MER29.b3 MER29 repetitive element ;	H09p01.x1 NCI CGAP Kid13 Homo saplens cDNA clone IMAGE:3146256 3' similar to contains MER29.b3	MER29 repetitive element;	RC1-CN0008-210100-012-a09_1 CN0008 Homo saplens cDNA	H.saplens DMA, DMB, HLA-Z1, IPP2, LMP2, TAP1, LMP7, TAP2, DOB, DQB2 and RING8, 9, 13 and 14	Sanes	DKFZp434E0422_r1 434 (synonym: htes3) Homo saptens cDNA clone DKFZp434E0422 5	EST380899 MAGE resequences, MAGJ Homo sapiens cUNA	wk25b11.x1 NCI_CGAP_Bm25 Homo sapiens cDNA done IMAGE:2413341 3' similar to contains PTR5.t2	twozwa w NCI CCAP Buck Home saniens cDNA circle IMAGE 2185140 3' similar to contains L1.b3 L1	repetitive element;	Homo sapiens protocadherin alpha 10 alternate isoform (PCDH-alpha10) mRNA, complete cds	Human olfactory receptor olfr17-201-1 (OR17-201-1) gene, olfactory receptor olfr17-32 (OR17-32) gene and	olfactory receptor pseudo_olfr17-01 (OR17-01) pseudogene, complete cds	Homo sapiens Sad1 unc-84 domain protein 2 (SUN2) mRNA, partial cds	EST178035 Colon carcinoma (HCC) cell line Homo sapiens cDNA 5' end	EST178035 Colon carcinoma (HCC) cell line Homo sapiens cDNA 5' end	AV750211 NPC Homo sapiens cDNA clone NPCBGH09 6'	Homo saplens glycine C-acctytransferase (2-amino-3-ketobutyrate-CoA ligase) (GCAT), mRNA	Homo sapiens NOD1 protein (NOD1) gene, exons 1, 2, and 3
Top Hit Database Source	П	EST_HUMAN	EST_HUMAN	LN	N.	LN	NT	EST HUMAN	EST_HUMAN	EST_HUMAN	NT	EST_HUMAN	FST HUMAN	7.1	EST_HUMAN	EST_HUMAN		L	EST_HUMAN	EST_HUMAN	NYFO ITI AGA	NICH I CO	EST HUMAN	TN		N	NT	EST_HUMAN	EST_HUMAN	EST_HUMAN	NT	NT
Top Hit Acession No.	.0E-36 AW855868.1	.0E-36 AW897638.1	.0E-36 AW 504143.1	11545901 NT	11418177 NT	.0E-36 AL163213.2	.0E-36 AF202723.1	.0E-37 AW009277.1	9.0E-37 AW009277.1	9.0E-37 W 22618.1	TN 6767574	8.0E-37 BE698077.1	0F-47 BE350197 4	1	3.0E-37 BE350127.1	9.0E-37 AW840840.1		8.0E-37 X87344.1	7.0E-37 AL042800.1	7.0E-37 AW968823.1	7 0022701	7.0E-37 MO17700.1	7.0F-37 AI536702.1	3.0E-37 AF169689.1		8.0E-37 U78308.1	6.0E-37 AF202723.1	5.0E-37 AA307123.1	5.0E-37 AA307123.1	5.0E-37 AV750211.1	7657117 NT	5.0E-37 AF149773.1
Most Similar (Top) Hit BLAST E Value	1.0E-36	1.0E-36	1.0E-36	1.0E-36	1.0E-36	1.0E-36	1.0E-36	9.0E-37	9.0E-37	9.0E-37	8.0E-37	8.0E-37	R 0E-37	100	8.0E-37	8.0E-37		8.0E-37	7.0E-37	7.0E-37	L	/:UE-3/	7.0F-37	6.0E-37		6.0E-37	6.0E-37	5.0E-37	5.0E-37	5.0E-37	5.0E-37	
Expression Signal	0.64	2.55	3.55	10.8	2.93	5.76	2.76	2.27	. 2.27	3.57	1.4	1.7	3 48	P. S	3.48	7.08		6.2	4.92	3.04		8.80	80	0.50		2.3	4.5	4.3	4.3	1.03	4.02	3.63
ORF SEQ ID NO:	37177	37895	38432			-			34088		29624		32AAB		32449		<u> </u>	34670		31320		37/00	37831					32741	32742	l		
SEQ ID NO:	23569	24259	24741	25029	Ι_	L	}	20612	l	1	16604	1		1	19135	1	L	21150	14469	18350	L	24073	24208	1	L	25575	L	L	1_	1_	24231	25242
Probe SEQ ID NO:	10534	11190	11662	12048	12340	12835	13131	7539	7539	12619	3436	5363	2040	2	5949	2998		8008	1313	5228		10994	11194	8634	3	12864	12984	6218	6218	8956	11160	12335

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Top Hit Descriptor	zB0b04.s1 Soares_feta_liver_spleen_1NFLS_S1 Homo saplens cDNA clone IMAGE:448015 3'	RC6-UM0014-210200-021-H05 UM0014 Homo sapiens cDNA	ak09c02.s1 Soares_parathyrold_tumor_NbHPA Homo sapiens cDNA clone IMAGE:1405442.3	DKFZp434L2418_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434L2418	DKFZp434[2418_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434[2418	EST373222 MAGE resequences, MAGF Homo sapiens cDNA	EST373222 MAGE resequences, MAGF Homo sapiens cDNA	DKFZp547G067_r1 547 (synonym: hfbr1) Homo saplens cDNA clone DKFZp547G067 5	аіЗ4605лл Barstead cdon HPLRB7 Homo sapiens cDNA chone IMAGE:2373896 3' similar to TR:Q13637 Q13537 SIMILAR TO POGO ELEMENT.;	Homo saplens mRNA for AML1, complete cds	Hamo sepiens mRNA for AML1, complete cds	AU 131202 NT2RP3 Homo sapiens cDNA clone NT2RP3002166 5	AU137202 NT2RP3 Homo sapiens cDNA clone NT2RP3002166 5	Homo sapiens chromosome 21 segment HS21C047	Home sapiens cytochrome P450, subfamily XXVIIA (steroid 27-hydroxytase, cerebrotendinous	Homo sanians DFAD/H (Asp.Glu-Ala-Asp/His) box odvoeofide 1 (DDX1) mRNA	601458531F1 NIH MGC 66 Homo sapiens cDNA clone IMAGE:3862086 5	Hamo sapiens mouse thiamin pyrophosphokinase hamdog (TPK1), mRNA	EST62931 Fetal heart II Homo sapiens cDNA 5' end	601067534F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3453657 51	601067534F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3453657 5'	601869157F1 NIH_MGC_17 Homo saplens cDNA clone IMAGE:4111406 5'	Homo sapiens J domain containing protein 1 isoform b (JDP1) mRNA, complete cds	Homo sapiens pescadillo (zebrafish) homolog 1, containing BRCT domain (PES1), mRNA	Homo sapiens pescadillo (zebrafish) homolog 1, containing BRCT domain (PES1), mRNA	Homo saplens chromosome 21 segment HS21C081	RC3-CT0347-210400-016-h03 CT0347 Homo sapiens cDNA	QV0-FN0180-280700-318-c10 FN0180 Homo sapiens cDNA	Mus musculus otogelin (Otog), mRNA	601072419F1 NIH_MGC_12 Homo sapiens cDNA done IMAGE:3458308 5'	zp21b02.r1 Stratagene neuroepithelium (#937231) Homo sapiens cDNA clone IMAGE:610059 5' similar to	contains L1.t2 L1 repetitive element :
Top Hit Database Source	EST_HUMAN	EST_HUMAN	EST HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST HUMAN	LN	LZ	EST_HUMAN	EST_HUMAN	님	1	- 1	FST HIMAN	LN	EST HUMAN	EST HUMAN	EST_HUMAN	EST_HUMAN	LN	±Ν	Ę	LΝ	EST_HUMAN	EST_HUMAN	F	EST_HUMAN		EST_HUMAN
Top Hit Acession	.0E-37 AA702794.1	.0E-37 AW 794502.1	4.0E-37 AA843806.1	3.0E-37 AL046956.1	3.0E-37 AL048956.1	3.0E-37 AW961150.1	3.0E-37 AW961150.1	.0E-37 AL138274.1	3.0E-37 AI749952.1	2.0E-37 D89790.1	2.0E-37 D89790.1	2.0E-37 AU131202.1	2.0E-37 AU131202.1	2.0E-37 AL163247.2	0.0007	4503210 N I	2.0E-37 REPRESSOR 1	11890617 NT	2.0E-37 AA346720.1	2.0E-37 BE537764.1	2.0E-37 BE537764.1	2.0E-37 BF204032.1	2.0E-37 AF176013.1	11417972 NT	11417972 NT	1.0E-37 AL163281.2	1.0E-37 AW862082.1	BF371719.1	7305360 NT	1.0E-37 BE546032.1		1.0E-37 AA171406.1
Most Similar (Top) Hit BLAST E Value	4.0E-37 /	4.0E-37	4.0E-37	3.0E-37	3.0E-37	3.0E-37	3.0E-37	3.0E-37	3.0E-37	2.0E-37	2.0E-37	2.0E-37	2.0E-37	2.0E-37		2.05-37	2.0E-37	2.0E-37	2.0E-37	2.0E-37	2.0E-37	2.0E-37	2.0E-37	2.0E-37	2.0E-37	1.0E-37	1.0E-37	1.0E-37	1.0E-37	1.0E-37		1.0E-37
Expression	2.97	0.68	0.56	3.42	3.42	1.54	4.02	0.7	0.72	0.89	0.89	2.53	2.53	1.32		0.0	5 5	80	3.72	0.47	0.47	2.32	10.07	1.44	4.19	6.95	1.03	2.34	0.89	1.12		3.50
ORF SEQ ID NO:	28741	32947			28333			32492		26666	26667	27328	27329	28267		30162	1	1	33353		34791	34829	38541			28417		31158		35019		35551
Exon SEQ ID NO:	15622	_			L	1	16206	19170	l	13629	13620	14270	14270	15162		1/136	1_	L	L	1	1	21309	ı	ı	ı	15290	16441	18183	19306		1	22012
Probe SEQ ID NO:	2495	6416	9556	2074	2074	2581	3030	5985	77.28	392	392	1105	1105	2021		388	702	-000 8678	6798	8185	8185	8227	11856	12797	13184	2154	3267	5055	6127	8409		8933

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			T	T	1	7			1	1		1	T	T		T	1	T	T			T	T			T	T		1				T	T	7
Too Hit Descriptor		Human somatic cytochrome c (HC1) processed pseudogene, complete cds	CM3-FT0096-140700-243-d07 FT0096 Homo sapiens cDNA	Rattus norvegicus multidomain presynaptic cytomatrix protein Plocalo (LOC56768), mKNA	Homo sapiens Grb2-associated binder 2 (KIAA0571), mRNA	602018401F1 NCL_CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4153992 5	Homo sapiens Grb2-associated binder 2 (KIAA0571), mRNA	Homo saplens DNA for Human P2XM, complete cds	EST384920 MAGE resequences, MAGL Homo saplens cDNA	601455722F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3859348 5'	Homo sapiens zinc finger protein ZNF287 (ZNF287), mRNA	Homo sapiens zinc finger protein ZNF287 (ZNF287), mRNA	Homo sepiens hypothetical protein FLJ20128 (FLJ20128), mRNA	Homo sapiens chromosome 12 open reading frame 3 (C12ORF3), mRNA	Hamo sapiens DNA for Human P2XM, complete cds	Homo sapiens adenylosuccinate (yase (ADSL), mRNA	EST383908 MAGE resequences, MAGL Homo saplens cDNA	Homo sapiens RIBIIR gene (partial), exon 8	Homo sapiens deiodinase, lodothyronine, type II (DIO2), transcript variant 2, mRNA	Homo sapiens delodinase, iodothyronine, type II (DIO2), transcript variant 2, mKNA	Homo sapiens RIBIIR gene (partial), exon 8	601450148F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3854074 5	B.taurus mitochondrial aspartate aminotransferase mRNA, complete CDS	B.taurus mitochondrial aspartate aminotransferase mRNA, complete CDS	Homo sapiens chromosome 12 open reading frame 3 (C12ORF3), mKNA	Homo saplens homeobox protein CDX4 (CDX4) gene, complete cas and rienking repeat regions	Homo sapiens HIRA interacting protein 4 (dnaJ-like) (HIRIP4), mKNA	SSU72 PROTEIN	SSU72 PROTEIN	601157633F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3504272 5	Homo sapiens chromosome 21 segment HS21C100	xw04d01.x1 NCL_CGAP_Bm53 Homo saplens cDNA done IMAGE:2827009 3	CMS-FT0181-140700-241-f07 FT0181 Homo sapiens cDNA	yv88b04.r1 Soares melanocyte 2NbHM Homo sapiens cDNA clone IMAGE:249775 5	y/88b04.rf Scares melanocyte ZNbHM Homo sapiens cDNA clone IMAGE. 2497733
Top Hit	Source	TN	EST HUMAN	NT	닏	EST_HUMAN	NT	NT	EST_HUMAN	EST_HUMAN	NT	. LN	TN	LN	NT	. LN	EST HUMAN	IN	TN	NT	LN	EST_HUMAN	ΙN	TN	NT	LNT	NT	SWISSPROT	SWISSPROT	EST_HUMAN	NT	EST_HUMAN	<b>EST_HUMAN</b>	EST_HUMAN	EST_HUMAN
Top Hit Acession	ó		1.0E-37 BE771814.1	10048482 NT	11436955 NT	8.0E-38 BF346221.1	11436955 NT	8.0E-38 AB002059.1	7.0E-38 AW972825.1	6.0E-38 BF033033.1	11425114 NT	11425114 NT	8923130 NT	11435947 NT	6.0E-38 AB002059.1	11418164 NT	1	5.0E-38 AJ237740.1	7549804 NT	7549804 NT	5.0E-38 AJ237740.1	5.0E-38 BE871610.1	4.0E-38 Z25466.1	4.0E-38 Z25466.1	11435947 NT	3.0E-38 AF003530.1	7549807 NT	P53538	P53538	3.0E-38 BE279301.1	3.0E-38 AL163300.2	3.0E-38 AW302461.1	3.0E-38 BF373664.1	3.0E-38 H85494.1	3.0E-38 H85494.1
<del></del>	BLAST E Value	1.0E-37 M22878.1	1.0E-37	9.0E-38	8.0E-38	8.0E-38	8.0E-38	8.0E-38	7.0E-38	6.0E-38	6.0E-38	6.0E-38	6.0E-38	6.0E-38	6.0E-38	6.0E-38	5.0E-38	5.0E-38	5.0E-38	5.0E-38	€.0E-38	5.0E-38	4.0E-38	4.0E-38	3.0E-38	3.0E-38	3.0E-38	3.0E-38 P53538	3.0E-38 P53538		3.0E-38		3.0E-38	3.0E-38	3.0E-38
Expression	Signal	2.19	1.94	1.72	1.96	1.21	1.37	1.44	1.7	1.98	0.98	0.98	0.59	4.27	99.9	1.79	6.0	4.57	0.94	77.0	96.0	1.63	4.28	428	1.15	4.42	1.49			0.61	5.80		6.53		2,11
ORF SEQ	Ö NÖ	37652		32398			27470			29299		L			32025	31861	26967			29961		33748		L				30119			33463				35470
Exon	다. 일 ::	24019	25447	19086	1		14408	26049	1	16283	18899	ı	1	1	L	١_	13926	1	l_	16957	l l	l	1.		14346	L	16948	L			26836	L_	<u> </u>	_	21930
Probe		10937	12671	2898	1249	2567	12735	13210	2254	3107	5706	5706	7482	12189	12704	13160	745	2525	3796	3971	5288	7172	121	121	1183	2167	3787	3958	3958	4736	6893	7393	7763	8851	8851

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Γ		П			П							Γ	Ι_		П			2	٣		7	_			П	J	7	-
	Top Hit Descriptor	Homo sapiens chromosome 21 segment HS21C048	Homo sapiens chromosome 21 segment HS21 C048	Homo sapiens chromosome 12 open reading frame 3 (C12ORF3), mRNA	Homo sapiens chromosome 21 segment HS21C048	Homo sapiens SMT3 (suppressor of mif two 3, yeast) homolog 2 (SMT3H2), mRNA	zw30d01.r1 Soares ovary tumor NbHOT Homo septens cDNA clone IMAGE:770785 5' similer to SW:MA12_RABIT P45701 MANNOSYL-OLIGOSACCHARIDE ALPHA-1,2-MANNOSIDASE;	zw30401.r1 Soares ovary tumor NbHOT Homo sapiens cDNA clone (MAGE:770785 5' simiter to SW:MA12_RABIT P45701 MANNOSYL-OLIGOSACCHARIDE ALPHA-1,2-MANNOSIDASE;	Homo saplens protein phosphatase 2C alpha 2 mRNA, complete cds	Homo sapiens keratin 18 (KRT18) mRNA	2x61409.r1 Soares testls. NHT Homo sepiens cDNA clone IMAGE:758129 5' similar to TR:G817957 G817957 GLYCINE RECEPTOR SUBUNIT ALPHA 4;	Homo sapiens mRNA for ankyrin B (440 kDa)	Homo sapiens mRNA for ankyrin B (440 kDa)	AV721103 HTB Homo sapiens cDNA clone HTBARH11 5	MR3-HT0487-150200-113-g01 HT0487 Homo sapiens cDNA	HSC18F031 normalized Infant brain cDNA Homo saplens cDNA clone c-18f03	Homo sapiens orphan G protein-coupled receptor HG20 (HG20) mRNA, complete cds	hu09g02.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3166130 3' similar to TR:C02710 C02710 GAG POLYPROTEIN.;	Homo saplens mRNA for KIAA0145 protein, partial cds	QV2-HT0698-080800-293-a05 HT0698 Homo sapiens cDNA	Homo sapiens laucina-rich repeat-containing G protein-coupled receptor 6 (LGR8) mRNA, partial ods	Homo sapiens leucine-rich repeat-containing G protein-coupled receptor 6 (LGR6) mRNA, partial cds	AV726988 HTC Homo saplens cDNA clone HTCAXH07 5'	Homo sapiens gene for kinesin-like protein, complete cds	Human topoisomerase I pseudogene 2	CHR220580 Chromosome 22 exon Homo sapiens cDNA clone C22_788 5'	E1 beta=pyruvate dehydrogenase beta (promoter) [human, placenta, Genomic, 1280 nt]	
	Top Hit Database Source	LΝ	NT	Ę	FN	N.	EST_HUMAN	EST HUMAN	LN LN	Ę	EST HUMAN	Т		T HUMAN	EST_HUMAN	EST_HUMAN	LN.	EST_HUMAN	IN	EST_HUMAN	LN	. LN	EST_HUMAN	TN	IN	EST_HUMAN	IN	
	Top Hit Acession No.	1.0E-38 AL163248.2	3.0E-38 AL163248.2	11435947 NT	2.0E-38 AL163248.2	5902097 NT	2.0E-38 AA437353.1	2.0E-38 AA437353.1		4557887 NT	2 0F-38 AA437181.1	Γ		2.0E-38 AV721103.1			2	2.0E-38 BE222256.1	20E-38 D63479.2	2.0E-38 BE712790.1	2.0E-38 AF190501.1	2.0E-38 AF190501.1	2.0E-38 AV726988.1	2.0E-38 AB012723.1	2.0E-38 M55630.1	H55641.1	S74906	
	Most Similar (Top) Hit BLAST E Value	3.0E-38	3.0E-38/	3.0E-38	2.0E-38	2.0E-38	2.0E-38	2.0E-38/	2.0E-38	2.0E-38	2.0F-38	2.0E-38			2.0E-38	2.0E-38	2.0E-38	2.0E-38	20E-38	2.0E-38	2.0E-38	l		2.0E-38	2.0E-38	2.0E-38	2.0E-38	
	Expression Signal	1.84	1.88	1.23	1.96	3.66	13.95	13.95	0.92	18.99	89 0	0.75	0.75	1.47	4.47	0.49	1.26	1.36	1.67	4.86	2.86	2.88	6.21	1.26	3.36	4.81	2.87	
	ORF SEQ ID NO:				26303					30824		l	ļ			35719	35786		37309	38467	38626	38627				32073		
	SEQ ID NO:	23214	24651	L	L	14565	J	<u> </u>	L	L		L	L	L	1_	1	22243	1		24771	24925			l	j	)	25425	
	Probe SEQ ID NO:	10177	11598	12990	61	1411	1678	1678	3622	4704	5252	5836	5836	7897	8680	9606	9165	9422	10665	11781	11939	11939	12244	12246	12546	12559	12632	

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		Т	Т	Т	Т	$\neg$	Т	Т	Т	Т	Т	Т	Т	1	6	Г	П	7	П	g T	7	٦			Т		Γ	7
Top Hit Descriptor	zu82b02.r1 Soares_testis_NHT Homo sapiens cDNA clone INAGE:742539 წ similar to contains element MER19 repetitive element ;	Homo sapiens guanine nucleotide binding protein-like 1 (GNL1), mRNA	Homo sapiens KIAA0173 gene product (KIAA0173), mRNA	Hamo sapiens cyclin K (CCNK) gene, exon 7	Homo sapiens mRNA for KIAA1442 protein, partial cds	Homo sapiens low density lipoprotein receptor-related protein 6 (LRP6) mRNA, and translated products	Homo sapiens chromosome 21 segment HS21C003	Homo sapiens chromosome 21 segment HS21C003	Homo sapiens hypothetical protein FLJ10600 (FLJ10600), mKNA	Homo sapiens chromosome 21 segment HS21C080	Mus musculus otogelin (Otog), mRNA	Mus musculus otogelin (Otog), mRNA	Homo sepiens mRNA for KIAA0612 protein, partial cds	Homo sapiens hypothetical protein FLJ10600 (FLJ10600), mRNA	ht09g01.x1 NCI_CGAP_Kid13 Homo sapiens cDNA done IMAGE:3148256 3' sImilar to contains MER29.b3 MER29 resettiive element :	Homo sariens chromosome 21 segment HS210084	2n/2707.r1 Stratagene pancreas (#937208) Homo sapiens cDNA clone IMAGE:526885 5'	Homo capiens ATPase, H+ transporting, lysosomal (vacudar proton pump) 16kD (ATP6C) mRNA	Homo sapiens estrogen receptor-binding fragment-associated gene 9 (EBAG9) mRNA	wh53r10.x1 NCI_CGAP_Kid11 Homo saplens cDNA clone IMAGE:2384491 3' similar to TR:P87890 P87890 POL PROTEIN;	Homo sapiens chromosome 21 segment HS21C027	QV1-BT0631-040900-357-{02 BT0631 Homo sapiens cDNA	7e34c03.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3284356 3' similar to WP:R151.6 CE00828 :	Homo sapiens X-linked anhidroitic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat	regions	at36b04.x1 Barstead colon HPLRB7 Homo sapiens cDNA clone IMAGE:2374063 3' similar to TR:Q15408 Q15408 NEUTRAL PROTEASE LARGE SUBUNIT ;contains LTR7.t1 LTR7 repetitive element ;	Domo serions hypothetical protein Ft 110803 (FL 110803) mRNA	ושמוום משופוו או אוא מתופות של מתייני הם והכבה לי הבי ברבה אייי בייי
Top Hit Database Source	T_HUMAN		LN	NT	NT	NT	ΝT	NT .	NT	NT	NT	NT	NT	LN	HIMAN	TN	EST HUMAN	LN	LN.	EST HUMAN	F	EST HUMAN	EST HUMAN		TN	EST HUMAN	2	_
Top Hit Acession No.	1.0E-38 AA401570.1	4885288 NT	7661969 NT	1.0E-38 AF270831.1	1.0E-38 AB037863.1	4505016 NT	1.0E-38 AL163203.2	1.0E-38 AL163203.2	8922543 NT	1.0E-38 AL163280.2	7305360 NT	7305360 NT	1.0E-38 AB014512.1	11422250 NT	1 OE 38 BE3501 27 1	4 05 20 14 482204 2	1.0E-36 AL 103264.2	4502312 NT	4758229 NT	8.0E-39 AI823404.1	7.0E-39 AL163227.2	6.0E-39 BF331829.1	6 0E-39 BE670394 1		5.0E-39 AF003528.1	5 0F-39 A1750154.1	F1 00000	11420203
Most Similar (Top) Hit BLAST E Value	1.0E-38	1.0E-38	1.0E-38	1.0E-38	1.0E-38	1.0E-38	1.0E-38	1.0E-38	1.0E-38	1.0E-38	1.0E-38	1.0E-38	1.0E-38	1.0E-38	200	1 00 30	1.0E-36/	8.0F-39	8.0E-39	8.0E-39	7.0E-39	6.0E-39	R 0E-30	23.7	5.0E-39	5.05.39	10.7	5.0E-39
Expression Signal	1.96	2.62	1.33	1.69	0.93	0.6	2.15	2.15	1.08	1.89	4.69	4.59	2.55	0.58	6	25	4.78 8.78	4 93	13	8.	7.08	2.4	200		1.64	0	3.5	<u>8</u>
ORF SEQ ID NO:		28310	28336	28815		30558					32672	32673					28804					37758			27259			_
Exen SEQ ID NO:	14282	L	L	L	17416	17579	1	1	Į.	1	l	19327	L	L	1	. 1	25877	1	L	.1	1		1	L	14201	1	J	25479
Probe SEQ ID NO:	1117	2055	2077	2564	4271	4439	4444	4444	4719	5268	8151	6151	7563	9354	999	0106	12403	2 2	1425	1876	2460	11047	19064	1000	1032	3050	OCOS.	12720

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Top Hit Descriptor	Chlarocebus aethiops mRNA for ribocomal protein S4X, complete cds	Homo sapiens chromosome 21 segment HS21C010	Homo sapiens EBNA-2 co-ectivator (100kD) (p100), mRNA	Homo sapiens EBNA-2 co-activator (100kD) (p100), mRNA	ac92g04,s1 Stratagene schizo brain S11 Homo saplens cDNA done IMAGE:1020438 3' similar to contains	OFR.DI OFR repoulte defining.	Tunio saptem Investoria symmetry, con re-	Hano saplens Diva to prostacycin synutase, excit z	Homo sapiens Ran GTPase activating protein 1 (KANGAP1), mKNA	QV0-FN0063-260600-278-c06 FN0063 Homo saptens cDNA	fmíc18 Regional genomic DNA specific cDNA library Homo saplens cDNA clone CR12-1	finfo16 Regional genomic DNA specific cDNA library Homo sapiens cDNA clone CR12-1	finfc16 Regional genomic DNA specific cDNA library Homo sapiens cDNA clone CR12-1	cx63a10.s1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:1660986 3' similar to SW.GTR5_RAT	P43427 GLUCOSE IRANSPORTER TYPE 5, SMALL INTESTINE:	οκ63a10.s1 Soares_NhHMPu_S1 Homo sapiens cDNA clone.IMAGE:1660986 3' similar to SW:GTR5_RAT   P43427 GLUCOSE TRANSPORTER TYPE 5, SMALL INTESTINE;	yp51c06 s1 Soares retina N2b4HR Homo saplens cDNA done IMAGE:190954 3'	601301607F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3636289 5	promrna-7.001 r bytumor Homo sapiens cDNA 5'	Homo sapiens homogentisate 1,2-dloxygenase gene, complete cds	PM0-BT0340-211299-003-d02 BT0340 Homo sapiens cDNA	тw21g02.s1 NCI_CGAP_GCB0 Homo sapiens cDNA clone IMAGE:1241138 3' similar to contains THR.13	THR repetitive element;	Homo sapiens chromosome 21 segment HS21C048	RC4-FN0037-290700-011-a10 FN0037 Homo sapiens cDNA	ng86f03.s1 NC[_CGAP_Prd Homo sapiens cDNA clone IMAGE:941693	zn06i02.r1 Stratagene hNT neuron (#537233) Homo sapiens cDNA clone IMAGE:546651 5'	Homo sapiens chromosome 21 segment HS21C002	Homo sapiens chromosome 21 segment HS21C002	Rattus norvegicus putative four repeat ion channel mRNA, complete cds	tu35e03.x1 NCI_CGAP_Pr28 Homo sapiens cDNA clone IMAGE:2253052 3'	Human mRNA for KIAA0209 gene, partial cds	Homo saplens KVLQT1 gene
Top Hit Database Source	NT	IN	NT	N		ESI HUMAN	Į.	Z	NT	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN		EST_HUMAN	EST HUMAN	EST_HUMAN	EST HUMAN	EST_HUMAN	N	EST_HUMAN		EST_HUMAN	LN	<b>EST_HUMAN</b>	EST_HUMAN	EST_HUMAN	님	IN	NT	EST_HUMAN	NT TA	님
Top Hit Acession No.	4.0E-39 AB015610.1	4.0E-39 AL163210.2	11422113 NT	11422113 NT				J84116.1	18177			3.0E-39 AA631949.1	3.0E-39 AA631949.1		3.0E-39 Al084557.1	3.0E-39 A1084557.1	3.0E-39 H37903.1	2.0E-39 BE409203.1	2.0E-39 AI525119.1	2.0E-39 AF000573.1	2.0E-39 AW372318.1		2.0E-39 AA720574.1	2.0E-39 AL163248.2	2.0E-39 BF370207.1	2.0E-39 AA508880.1	2.0E-39 AA080867.1	2.0E-39 AL163202.2	2.0E-39 AL163202.2	2.0E-39 AF078779.1	2.0E-39 AI686660.1	2.0E-39 D86964.1	1.0E-39 AJ006345.1
Most Similar (Top) Hit BLAST E Value	4.0E-39	4.0E-39	4.0E-39	4.0E-39		4.0E-39	4.0E-39	4.0E-39 D84116.1	4.0E-39	4.0E-39	3.05-39	3.0E-39	3.0E-39		3.0E-39	3.0E-39	3.0E-39	2.0E-39	2.0E-39	2.0E-39	2.0E-39		2.0E-39	2.0E-39	2.0E-39	2.0E-39	2.0E-39	2.0E-39	2.0E-39	2.0E-39	2.0E-39	2.0E-39	1.0E-39
Expression Signal	4.39	6.0	9.0	9.0		1.02	0.46	0.46	6.36	2.56	11.96	11.96	11.96		6:20	69'9	5.72	7.78	11.55	3.9	33.59		4.48	1.89	1.74	4.45	2.08	0.68	89'0	0.63	0.79	2.13	2.83
ORF SEQ ID NO:	26782	29835						36166			26297	26298	26299		38348	38349							28279	28928	30649		34073	L	34252			38452	
SEO ION OC.	13756	16826	19136	19138			-1	. 1	25494	25586	13287	13287		1	25180	25180	1_	1_	L	14223	14713		15171	15812	17662		20599	L	20767	L	ı	1	Ш
Probe SEQ ID NO:	564	3983	2950	5950		8267	9530	9530	12744	12884	48	48	48		12238	12236	12284	920	935	1057	1560		2030	2692	4523	5608	7526	7702	7702	8505	9826	11716	1543

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Datebase Source	Top Hit Descriptor
55	14695	27775	2.83	1.0E-39	0E-39 AJ006345.1	LN	Homo sapiens KVLQT1 gene
1561	14714	27791	5.96	1.0E-39	7657020 NT		Homo sapiens DKFZp434P211 protein (DKFZP434P211), mRNA
1783	14912		1.14	1.0E-39	0E-39 H55224.1		CHR220163 Chromosome 22 exxn Homo saplens cDNA clono C22_205 5
4782	L		9.32	1.0E-39	0E-39 AW951995.1		EST364065 MAGE resequences, MAGB Homo saplens cDNA
4782				1.0E-39	0E-39 AW951995.1	EST HUMAN	EST364065 MAGE resequences, MAGB Homo sapiens cDNA
4824	17957	30943	9.13	1.0E-39	7657020 NT		Homo sapiens DKFZp434P211 protein (DKFZP434P211), mRNA
5474	18673	31686	0.82	1.0E-39	· 11417342 NT	TN	Homo sapiens sema domain, seven furombospondin repeats (type 1 and type 1-lika), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 5A (SEMA5A), mRNA
5474	18673	31687	0.82	1.0E-39	11417342 NT	Ŋ	Homo sapiens sema domain, seven thrombospondin repeats (type 1 and type 1-like), transmembrane domain (TM) and short cytoplasmic domain, (semaphorh) SA (SEMASA), mRNA
5747	]	1		-	0E-39 T80876.1	EST_HUMAN	yd26g06.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:109402 5' similar to contains Alu repetitive element,contains LTR1 repetitive element ;
5781	18973		4.65	1.0E-39	.0E-39 AJ278170.1	NT	Mus musculus mRNA for neuronal interacting factor X 1 (NIX1) (Nix1 gene)
5781	18973		4.65	-	.0E-39 AJ278170.1	NT	Mus musculus mRNA for neuronal interacting factor X 1 (NIX1) (Nix1 gene)
8965	J		1.95	1	11436736 NT	NT	Homo sepiens tubby like protein 3 (TULP3), mRNA
7521	20594	34069	2.15	1	.0E-39 D78132.1	NT	Homo sapiens mRNA for ras-related GTP-binding protein, complete cds
8762	21841	35382	1.04	1	.0E-39 O46530	SWISSPROT	RIBONUCLEASE K6 PRECURSOR (RNASE K6)
11165	24236	37867	1.4		4759051 NT	NT	Homo sapiens ribosomai protein S6 kinase, 90kD, polypeptide 5 (RPS6KAD) mKNA
8	13761	26785	2	9.0E-40		NT	Homo sapiens UDP-glucosc pyrophosphorylase 2 (UGP2), mRNA
1283	14420		16.02	9.0E-40		NT	Homo saplens AE-binding protein 1 (AEBP1) mRNA
1283	14420	27485	16.02		4755145 NT	K	Homo sapiens AE-binding protein 1 (AEBP1) mRNA
1480	14633	27718	16.75	9.0E-40	4507512 NT	Ľ	Homo sapiens tissue inhibitor of metalloproteinase 3 (Sorsby fundus dystropny, pseudoinitaminatory) (Timr 5), . mRNA
3885		L		1	9.0E-40 4503764 NT	LN	Homo sapiens fragile X mental retardation 1 (FMR1) mRNA
4081	L	L	3.99	L	AB033070.1	TN	Homo sapiens mRNA for KIAA1244 protein, partial cots
4466	17606		5.63		4507848 NT	NT	Homo saplens ubiquitin specific protease 13 (Isopeptidase T-3) (USP13) mRNA
3106	L	L	1.04	L	8.0E-40 AA078165.1	EST_HUMAN	7H15A04 Chromosome 7 HeLa cDNA Library Homo sapiens cDNA clone 7H15A04
4033	17189		3.43		8.0E-40 BE396541.1	EST_HUMAN	601288958F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3619166 5
7894	20948	34462	2.21		.0E-40 U60325.1	Ľ	Human DNA polymerase gamma mRNA, nuclear gene encoding mitochondrial protein, complete cds
7894	20946	34453	2.21		.0E-40 U60325.1	N	Human DNA polymerase gamma mRNA, nuclear gene encocling mitochondrial protein, complete cds
11136	1				.0E-40 AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
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Page 288 of 550 Table 4 Single Exon Probes Expressed in Placenta

										_,					_,	_			_	-	<u>.                                     </u>	-		_	÷			_		~~~	·
	Top Hit Descriptor	EST706227 T-cell lymphoma Homo saplens cDNA 6' end similar to similar to zinc finger protein family	EST70527 T-cell lymphoma Homo saplens cDNA 5' end similar to similar to zinc finger protein family	hz40g01.x1 NCI_CGAP_GC6 Homo seplens cDNA clone IMAGE:3210480 3'	Homo sapiens KIAA0211 gene product (KIAA0211), mRNA	Homo sapiens fatty acid desaturase 1 (FADS1), mRNA	Homo sapiens fatty acid desaturase 1 (FADS1), mRNA	AV653028 GLC Homo sapiens cDNA clone GLCDGF04 3'	AV653028 GLC Homo sapiens cDNA clone GLCDGF043'	Homo sapiens chromosome 21 segment HS210085	tt81b01,x1 NCI_CGAP_Pr28 Homo septens cDNA clone IMAGE:2248873 3' similar to TR:073505 O73505 POL PROTEIN.;	Homo sapiens X-linked anhidrolitic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat	regions	Homo sapiens KIAA0433 protein (KIAA0433), mRNA	AU127831 NT2RP2 Homo sapiens cDNA done NT2RP2002172 5'	m34e10.r1 NCI_CGAP_Br4 Hama seplens cDNA clone IMAGE:1222122	PM0-BN0167-070500-002-h12 BN0167 Homo sapiens cDNA	PM0-BN0167-070500-002-h12 BN0167 Homo sapiens cDNA	RC1-CN0017-120200-012-e04 CN0017 Homo sapiers cDNA	wh12f07.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clane IMAGE:2380549 3'	21.6h09.s1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:377153 3	Homo sapiens ribosomal protein S6 kinase, 70kD, polypeptide 1 (RPS6KB1) mKNA	Homo sapiens sema domain, seven thrombospondin repeats (type 1 and type 1-like), transmembrane domain	(TIVI) and Short cyphastine domain, seminary or (Chieron), improving the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company	Homo sapiens HBV associated racun (AAF4) IIINIVA	Rattus novegicus putative four repeat ion channel mikNA, complete cos	Rattus norvegicus putetive four repeat ion channel mRNA, complete cds	Human mRNA for KIAA0209 gene, partial cds	Homo sapiens serine threonine protein kinase (NDR), mRNA	qg52h08.x1 Soares_tests_NHT Homo sapiens cDNA clone IMAGE:1838847 3'	xr24e10.x1 NCI_CGAP_Ut4 Homo sapiens cDNA clone IMAGE:2761098 3' similar to SW:RS5_MOUSE P97461 40S RIBOSOMAL PROTEIN S5. ;
	Top Hit Database Source	EST_HUMAN		L HUMAN	NT	NT	. 1	EST HUMAN	EST_HUMAN	NT	EST HIMAN		Z	L	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HÜMAN	EST_HUMAN	EST_HUMAN	NT.		2	LN	NT	NT	LΝ	NT.	EST_HUMAN	EST_HUMAN
)	Top Hit Acession No.	6.0E-40 AA361275.1	6.0E-40 AA361275.1	3E50476	7661999 NT		11439783 NT	6.0E-40 AV653028.1	6.0E-40 AV653028.1	5.0E-40 AL163285.2	4 DF 40 AIRBRD05 1		.0E-40 AF003628.1	7662117 NT	.0E-40 AU127831.1	4.0E-40 AA742809.1	BE009416.1	4.0E-40 BE009416.1	4.0E-40 AW841585.1	3.0E-40 AI925949.1	.0E-40 AA055118.1	4506736 NT		11417342NI	5454167 NT	3.0E-40 AF078779.1	3.0E-40 AF078779.1	3.0E-40 D86964.1	6005813 NT	2.0E-40 A1223036.1	2.0E-40 AW303868.1
	Most Similer (Top) Hit BLAST E Value	6.0E-40	6.0E-40	6.0E-40	6.0E-40	6.0E-40	6.0E-40	6.0E-40	6.0E-40	5.0E-40	4 0F 40		4.0E-40	4.0E-40	4.0E-40	4.0E-40	4.0E-40	١			ຶ່	3.0E-40		3.0E-40	3.0E-40	3.0E-40	L				
	Expression Signal	9.91	9.91	1.85	1.38	3.04	3.04	60.09	60.9	2.75	å		6.81	7.2	0.64	86.9	5.84	5.84				99.0		7.06		1.27	1.6	,			5.58
	ORF SEQ ID NO:	29011	29012			33544			36812					30635	34672	34785		35882		30385	ļ	33137		33328							
	Exon SEQ ID NO:	15904	15904	ľ	19449	20128	20128	ı	23219	15791	i	1	15310	ı		L		1	1	17396	l	19752	١.	- 1		22247	ì	ì		1	
	Probe SEQ ID NO:	2788	2788	9090	6275	7075	7075	10182	10182	2670	1005	1920	2175	4508	8070	8181	9255	9255	10955	4250	4993	6592		6777	8575	9169	9412	10899	11544	335	817

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Top Hit Descriptor	AV731601 HTF Homo sapiens cDNA clone HTFAZE05 5	Homo saplens proteasome (prosome, macropain) subunit, alpha type, 7 (Powa 7) inc.va, aru uaisaaca products	Homo sepiens proteasome (prosome, macropaln) subunit, alpha type, 7 (PSMA7) mKNA, and transated products	wt90a11.x1 NCI_CGAP_GC6 Homo sepiens cDNA clone IMAGE:2514716 3' similar to TR:091929 Q91929 ZINC EINGER PROTEIN	Homo saplens adentifyl cyclase-associated protein 2 (CAP2) mRNA	R01121567F1 NIH MGC 20 Homo sepiens cDNA clone IMAGE:3345784 5	Homo sapiens adenylyl cyclase-associated protein 2 (CAP2) mRNA	Homo sapiens chromosome 21 segment HS21 CO80	Homo saplens chromosome 21 segment HS21C080	nc09a09.s1 NCI_CGAP_Prf Homo sapiens cDNA clone IMAGE:1007608	601460375F1 NIH MGC_68 Homo sapiens cDNA clone IMAGE:3863803 5	b578a10.7/ NIH_MGC_10 Homo sepiens cDNA clone IMAGE:3048570 5' sImitar to 1R:Q92158 Q92158 SENTAXIN 17:	Homo caniens sorting nexth 3 (SNX3) mRNA	I thin depoils do well a server of the server of the server of the server of the server of the server of the server of the server of the server of the server of the server of the server of the server of the server of the server of the server of the server of the server of the server of the server of the server of the server of the server of the server of the server of the server of the server of the server of the server of the server of the server of the server of the server of the server of the server of the server of the server of the server of the server of the server of the server of the server of the server of the server of the server of the server of the server of the server of the server of the server of the server of the server of the server of the server of the server of the server of the server of the server of the server of the server of the server of the server of the server of the server of the server of the server of the server of the server of the server of the server of the server of the server of the server of the server of the 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zinc finger protein 200 (21/17 200) Illinning, and defined proteins 200 (21/17 200) Illinning september CDNA clone IMAGE 418317 3	Ar/911.st Source feed liver spices, in the spices of the second liver spices of the second liver spices of the second liver spices of the second liver spices of the second liver spices of the second liver spices of the second liver spices of the second liver spices of the second liver spices of the second liver spices of the second liver spices of the second liver spices of the second liver spices of the second liver spices of the second liver spices of the second liver spices of the second liver spices of the second liver spices of the second liver spices of the second liver spices of the second liver spices of the second liver spices of the second liver spices of the second liver spices of the second liver spices of the second liver spices of the second liver spices of the second liver spices of the second liver spices of the second liver spices of the 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NCI CCGAP AAT Homo sapiens contained invalor, 390 of 5	IN4204.51 NCI CGAP ANT HOMO SAPIENS CLINA CICUR INVOICE BOUND 3	POL POLYPROTEIN JUDA FAINS: PROTEASE; REVENSE INAVIOUS FAIL FAIL FAIL FAIL FAIL FAIL FAIL FAIL	AU149345 N 1 ZKM4 Home sapiens control cone in I ZKM+0012 2	nposhto3 s1 NCI_CGAP_Pr3 Homo sapiens cUNA clone invade::1113co1 suring to 11.01.35co.	Inposhio3.51 NCI_CGAP_Pr3 Homo saplens cDNA clone IMAGE:1115861 similar to TR:G1138406	G1136408 KIAA0173 PROTEIN.;	Homo sapiens chromosome 21 segment HS21C046	MR2-CT0222-211099-002-e10 CT0222 Homo capiens cDNA	7836a02.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:284002.5	Homo sapiens chromosome 21 segment HS210303	wp04h04x1 NCI_CGAP_KId11 Home sapiens cDNA clone IMAGE:24636953	Wp04h04.X1 NCI_CGAP_NIBTT DID bequelle vertex critical control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of
Top Hit Database Source	EST HUMAN	F	<del>\</del>	Note that the second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second se	5.1 EST TOWN	EST LIMAN	LN L	L Z	E	EST HUMAN	EST HUMAN		EST TOWAR	Z	LN L	EST HUMAN	EST_HUMAN	EST HUMAN	EST_HUMAN	SWISSPROT	EST_HUMAN	EST HUMAN		EST HUMAN	N	EST_HUMAN	EST_HUMAN	NT	EST_HUMAN	EST_HUMAN
Top Hit Acession No.	.0E-40 AV731601.1	4506188 NT	4506188INT		2.0E-40 A1908304.1	3	2.0E-40 BE27.3552.1		2.0E-40 At 163280.2	Ì			.0E-40 BE018348.1	450/14ZIN1	4508012 NT	.0E-40 W92708.1	1.0E-40 W92708.1	1.0E-40 AA573201.1	.0E-40 AA573201.1	.0E-40 P26808	.0E-40 AU148345.1	0F-40 AA614255.1		1.0E-40 AA614255.1	1.0E-40 AL 163246.2	1.0E-40 BF334112.1	9.0E-41 W01596.1	8.0E-41 AL163203.2	7.0E-41 AI934364.1	7.0E-41 A1934364.1
Most Similar (Top) Hit BLAST E Vatue	2.0E-40	2.0E-40	2 DE 40	2	2.0E-40	2.05	2.0F-40	2 OF 40	2.0E-40	1.06.40	1.0E-40		1.0E-40	1.0E-40	1.0E-40	1.0E-40	1.0E-40	1.0E-40	1.0E-40	1.0E-40	1.0E-40									
Expression Signal	233	28	a c	0.7	1.39	17.7	7.05	1 43	1 43	1.2	1.82		3.88	2.14	3.69	0.68	99:0	1.83	1.83	0.82	6.41	1 49		1.49		6.94				2.52
ORF SEQ ID NO:		28233			8389	Dice?	20278		1		28922				30851	32912		33763	33764	33922	37858		1	38684			30064			
SEQ ID	15016	15130	7670	20130	- 1	-1	15871	1.	19150	1	1	1	- }	16542	17868	19554	L	<u> </u>	1	١_	L	l	L	24978	1_			1	1	<u></u>
Probe SEQ ID NO:	1872	1088	3	888	2133	2238	2754	2021	2021	200	9886	3	2750	3370	4733	6385	6385	7236	7236	7381	11157	7,003		11993	12076	12687	3906	8108	8	851

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Table 4

Single Exon Probes Expressed in Placenta

	_							_		_,				_	_		-11111- 11 6-	1100		··-	٠,	-;:			-110-	<u></u>
Top Hit Descriptor	Homo sapiens hypothetical protein FLJ13188 (FLJ13188), mRNA	Homo sapiens a disIntegrIn and metalloproteinase domain 22 (ADAM22), mRNA	Homo seplens IQ motif containing GTPase activating protein 1 (IQGAP1), mRNA	Human pletelet activating factor acetylhydrolase, brain isoform, 45 kDa subunit (US1) gene, exons 3 and 4	Homo sapiens guanine nucleotide binding protein 10 (GNG10) mRNA	Homo saplens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced	Homo saplens pescadillo (zebrafish) homolog 1, containing BRCT domain (PES1), mRNA	Homo sapiens DSCR5b mRNA, complete cds	Homo sapiens Down syndrome candidate region 1 (DSCR1), mRNA	UI-H-BW 1-emp-b-03-0-UI s1 NCI_CGAP_Sub7 Home sepiens cDNA clone IMAGE:3070421 3	ho64f08.x1 Soares_NFL_T_GBC_S1 Homo saplens cDNA clone IMAGE:3042183 3' similar to contains MER32.b3 MER32 repetitive element ;	yc03e10.s1 Stratagene lung (#937210) Homo sapiens cDNA clone IMAGE:79626 3'	Homo saplens target of myb1 (chicken) homolog (TOM1), mRNA	PM4-BT0341-251199-002-F11 BT0341 Homo sapiens cDNA	QV6-HT0367-150200-114-g09 HT0367 Homo sapiens cDNA	AU118344 HEMBA1 Homo sepiens cDNA clone HEMBA1005583 57	ow45e06.s1 Soares_parathyroid_tumor_NbHPA Homo sapiens cDNA clone IMAGE:1649794.3' similar to TR:000597 CYTOCHROME C.LIKE POLYPEPTIDE, ;contains LTR5.b1 LTR5 repetitive element :	cw45e06.s1 Soares_parattyroid_tumor_NbHPA Homo capiens cDNA clone IMAGE:1649794 3' similar to .TR:000597 000597 CYTOCHROME C-LIKE POLYPEPTIDE.;contains LTR6.b1 LTR5 repetitive element.	Homo sapiens gene for activin receptor type IIB, complete cds	tm96c04.x1 NCI_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2165958 3' similar to contains OFR.b1 OFR repetitive element;	Horno sapiens 969 kb contig between AML1 and CBR1 on chromosome 21q22; segment 1/3	Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22; segment 1/3	H.sapiens Divase I hypersensitive site (HSS-3) enhancer element	AV758295 BM Homo sepiens cDNA clone BMFBHC06 5'	601888096F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE::4122119 5	AV710480 Cu Homo sapiens cDNA clone CuAACCU/ 5
Top Hit Database Source	Z L	NT	NT	NT	TN.	Ŋ	TN	LN	NT	EST_HUMAN	EST_HUMAN	EST HUMAN	LZ	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST HUMAN	LN	EST HUMAN	IN	NT	LN	EST HUMAN	EST_HUMAN	EST_HUMAN
Top Hit Acession No.	11545770 NT	11419208 NT	11433010 NT	172335.1	4758445 NT	7.0E-41 AF223391.1	11417972 NT	6.0E-41 AB037163.1	7657042 NT	6.0E-41 BF513783.1	6.0E-41 AW873637.1	T62628.1	4885639 NT	5.0E-41 BE067042.1	4.0E-41 BE156318.1	.0E-41 AU119344.1	.0E-41 Al027117.1	4.0E-41 Al027117.1	4.0E-41 AB008681.1	4.0E-41 AI500406.1	.0E-41 AJ229041.1	.0E-41 AJ229041.1	1.0E-41 X926B5.1	4.0E-41 AV758295.1	1.0E-41 BF304683.1	4.0E-41 AV710480.1
Most Similar (Top) Hit BLAST E Value	7.0E-41	7.0E-41	7.0E-41	7.0E-41 U72335.1	7.0E-41	7.0E-41	7.0E-41	6.0E-41	6.0E-41	6.0E-41	6.0E-41	5.0E-41 T62628.1	5.0E-41	5.0E-41	4.0E-41	4.0E-41	4	4.0E-41	4.0E-41	4.0E-41	4.0E-41	4.0E-41	4.0E-41			
Expression Signal	0.9	2.71	1.04	96.0	2.06	1.41	8.58	1.13	3.09	1.31	1.25	1.37	1.17	2.34	1.69	2.37	14.6	14.6	3.34	7.72			2.13	1.8		7.38
ORF SEQ ID NO:	31450	32651	33012	31473		38620		26543	28443			28092				27342	27670		27687					L	36519	
SE on No:	18581	15311	19650	18559	24758	24917	26028	13508	15314	21240	25952	l	1	Ł	13599	14287	] ,	14595	1	I	1	1	17407	19797	22935	24954
Probe SEQ ID NO:	6379	6132	6483	7133	11718	11931	13182	291	2179	8158	13156	1845	4223	6678	402	1122	1442	1442	1454	1665	2953	2953	4262	6638	9895	11969

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Γ-	1	T	7	7		Т	7	Т	T	7	Т	Т	Ţ	Т	Т	T	7	┑	7	Ï	*1645	Ť	j	T	Ţ	T	Ť	T	Т	Ť	Ť	Ï	Т	7
	Top Hit Descriptor	AV708431 ADC Homo saplens cDNA clone ADCARE02 5'	601508315F1 NIH_MGC_71 Homo saplens cDNA clone IMAGE:3910059 5'	Horno saptens PAD-H19 mRNA for peptidylarginine deiminase type II, complete ode	Hamo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes,	complete cds)	H. sapiens mRNA for putative p64 CLCP protein	Homo sapiens mRNA for KIAA1387 protein, partial cds	yi75d08.r1 Soares breast 2NbHBst Homo sapiens cDNA clone IMAGE:154575 5	QV0-BN0040-170300-160-h08 BN0040 Homo sapiens cDNA	QV0-BN0040-170300-160-h08 BN0040 Homo sapiens cDNA	ef17f10.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1031947 3'	601762940F1 NIH_MGC_20 Homo capiens cDNA clone IMAGE:4026081 5	Human ribosomal protein L23a mRNA, complete cds	EST35818 Embryo, 8 week I Homo sapiens cDNA 5' end	Human mRNA for KIAA0207 gene, complete cds	G.gorilla DNA for ZNF80 gene homolog	Human ribosomal protein L23a mRNA, complete cds	zo8b04.r1 Scares_total_fetus_Nb2HF8_9w Homo sapiens cDNA done IMAGE:785639 5	Homo sapiens son of sevenless (Drosophila) homolog 1 (SOS1) mRNA	Homo saplens chromosome 21 segment HS210067	Homo sapiens chromosome 21 segment HS21C067	no12c07.s1 NG_CGAP_Phe1 Homo sapiens cDNA clone IMAGE:1100460 3' similar to gb:X52851_ma1 PEPTIDYL-PROLYI, CIS-TRANS ISOMERASE A (HUMAN);	Homo sapiens integrin, beta 8 (ITGB8) mRNA	Homo sapiens homolog of Nedd5 (hNedd5) mRNA, complete cds	Human B-cell specific transcription factor (BSAP) mRNA, complete cds	Human B-cell specific transcription factor (BSAP) mRNA, complete cds	EST31723 Embryo, 12 week I Homo saplens cDNA 5' end	ZINC FINGER PROTEIN 135	Homo saplens KIAA0433 protein (KIAA0433), mRNA	Homo sapiens KIAA0433 protein (KIAA0433), mRNA	EST84555 Colon adenocarcinoma IV Homo sapiens cDNA 5 end	Homo saplens nuclear factor of activated T-cells, cytoplasmic 2 (NFATC2), mKNA	601445647F1 NIH_MGC_65 Homo saplens cDNA clone IMAGE:3849803 5
1	l op Hit Detabase Source	EST HUMAN	EST_HUMAN	TN		LN-	ΙΝ	NT	EST_HUMAN	EST HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	TN	EST_HUMAN	LΝ	F	F	EST_HUMAN	TN	TN	NT	EST_HUMAN	۲	NT	NT	TN	EST_HUMAN	SWISSPROT	TN	TN	EST_HUMAN	TN	EST_HUMAN
	Top Hit Acesslon No.	4.0E-41 AV708431.1	.0E-41 BE887118.1	.0E-41 AB030176.1		3.0E-41 AB026898.1	(87689.1	3.0E-41 AB037808.1	354765.1	3.0E-41 AW994941.1	3.0E-41 AW 994941.1	3.0E-41 AA609768.1	3.0E-41 BF125922.1	2.0E-41 U43701.1	2.0E-41 AA331940.1	.0E-41 D86962.1	.0E-41 X89631.1	2.0E-41 U43701.1	2.0E-41 AA449549.1	5032106 NT	2.0E-41 AL163267.2	2.0E-41 AL163267.2	2.0E-41 AA584575.1	4504778 NT	2.0E-41 AF038404.1	2.0E-41 M96944.1	2.0E-41 M96944.1	2.0E-41 AA328265.1	P52742	11417118 NT	11417118 NT	2.0E-41 AA372637.1	11420516 NT	1.0E-41 BE869735.1
Most Similar	ST E	4.0E-41	4.0E-41	3.0E-41		3.0E-41	3.0E-41 X87689.1	3.0E-41	3.0E-41 R54765.1	3.0E-41	3.0E-41	3.0E-41	3.0E-41	2.0E-41	2.0E-41	2.0E-41	2.0E-41	2.0E-41	2.0E-41	2.0E-41	2.0E-41	2.0E-41	2.0E-41	2.0E-41	2.0E-41	2.0E-41	2.0E-41	2.0E-41	2.0E-41 P52742	2.0E-41	2.0E-41	2.0E-41		
	Expression Signal	1.3	1.61	1.8		4.03	11.76	1.23	1.7.0	1.36	1,36	1.98	1.43	31.25	2.17	1.26	5.52	11.99	0.69	0.69	123	123	0.6	96.0	9.27	1.38	1.36	1.42	1.65	99.0	0.56	2.87	1.2	1.05
	ORF SEQ ID NO:		31942			30575	31869							27827		28559	L	27827		30097		30863								L				29470
	SEQ ID	25917	ì	1	1	17595	18804	19676	21017	25099	<u> </u>	25153	ı	1_			L	1_	1	1	1	١.,	<u> </u>	L	L	1	21341	1	1_	1	L	L	L	
	Probe SEQ ID NO:	12900	13110	970		4455	6099	6511	7967	12119	12119	12196	12783	1871	2013	2293	2341	2889	3406	3941	4744	4744	5656	6763	7850	8259	8259	8288	9175	9617	9617	11775	13148	3276

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	Top Hit Descriptor	601445647F1 NIH_MGC_65 Hamo saplens cDNA clone IMAGE:3849803 5'	Mus musculus tubulin alpha 6 (Tuba6), mRNA	qf75c10.x1 Soares_test(s_NHT Homo sapiens cDNA clone IMAGE:1755858 31	Homo sapiens hypothetical protein FLJ20454 (FLJ20454), mRNA	RC0-HT0613-210300-032-g01 HT0613 Homo sapiens cDNA	Homo sapiens hypothetical C2H2 zinc finger protein FLJ22504 (FLJ22504), mRNA	Homo sapiens hypothetical C2H2 zinc finger protein FLJ22504 (FLJ22504), mRNA	Homo sapiens homeobox protein CDX4 (CDX4) gene, complete cds and flanking repeat regions	Homo sapiens DNA, DLEC1 to ORGTL4 gene region, section 1/2 (DLEC1, ORG1L3, ORC1 L4 genes, complete eds)	rth07c02.st NOL_CGAP_Thy1 Homo sapiens dDNA clone IMAGE:943586 similar to TR:C434304 G434304 367BP EXPRESSED SEQUENCE TAG MRNA;	xc97a04.x1 NCI_CGAP_Brn35 Homo saplens cDNA clone IMAGE:2592174 3' similar to contains OFR.t2	OFR repetitive element ;	Homo sapiens chromosome 21 segment HS21C085	y/38g04.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:129174.5	qf58g12.x1 Soares_testis_NHT Homo saplens cDNA clone IMAGE:17542783	Homo sapiens phosphatdyfinositol 4-kinase 230 (pl4K230) mRNA, complete cds	Homo sapiens phosphattdylinositol 4-kinase 230 (pł4K230) mRNA, complete cds	xp29f08.x1 NCI_CGAP_HN10 Homo sepiens cDNA done IMAGE:2741799 3' simitar to contains L1.f1 L1 repetitive element;	Homo sapiens mRNA for KIAA1067 protein, partial cds	Homo sapiens mRNA for KIAA 1067 protein, partial cds	Homo saplens Xq pseudoautosomal region; segment 1/2	hv31e11.x1 NCI_CGAP_Lu24 Homo saplens cDNA clone IMAGE:3175052 3	Homo saplens SET domain and mariner transposase fusion gene (SETMAR) mRNA	Homo sapiens SET domain and mariner transposase fusion gene (SE IMAR) mRNA	Homo sepiens ubiquitin protein ligase E3A (human papilioma virus E6-associated protein, Angelman syndrome) (UBE3A), mRNA	Homo sapiens ubiquitin protein ligase E3A (human papilloma virus E6-associated protein, Angelman syndrome) (UBE3A), mRNA	Homo saplens myotubularin related protein 3 (MTMR3), mRNA	Homo sapiens multifunctional calcium/calmodulin-dependent protein kinase II delta2 isoform mRNA, complete cds
ì	Top Hit Database. Source	EST_HUMAN		EST_HUMAN		HUMAN			NT	L	EST HUMAN	$\overline{}$	EST_HUMAN			L HUMAN	NT	LN	EST HUMAN	F.	NT	LN	T_HUMAN	NT	N	TN	¥	뉟	LN.
	Top Hit Acession No.	0E-41 BE869735.1	6678468 NT	1.0E-41 AI217868.1	11526291 NT	9.0E-42 BE179191.1	11560151 NT	9.0E-42 11560151 NT		8.0E-42 AB026898.1	8.0E-42 AA493896.1	l	8.0E-42 AW088062.1		.0E-42 R10963.1	.0E-42 AI204358.1	6.0E-42 AF012872.1	4F012872.1	4W238656.1	AB028990.1	6.0E-42 AB028990.1	5.0E-42 AJ271735.1	5.0E-42 BE217913.1	573003B NT	5730038 NT	11433063 NT	11433063 NT	11417957 NT	.0E-42 AF071569.1
	Top) Hit (Top) Hit (Top) Hit (Top) Hit (Top)	1.0E-41	1.0E-41	1.0E-41	1.0E-41	9.0E-42	9.0E-42	9.0E-42	8.0E-42	8.0E-42	8.0E-42		8.0E-42	7.0E-42	7.0E-42	7.0E-42	6.0E-42	6.0E-42	6.0E-42	1	1	5.0E-42	5.0E-42	5.0E-42	5.0E-42	5.0E-42	5.0E-42	5.0E-42	"
	Expression Signal	1.05	9.46	1.57	1.67	1.19	2.81	2.81	5.34	8.63	30.09		2.91	2.23	0.5	1.32	3.24	3.24	3.6	1.88	1.5	8.9	1.56	3.05	1.14	0.94		2.57	
	ORF SEQ ID NO:	29471	30811	36243			36011	36012	26702	28439	i					36124	28155	28156	·	31824			26683			33385		L	
	Exan SEQ ID NO:	16450	L	_	L	L		<u> </u>	l	15311	1	1	25904	14128	1	1	15048	15046		L		13364	<u> </u>		L	l		1	1 1
	Probe SEQ ID NO:	3276	4689	9618	12334	8717	9375	8375	475	2176	12375		12396	955	9998	8445	1903	1903	7363	5584	5834	138	451	499	200	6825	6825	6941	7351

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Top Hit Descriptor	Homo sepiens mRNA for KIAA1294 protein, partial cds	Homo sapiens 3-hydroxyanthranilate 3,4-dloxygenase (HAAO), mRNA	Homo sapiens 3-hydroxyarthranilate 3,4-dioxygenase (HAAO), mRNA	Homo sepiens hypothetical protein FLJ20163 (FLJ20163), mRNA	Homo sapiens MHC class 1 region	Homo sapiens MHC class 1 region	Homo sapiens ribonuclease III (RN3) mRNA, complete cds	H.saplens PROS-27 mRNA	Homo sapiens SNARE protein kinase SNAK mRNA, complete cds	Homo sapiens regulatory factor X, 4 (influences HLA class II expression) (RFX4) mRNA	Homo sapiens zinc finger protein 177 (ZNF177) mRNA	Homo sapiens DKFZP564O2082 protein (DKFZP564O2082), mRNA	CMO-BT0282-171299-127-b03 BT0282 Homo sapiens cDNA	RC1-ST0278-040400-018-h11 ST0278 Homo sapiens cDNA	RC1-ST0278-040400-018-h11 ST0278 Homo sapiens cDNA	ti11d02:x1 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2130147 3'	601458531F1 NIH_MGC_66 Homo saplens cDNA clone IMAGE:3862086 5'	RCO-TN0079-110900-024-g07 TN0079 Homo sapiens cDNA	AV690218 GKC Homo sapiens cDNA clone GKCCBB08 5	RC3-NN0070-270400-011-h10 NN0070 Homo sapiens cDNA	2819293.3prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2819293 3'	EST367438 MAGE resequences, MAGC Homo sapiens cDNA	EST367438 MAGE resequences, MAGC Homo sapiens cDNA	ow83d05.x1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1653417 31	601061284F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3447620 5'	RIBONUCLEASE K3 (RNASE K3)	RIBONUCLEASE K3 (RNASE K3)	Homo sapiens chromosome 21 segment HS21 C046	Human endogenous retrovirus pHE.1 (ERV9)	UI-H-BI1-eith-e-04-0-UI.s1 NCI_CGAP_Sub3 Horno sapiens cDNA clone IMAGE:2721871 3'	Homo sapiens partial C9 gene for complement component C9, exon 1	Homo sapiens partial C9 gene for complement component C9, exon 1	Homo sapiens NADH-ublquinane oxidareductase AGGG subunit precursor homolog mRNA, nuclear gene encoding mitochondrial protein, complete ods
Top Hit Database Source	LN LN		NT	LN	Į.	TN	TN	NT	NT	NT	NT	Ľ	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	SWISSPROT	SWISSPROT	F	NT.	EST_HUMAN	F	F	ĽN.
Top Hit Acession No.	5.0E-42 AB037715.1	11431168 NT	11431168 NT	8923162 NT	4.0E-42 AF055066.1	4.0E-42 AF055068.1	4.0E-42 AF189011.1		4.0E-42 AF246219.1	4506496 NT	4508008 NT	7661635 NT	4.0E-42 AW371201.1	4.0E-42 AW818630.1	4.0E-42 AW818530.1	4.0E-42 AI435225.1	4.0E-42 BF035327.1	2.0E-42 BF376834.1	2.0E-42 AV690218.1	2.0E-42 AW898344.1	2.0E-42 AW250059.1	2.0E-42 AW955368.1	2.0E-42 AW955368.1	2.0E-42 AI052586.1	2.0E-42 BE538919.1	981649	981649	2.0E-42 AL163246.2	X57147.1	1.0E-42 AW 295809.1	1.0E-42 AJ251818.1	1.0E-42 AJ251818.1	1.0E-42 AF067166.1
Most Similar (Top) Hit BLAST E Value	5.0E-42	5.0E-42	5.0E-42	6.0E-42	4.0E-42	4.0E-42	4.0E-42	4.0E-42 X59417.1	4.0E-42	4.0E-42	4.0E-42	4.0E-42	4.0E-42	4.0E-42	4.0E-42	4.0E-42	4.0E-42	2.0E-42	2.0E-42	2.0E-42	2.0E-42	2.0E-42	2.0E-42	2.0E-42	2.0E-42	2.0E-42 P81649	2.0E-42 P81649	2.0E-42	1.0E-42 X57147.1	1.0E-42	1.0E-42	1.0E-42	
Expression Signal	2.88	0.55	Ò.55	1.77	5.6	5.6	1.82	1.39	1.1	4.67	17.64	0.93	0.57	2.32	2.32	1.43	1.69	3.79	1,6	4.24	3.6	11.82	11.82	0.9	1.28	0.64	0.64	1.53	1.75	2.2		1.74	
ORF SEQ ID NO:	35599	37487	37488	37955		27003	27312	30442	30469	30488	30825	31372		L		l					28742				36885							27346	
Exon SEQ ID NO:	22057	1	23866	24315	13953	13953	14256	17454	17486	17507	17841	18404	23734	23968	23968	24309	24695	14665	15593	15610	į.	1	ı	ı	23084	23295	23295	25018	13932	14233	Ł	L	1 1
Probe SEQ ID NO:	8978	10832	10832	11246	772	772	1091	4311	4343	4364	4708	5285	10701	10884	10884	11240	11698	1512	2466	2483	2496	5875	5875	6892	10046	10280	10280	12037	752	1067	1125	1125	1271

. Page 294 of 550 Table 4 Single Exon Probes Expressed in Placenta

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Top Hit Descriptor	Homo saplens NADH-ubiquinane oxidoreductase AGGG subunit precursor homolog mRNA, nuclear gene encoding mitochondrial protein, complete cds	Homo sapiens rec (LOC51201), mRNA	Homo sapiens PDNP1 gene, exon 17	Homo sapiens major histocompatibility complax, class II, DM alpha (HLA-DMA) mRNA	Homo sapiens origin recognition complex, subunit 5 (yeast homolog)-like (ORC5L) mRNA, and translated products	Homo sapiens KIAA0255 gene product (KIAA0255), mRNA	Homo saplens Gdgi vesicular membrane trafficking protein p18 (BET1) mRNA	Homo saplens chromosome 21 segment HS21C067	Homo saplens chromosome 21 segment HS21C080	RC3-ST0197-161099-012-a03 ST0197 Homo sapiens cDNA	Homo saplens proteasome inhibitor (PI31), mRNA	Homo saplens proteasome inhibitor (PI31), mRNA	Homo sapiens ryanodine receptor 3 (RYR3) mRNA	601304125F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3638310 5'	Homo sapiens chromodomain protein, Y chromosome-like (CDYL) mRNA	AV736824 CB Homo saplens cDNA clone CBLAKH08 5'	AV736824 CB Homo sapiens cDNA clone CBLAKH08 5'	Homo sapiens hypothetical protein FLJ20297 (FLJ20297), mRNA	Homo saplens hypothetical protein FLJ20297 (FLJ20297), mRNA	Homo sapiens hypothetical protein FLJ20297 (FLJ20297), mRNA	y/08e11.r1 Soaros placenta Nb2HP Homo sapiens cDNA clone IMAGE:148172 5	2822251.5prime NIH_MGC_7 Homo capiens cDNA clone IMAGE:2822251 5	wp69b01.x1 NOL_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2466985 3' similar to TR:015475 O45475 LINNAMED HERV-H PROTEIN contains LTR2 b1 LTR7 repetitive element :	ne72d08.51 NCI_CGAP_Ew1 Homo saplens cDNA clone IMAGE:309803 similar to gb:L05095 60S	RIBOSOMAL PROTEIN L30 (HUMAN);	AV708201 ADC Homo sepiens cDNA done ADCACC10 5'	#26c04.x1 NCI_CGAP_Brn23 Homo capions cDNA clone IMAGE:2097318 3' similar to SW:BRR2_YEAST P32639 PRE-MRNA SPLICING HELICASE BRR2 ;	Homo saplens ATP-binding cassette, sub-family C (CFTR/MRP), member 3 (ABCC3), transcript varient MRP38 mRNA	בינה ווון לישה זי ווון
Top Hit Dafabase Source	TN	NT	IN	LN TN	·	¥	Ŋ	NT	±N	EST_HUMAN	NT	LN	TN	EST_HUMAN	NT	EST_HUMAN	EST_HUMAN	LN	FZ	N.	EST_HUMAN	EST_HUMAN	EST WINAM	Name of Con	EST_HUMAN	EST_HUMAN	EST HUMAN	L	
Top Hit Acession No.	1.0E-42 AF067166.1	11423219 NT	1.0E-42 AF110296.1	5174458 NT	4505524 NT	7662027 NT	5031610 NT	1.0E-42 AL163267.2	1.0E-42 AL163280.2	1.0E-42 AW813617.1	5803122 NT	5803122 NT	4506758 NT	1.0E-42 BE408611.1	TN 6967574	8.0E-43 AV736824.1	8.0E-43 AV736824.1	23276	8023276 NT	8923276 NT	8.0E-43 H13952.1	7.0E-43 AW246442.1	7 OC 42 A 1026748 4		6.0E-43 AA491890.1	6.0E-43 AV708201.1	6.0E-43 AI421540.1	TN 6769200	
Most Similar (Top) Hit BLAST E Value	1.0E-42	1.0E-42	1.0E-42	1.0E-42	1 OF-42	1.0E-42	1.0E-42	1.0E-42	1.0E-42	1.0E-42	1.0E-42	1.0E-42	1.0E-42	1.0E-42	9.0E-43	8.0E-43	8.0E-43	8.0E-43	8.0E-43	8.0E-43	8.0E-43	7.0E-43	1 05 42	1.0	6.0E-43	6.0E-43	6.0E-43	8.00.42	0.0E-45
Expression Signal	11.99	1.15	1.18	1.42	9	3.31	1.11	66.0	3.47	19:0	2.37	2.37	6.13	1,39	6.16	20.77	20.77	5.12	5.12	5.12	0.72	7.48	000	9	11.62	4.03	252.27	0	2.03
ORF SEQ ID NO:	27499	27977	28349	28849	<u>.</u>	Ì	30054	30202		Ì.	30984		31020	38169		L				L							31068		32971
Exon SEQ ID NO:	16033	14884	15227	15733	18205	16980	17054	17192	17504	17851	18000	18000	18031	24501	23326	13855	_	1	1	L	19006	16892	<u> </u>	75077	14529	ı			19608
Probe SEQ ID NO:	1271	1735	2087	2609	3020	3790	3895	4036	4361	4716	4867	4867	4901	11440	10291	699	699	718	718	718	5816	3731	000	0050	1374	2657	4963	7	<b>8</b> 41

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Top Hit Descriptor	hd30b04.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2910991 3' similar to contains MER1.t3 MER1 mER1 repositive element ;	7735606.r1 Soares_NhHMPu_S1 Homo saplens cDN4 clone IMAGE:065410 6' similar to TR:G529641 G529641 DB1, COMPLETE: CDS. ;contains element PTR7 repetitive element;	DKFZp761L1712_r1 761 (synonym: hamy2) Homo sapiens cDNA clone DKFZp761L1712 5	Homo sapiens chromosome 21 segment HS21C013	EST96033 Testis I Hamo sapiens cDNA 5' end	AV732578 HTF Homo sapiens cDNA clone HTFANC06 5'	tw22e07.x1 NCi_CGAP_Brn52 Homo saplens cDNA clone IMAGE:2260452 3'	tw22e07.x1 NCI_CGAP_Brn52 Homo sapiens cDNA clone IMAGE:2260452.3	zv54a03.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:757420 5'	zv54e03.r1 Soares_testis_NHT Homo sapiens cDNA clone iMAGE:757420 5'	yu49g12.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:229510 6	aa33d08.r1 NCI_CGAP_GCB1 Homo saplens cDNA clone IMAGE:815055 5'	0052c10.x5 NCI_CGAP_Lu5 Homo saplens cDNA clone IMAGE:1569810 3' similar to TR:P90591 P90591	PV14 GENE.;	DKFZp434D0119_r1 434 (synonym: htes3) Homo sepiens cDNA clone DKFZp434D0119	MR2-SN0007-290400-004-c02 SN0007 Homo sapiens cDNA	55a4 Human retina cDNA randomly primed sublibrary Homo sapiens cDNA	Homo sapiens X-linked anhidroitic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat	regions	oy47h03.x1 NCI_CGAP_Bm23 Homo sapiens cDNA clone IMAGE:1669013 3'	Homo sapiens glycyt-tRNA synthetase (GARS), mRNA	Homo sapiens protocadherin beta 8 (PCDHB6), mRNA	qj76a02.x1 NCI_CGAP_Kid3 Homo sapiens cDNA clone IMAGE:1865354 3' similar to contains MER10.t3	MER10 repetitive element;	qj76a02.x1 NCI_CGAP_Kid3 Homo saplens cDNA clone IMAGE:1865354 3' similar to contains MER10.t3	MER10 repetitive element;	Homo sapiens zinc finger protein 161 (ZNF161), mRNA	ygo6b05.r1 Soares Infant brain 1NIB Homo sapiens cDNA clone IMAGE:31363 5' similar to contains MER10	repetitive element;	thg2b12.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2126111 3' similar to TR:002710 002710 GAG POLYPROTEIN ;	
Top Hit Database Source	EST_HUMAN	EST_HUMAN	EST HUMAN	NT	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN		EST_HUMAN	EST_HUMAN	EST_HUMAN	EST HUMAN		NT	EST_HUMAN	LN.	N		EST_HUMAN		EST_HUMAN	LZ		EST HUMAN	FST HUMAN	
Top Hit Acession No.	6.0E-43 AW468897.1		6.0E-43 AL119158.1	5.0E-43 AL163213.2		5.0E-43 AV732578.1	5.0E-43 AI613509.1	5.0E-43 AI613509.1	5.0E-43 AA442271.1	5.0E-43 AA442271.1	5.0E-43 H74277.1	.0E-43 AA465288.1		5.0E-43 AI733244.1	5.0E-43 AL049110.1	5.0E-43 AW863007.1	5.0E-43 W 29011.1		4.0E-43 AF003528.1	.0E-43 Al056338.1	TN 6009669	11416793 NT		.0E-43 AI244341.1		.0E-43 AI244341.1	TN 7865009		4.0E-43 R20950.1	0F-43 Al436093 1	The state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the s
Most Similar (Top) Hit BLAST E Value	6.0E-43	6.0E-43	6.0E-43	5.0E-43	5.0E-43	5.0E-43	5.0E-43	5.0E-43	5.0E-43	5.0E-43	5.0E-43	5.0E-43		5.0E-43	5.0E-43	5.0E-43	5.0E-43		4.0E-43	4.0E-43	4.0E-43	4.0E-43		4.0E-43		4	4.0E-43		_		
Expression Signal	1.8	1.77	2.45	1.82	3.4	1.59	6.0	0.69	0.64	0.64	0.73	4,09		2.6		4.53			4.4	1.09	99'0	1.6		5.18		5.18	1.02		2.7	1 23	}
ORF SEQ ID NO:	33518	36696					33512				Ĺ	36272			37295		١		27227		33028	l		34975	_	34976	l				
Exen SEQ ID NO:	20101	23094	24424		ı	l			21462	21462	22169	22706		23643	23685	24080	24282		15987	18576	19665	١_		21452			23556		25227	1_	
Probe SEQ ID NO:	7048	10086	11363	145	515	2908	6435	7043	8381	8384	0806	9564		10609	10651	11001	11213		995	5373	6499	7280		8371		8371	10521		12311	12030	322

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Table 4
Single Exon Probes Expressed in Placenta

Top Hit Descriptor	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced	H.sapiens gene encoding La autoantigen	Г	7	AML1-EVI-1=AML1-EVI-1 fusion protein {rearranged translocation} {human, leukemic cell line SKH1, mRNA  Mulant 5938 ntl	T	Human TBXAS1 gene for thromboxane synthase, promoter region and expn 1	Mus musculus otogelin (Otog), mRNA	Mus musculus otogelin (Otog), mRNA	Human ribosomal RNA upstream binding transcription factor (UBTF) gene, partial cds	Г		Homo sapiens hypothetical protein (HSA011916), mRNA	Homo sapiens similar to ornithine carbamoyfiransferase (H. sapiens) (LOC63648), mRNA	Homo sapiens SET domain and mariner transposase fusion gene (SETMAR) mRNA	qd61c09.x1 Soares_testie_NHT Homo sapiens cDNA done IMAGE:1733968 3' similar to contains PTR7.t3 AN PTR7 PTR7 repetitive element;	hingand v1 NCI CGAP Brn41 Homo satiens cDNA clone IMAGE:3173750 3' similar to contains element				Human ribosomai protein L23a mRNA, complete cds	AN FB1G5 Fetal brain, Stratagene Homo sepiens cDNA clone FB1G5 3'end similar to LINE-1	Homo sapiens Ras-like GTP-binding protein (RAB27A) gene, exons 1b and 2	Homo sapiens Ras-like GTP-binding protein (RAB27A) gene, exons 1b and 2	Homo sapiens chromosome 21 segment HS21C084	Γ	Homo sapiens pyruvate dehydrogenase khase, Isoenzyrne 3 (PDK3) mRNA	Homo sapiens Sp4 transcription factor (SP4) mRNA	Homo saplens Sp4 transcription factor (SP4) mRNA
Top Hit Database Source	F	LN LN		ES! HUMAN	F	EST HUMAN	Į Į	N	ΙN	N		EST_HUMAN	LN	TN	N	EST HUMAN		EST HUMAN	EST_HUMAN	EST_HUMAN	Σ	EST HUMAN	L.	F	Ν	EST_HUMAN	LN	N.	TN
Top Hit Acession No.	3.0E-43 AF223391.1	3.0E-43 X97869.1		3.0E-43 RB3422.1	3 0F 43 Sepuno 1	3.0E-43 AA548154.1	3.0E-43 D34613.1	7305360 NT	T306360 NT	3.0E-43 U65487.1		AA45882	7661721 NT		5730038 NT	2 DE-43 A1190764.1		2.0E-43 BE222778.1	2.0E-43 BE222778.1	2.0E-43 AW 207390.1	2.0E-43 U43701.1	2.0E-43 T03007.1	1.0E-43 AF154836.1	1.0E-43 AF154836.1	1.0E-43 AL163284.2	1.0E-43 BF348283.1	4885544 NT	4507168 NT	4507168 NT
Most Similar (Top) Hit BLAST E Value	3.0E-43	3.0E-43		3.0E-43	2 OF 13	3.0E-43	3.0E-43	3.0E-43	3.0E-43	3.0E-43		3.0E-43	3.0E-43	3.05-43	3.0E-43	2 0E-43		2.0E-43	2.0E-43	2.0E-43	2.0E-43	2.0E-43	1.0E-43	1.0E-43	1.0E-43	1.0E-43	1.0E-43	1.0E-43	1.0E-43
Expression Signal	3.46	2.52		1.1	1 20	0.0	0.94	1.58	1.56	5.09		4.39	-	0.68	1.42	7.24		1.	1.2	129	3.16	4.75	2.95		4.12	4.73	0.88	6.84	6.84
ORF SEQ ID NO:		27971		28377	76000		32515	33016	33017	1	_		35639		1_			33152	33153				27917	L		İ		33291	
SEQ ID NO:	14399	14880	l	16055	1007	1	L.		19654	20019			22099	1	ı		1	19764	19764	Ł	L	L	1_	14833	14891	15902	18723	19900	1
Probe SEQ ID NO:	1240	1730		2120	.000	4405	6014	6487	6487	6867		8357	9020	10068	12026	8		6604	6604	7428	8503	11476	1681	1681	1742	2786	5526	6744	6744

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Top Hit Descriptor	yg40e01.r1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:34732 & similar to SP:BD38_MOUSE P28656 BRAIN PROTEIN DN38;	Homo sapiens vacudar sorting protein 35 (VPS35) mRNA, complete cds	Hamo sapiens 8422.1 region and MTG8 (CBFA2T1) gene, partial cds	EST375749 MAGE resequences, MAGH Homo saplens cDNA	EST365299 MAGE resequences, MAGB Homo saplens cDNA	wr87h01.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE::2494705 3		┱	_				$\Box$	Homo sapiens small proline-rich protein 2C (SPRR2C), mRNA	Homo saplens small proline-rich protein 2C (SPRR2C), mRNA	Homo sapiens mRNA for thymidine kinase, partial	Homo saplens myosin mRNA, partial cds	Homo sapiens polymerase (RNA) II (DNA directed) polypeptide F (POLR2F), mKNA	Homo sapiens putative nuclear protein (HRIHFB2122), mKNA	Homo sapiens protein kinase C, alpha binding protein (PRKCABP), mKNA			Home sapiens LIM domain-containing preferred translocation partner in lipoma (LTT) minute.	Homo sapiens minisatellite ms32 repeat region	Homo saptens minisatellite ms3z repeat region	Homo sapiens chromosome 21 segment HS21C084	Home sapiens chromosome 21 unknown mRNA				Homo sapiens KIAA0831 gene (partial), XII3 gene and L.C.I.F.L.I gene	Homo sapiens KIAA0851 gene (partial), X I 3 gene and LZ I FL1 gene
Top Hit Database Source	EST_HUMAN	NT	NT	EST HUMAN	EST_HUMAN	EST_HUMAN	NT	EST_HUMAN	EST_HUMAN	NT	EST_HUMAN	EST_HUMAN	N	LN LN	N	NT	NT	NT	N	NT		EST HUMAN	LN-1	N	NT	NT	TN	M	EST_HUMAN	EST_HUMAN	N	N N
Top Hit Acession No.	1.0E-43 R19751.1	1.0E-43 AF175265.1	1.0E-43 AF198490.1	1.0E-43 AW963676.1	1.0E-43 AW953229.1	1.0E-43 AI984961.1	24378		1.0E-43 AI675416.1	1832	8.0E-44 AI222985.1	8.0E-44 AI222985.1	8.0E-44 X94354.1	11423497 NT	11423497 NT	8.0E-44 Y10498.2	8.0E-44 L29139.1	11527389 NT	11418086 NT	11418099 NT	11418086 NT	7.0E-44 R06035.1	5031886 NT	7.0E-44 AF048729.1	7.0E-44 AF048729.1	7.0E-44 AL163284.2	7.0E-44 AF231919.1	7.0E-44 AF231919.1	7.0E-44 AU159839.1	8.0E-44 Z20946.1	5.0E-44 AJ289880.1	5.0E-44 AJ289880.1
Most Similar (Top) Hit BLAST E Value	1.0E-43	1.0E-43	1.0E-43	1.0E-43	1.0E-43	1.0E-43	1.0E-43	1.0E-43	1.0E-43	9.0E-44	8.0E-44	8.0E-44	8.0E-44	8.0E-44	8.0E-44	8.0E-44	8.0E-44	8.0E-44	8.0E-44	8.0E-44	8.0E-44	7.0E-44	7.0E-44	7.0E-44	7.0E-44	7.0E-44						
Expression Signal	1.19	9.0	2.17	28.54	0.66	5.81	3.05	2.29	3.16	3.21	5.32	5.32	2.86	0.5	0.5	2.87	1.76	2.89	2.17	1.85	2.29	1.13	1.19	4.44	4.44	2.71	0.85	0.85	2.39	0.67	4.25	2.42
ORF SEQ ID NO:	31488		_	35659					32071		27153							32065	31946	31760	31946	L	28573		29230		30479				-	
Exon SEQ ID NO:	18533		21338	22116	L		L	25189	25373	١.	1	14088	_	L			L	1_	١	1_	1	13862	L	L	16207	17123	17499		١	L	13530	13553
Probe SEQ (D NO:	7106	8117	8258	9037	10498	11208	11647	12248	12550	12805	913	913	8736	10545	10545	11436	11987	12501	12544	12945	13126	929	2307	3031	3031	3965	4356	4356	8379	6229	314	342

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Signal 2 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3				_	_		-	_		_	_	_		_			_	_		_	_,	- 1	_			-		$\neg$	-		_	_
Exon         Most Similar         Most Similar         Top Hit Acession         Top Hit Acession         Top Hit Acession         Top Hit Acession         Top Hit Acession         Top Hit Acession         Top Hit Acession         Top Hit Acession         Top Hit Acession         Top Hit Acession         Top Hit Acession         Top Hit Acession         Top Hit Acession         Top Hit Acession         Top Hit Acession         Top Hit Acession         Top Hit Acession         Top Hit Acession         Top Hit Acession         Top Hit Acession         Top Hit Acession         Top Hit Acession         Top Hit Acession         Top Hit Acession         Top Hit Acession         Top Hit Acession         Top Hit Acession         Top Hit Acession         Top Hit Acession         Top Hit Acession         Top Hit Acession         Top Hit Acession         Top Hit Acession         Top Hit Acession         Top Hit Acession         Top Hit Acession         Top Hit Acession         Top Hit Acession         Top Hit Acession         Top Hit Acession         Top Hit Acession         Top Hit Acession         Top Hit Acession         Top Hit Acession         Top Hit Acession         Top Hit Acession         Top Hit Acession         Top Hit Acession         Top Hit Acession         Top Hit Acession         Top Hit Acession         Top Hit Acession         Top Hit Acession         Top Hit Acession         Top Hit Acession         Top Hit Acession         Top Hit Acession         Top	Top Hit Descriptor	In40d02.x1 NO_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2170083 3' similar to contains OFR.t1 OFR OFR repetitive element ;	AU124571 NT2RM4 Homo sapiens cDNA clone NT2RM4000218 5	Homo saplens chromosome 21 segment HS21C103	II11402.x1 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2130147 3'	801508601F1 NIH_MCC_71 Homo sapiens dDNA clone IMAGE:3910152 5'	Human fibrillin (FBN1) locus polymorphism	RC3-HT0585-010400-023-d08 HT0585 Homo saplens oDNA	Homo saptens carboxyl terminal LIM domain protein (CLIM1) mRNA, complete cds	Homo sapiens keryopherin alpha 6 (importin alpha 7) (KPNA6), mRNA	ap18b05.r1 Stratagene fetal retina 937202 Homo sapiens cDNA clone IMAGE:609777 5	601510547F1 NIH_MGC_71 Homo capiens cDNA clone IMAGE:3912010 5	Sus scrofa domestica submaxillary apomucin mRNA, complete cde	Homo sapiens DEAD/H (Asp-Glu-Alæ-Asp/His) box polypeptide 1 (DDX1) mRNA	Homo sapiens DEAD/H (Asp-Giu-Ala-Asp/His) box polypeptide 1 (DDX1) mRNA	Homo sepiens transmembrane trafficking protein (TMP21), mRNA	Homo saplens transmembrane trafficking protein (TMP21), mRNA	Homo saplens RAB36 (RAB36) mRNA, complete cds	hw14g06.x1 NCI_CGAP_Lu24 Homo saplens cDNA clone IMAGE:3182838 3' similar to SW::OXYB_HUMAN P22059 OXYSTEROL-BINDING PROTEIN: ;	Homo sapiens tissue-type bone marrow zinc finger protein 4 mRNA, complete cds	Homo saplens tumor necrosis factor (ligand) superfamily, member 10 (TNFSF10) mRNA	Human mRNA for integrin alpha subunit, complete cds	Homo sapiens adaptor-related protein complex 4, sigma 1 subunit (CLAPS4), mRNA	Homo saplens DNA for amyloid precursor protein, complete cds	PM4-SN0016-120500-003-e04 SN0016 Homo sapiens cDNA	Homo saplens chemokine (C-C motif) receptor 9 (CCR9), mRNA	Homo sapiens general transcription factor 2-1 (GTF2I) mRNA, alternatively spliced product, complete cds	Homo sapiens glutamate receptor, metabotropio 3 (GRM3), mRNA	Homo sapiens glutamate receptor, metabotropic 3 (GRM3), mRNA	Homo sapiens vesicle transport-related protein (KIAA0917), mRNA	Homo sapiens vesicle transport-related protein (KIAA0917), mRNA	601286914F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3613586 5'
Exam NO: NO: NO: NO: NO: NO: NO: NO: NO: NO:	Top Hit Database Source	EST_HUMAN	EST_HUMAN	NT	EST_HUMAN	EST_HUMAN	TN	EST_HUMAN	NT	NT		EST HUMAN	IN	IN	LN	TN	LN	NT	EST HUMAN	FN	FX	NT	LN	TN	EST_HUMAN	LN	FN	F	된	뒫	Ę	EST_HUMAN
Exon         ORF SEQ         Expression         Most Similar           SEQ ID         ID NO:         Signal         ICap) Hit           27726         1.39         5.0E-44           22726         1.39         5.0E-44           16068         29678         4.27         4.0E-44           20708         34187         0.89         4.0E-44           21547         38077         0.89         4.0E-44           21647         38077         0.89         4.0E-44           24570         38247         0.87         4.0E-44           14240         27287         1.43         5.0E-44           14383         27286         1.43         3.0E-44           14383         27286         1.43         2.0E-44           14383         27456         0.63         3.0E-44           14383         27456         0.63         3.0E-44           14383         27456         1.43         2.0E-44           14554         27656         1.43         2.0E-44           14564         27656         3.61         2.0E-44           15753         28484         3.07         2.0E-44           15756         28879	Top Hit Acession No.	AI568523.1	NU124571.1	AL163303.2	11435225.1	3E883178.1	21948.1	3E176618.1	J90878.1	6912477	\A169851.1	3E884820.1	4F005273.1	4826685	4826685	5803200	5803200	4F133588.1	BE 465325.1	AF070651.1	4507592	025303.1	5901933	D87675.1	AW864379.1	11449901	AF038968.1	11419226	11419226	7706370	7706370	BE389058.1
Exan         ORF SEQ         Expression           NO:         Signal           NO:         Profession           27728         10668           16688         29678         4           16688         29678         4           16553         34187         0           20708         3453         0           24570         38247         6           14240         27287         1           14240         27287         1           14240         27287         1           14240         27287         1           14333         27456         3           14383         27456         3           14365         28424         3           15728         1436         2768           15728         28424         3           15728         28424         3           15728         28434         1           15726         28879         0           15726         28879         0           1654         32744         1           1861         34122           2064         34122           21703 <td>Similar p) Hit ASTE atue</td> <td>5.0E-44</td> <td>5.0E-44</td> <td>4.0E-44</td> <td>4.0E-44</td> <td>4.0E-44</td> <td>4.0E-44</td> <td>4.0E-44</td> <td>4.0E-44</td> <td>3.0E-44</td> <td>3.0E-44</td> <td>3.0E-44</td> <td>3.0E-44</td> <td>2.0E-44</td> <td>2.0E-44</td> <td>2.0E-44</td> <td>2.0E-44</td> <td>2.0E-44</td> <td>2.0E-44</td> <td>2.0E-44</td> <td>2.0E-44</td> <td>2.0E-44</td> <td>2.0E-44</td> <td>2.0E-44</td> <td>2.0E-44</td> <td>2.0E-44</td> <td>2.0E-44</td> <td></td> <td></td> <td>ĺ</td> <td>2.0E-44</td> <td></td>	Similar p) Hit ASTE atue	5.0E-44	5.0E-44	4.0E-44	4.0E-44	4.0E-44	4.0E-44	4.0E-44	4.0E-44	3.0E-44	3.0E-44	3.0E-44	3.0E-44	2.0E-44	2.0E-44	2.0E-44	2.0E-44	2.0E-44	2.0E-44	2.0E-44	2.0E-44	2.0E-44	2.0E-44	2.0E-44	2.0E-44	2.0E-44	2.0E-44			ĺ	2.0E-44	
Exan ORF NO: DO ID ID ID ID ID ID ID ID ID ID ID ID ID	Expression Signal	4.12	1.39	4.27	0.89	0.67	0.86	0.71	5.64	5.1	5.11	0.65	0.63	1.43	1.43	3.61	3.61	6.82	3.1	3.07	1.28	0.94	2.3	1.34	1.75	1.75	2.18	3.8	3.8	0.7	0.7	1.8
	ORF SEQ ID NO:			29678										L	Ŀ					L		L				L	<u> </u>	L	L	L		
Probe SEQ ID NO: NO: 1 8072 11513 11674 1174 1174 1174 1174 1174 1174 117	Exan SEQ ID NO:	21154	22728	16668	18253	20708	21547	22158	24570	14975	16342	21020	1_		<u> </u>		ட	L.		1_	١.	L	<u> </u>	_		1	<u></u>	1	l	L	L	1
	Probe SEQ ID NO:	8072	9584	3501	5128	7639	8466	8079	11513	1827	3167	7970	9719	1074	1074	1234	1234	1340	1400	2219	2605	2642	2676	3559	4692	6220	9669	7572	7572	8623	8623	8819

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Top Hit Descriptor	TCBAP1E2795 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project≔TCBA Homo sapiens cDNA clone TCBAP2795	Homo sapiens neuronal cell adhesion molecule (NRCAM) mRNA	Homo sapiens Misshapen/NIK-related kinase (MINK), mRNA	Homo sapiens Misshapen/NIK-related kinase (MINK), mRNA	RC1-CT0249-030300-026-h12 CT0249 Homo saplens cDNA	RC1-BN0039-110300-012-b01 BN0039 Homo saptens cDNA	Homo sapiens chromosome 21 segment HS21C103	zw53d02.r1 Soares_total_fetus_Nb2HF9_9w Homo sapiens cDNA clone IMAGE:773763 5' sImilar to contains THR.t3 THR repetitive dement ;	zw53d02.r1 Soares_total_fetus_NbZHF8_9w Homo saptens cDNA clone IMAGE:773763 5' similar to	contains I HK.t3 I HK repeature element ;	Homo sapiens transcription factar IGHM enhancer 3, JM11 protein, JM4 protein, JM5 protein, T54 protein, JM10 protein, A4 differentiation-dependent protein, triple LIM domain protein 6, and synaptophysin genes,	complete cds; and L-type calcium channel az	aa01c09.s1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:811984 31	Homo sapiens alpha satellite DNA, M1 monomer type	Homo sapiens alpha satellite DNA, M1 monomer type	EST379147 MAGE resequences, MAGJ Homo sapiens cDNA	EST379147 MAGE resequences, MAGJ Homo sapiens cDNA	Homo sapiens chromosome 21 segment HS21C009	qx88g07.x1 NCI_CGAP_GC6 Homo saplens cDNA clone IMAGE:2009628 3'	AV714608 DCB Homo sapiens cDNA clone DCBBYE03 5'	Homo sapiens Sushi domain (SCR repeat) containing (BK65A6.2), mRNA	RC1-CT0198-150999-011-C08 CT0198 Hamo saplens cDNA	RC1-CT0198-150999-011-C08 CT0198 Homo sapiens cDNA	Homo sapiens hypothetical protein FLJ10379 (FLJ10379), mRNA	Homo sapiens hypothetical protein FLJ10379 (FLJ10379), mRNA	Homo sapiens mRNA for KIAA0995 protein, partial cds	Homo sapiens TRK-fused gene (NOTE: non-standard symbol and name) (TFG) mRNA	Homo sapiens TRK-fused gene (NOTE: non-standard symbol and name) (TFG) mRNA	EST90893 Synovial sarcoma Homo saplens cDNA 5' end	wb89c06.x1 NCI_CGAP_Pr28 Homo sepiens cDNA clone IMAGE:2313802 3' similar to contaîns L1.t1 L1 repositive element ;
Top Hit Database Source	EST_HUMAN	IN	TN	N	EST_HUMAN	EST_HUMAN	IN	EST HUMAN		EST_HUMAN	ļ	LN	EST_HUMAN	TN	NT	EST_HUMAN	EST_HUMAN	TN	EST_HUMAN	EST_HUMAN	L	EST_HUMAN	EST_HUMAN	INT	LN	FN	N-	L	EST_HUMAN	EST_HUMAN
Top Hit Acession No.	2.0E-44 BE244902.1	4826863 NT	7657334 NT	7657334 NT	1.0E-44 AW853132.1	1.0E-44 AW 994803.1	1.0E-44 AL163303.2	1 0E-44 AA434554 1		1.0E-44 AA434554.1		1.0E-44 AF196779.1	1.0E-44 AA455869.1	1.0E-44 AJ130755.1	1.0E-44 AJ130755.1	1.0E-44 AW967073.1	1.0E-44 AW967073.1	1.0E-44 AL163209.2	1.0E-44 AI337183.1	1.0E-44 AV714608.1	10092664 NT	1.0E-44 AW846967.1	1.0E-44 AW846967.1	B922391 NT	B922391 NT	9.0E-45 AB023212.1	5174718 NT	5174718 NT	8.0E-45 AA377985.1	6.0E-45 AI675425.1
Most Similar (Top) Hit BLAST E Value	2.0E-44	2.0E-44	1.0E-44	1.0E-44	1.0E-44	1.0E-44	1.0E-44	1.0E.44		1.0E-44		1.0E-44	1.0E-44	1.0E-44	1.0E-44	1.0E-44	1.0E-44	1.0E-44	1.0E-44	1.0E-44	1.0E-44	1.0E-44	1.0E-44	9.0E-45	9.0E-45	9.0E-45	8.0E-45	8.0E-45	8.0E-45	6.0E-45
Expression Signal	4.59	1.56	5.24	5.24	1.63	1.96	8.06	8.17		6.17		1.74	ဇ	0.68	99.0	0.91	16.0	96:0			3.47		3.21		0.98	1.41	3.9	6		
ORF SEQ ID NO:			26306		26804	L		28563		28564		29043		31314	31315	35070	L	35466	L		38505	38574			L		l			
Exon SEQ ID NO:	25122	L	L	13292	ı	1	14758			15431	1	15932	16979	18343	18343	L	L	_	L	L	24809	24878	24878	L	L	L	L	L		
Probe SEQ ID NO:	12152	12730	ន	53	594	1224	1805	2200		2299		2818	3819	5221	5221	8460	8460	8848	9227	11264	11820	11890	11890	4701	4701	6787	2591	5193	8298	1583

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											_		_	_							_		_	_	_			_		_	_
Top Htt Descriptor	au83h07.x1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2782909 3' similar to SW:R13A_HUMAN P40429 60S RIBOSOMAL PROTEIN L13A;	Homo sapiens ADP-ribosylation factor OTPase activating protein 1 (ARFGAP1), mRNA	Homo sepiens chromosome 21 segment HS21C003	CM4-CN0044-180200-515-f01 CN0044 Horno sapiens cDNA	tg94f07.x1 NCI_CGAP_CLL1 Homo saplens cDNA clone IMAGE:2116453 3' similar to SW:PAX1_MOUSE   P09084 PAIRED BOX PROTEIN PAX-1.;	272403.s1 Sogres_testis_NHT Homo saplens oDNA clone IMAGE:727877 3' similar to contains element	Homo saniens MCP-1 dene and enhancer region	Homo sapiens MCP-1 gene and enhancer region	Homo sapiens mRNA for inducible nitric oxide synthase, complete cds	Homo saplens mRNA for Inducible nitric oxide synthase, complete cds	Hamo sapiens zinc finger protein 277 (ZNF277), mRNA	Homo sapiens zinc finger protein 277 (ZNF277), mRNA	Homo sapiens bone morphogenetic protein 5 (BMP5), mRNA	Homo sapiens programmed cell death 5 (PDCD5), mRNA	Homo saplens golgin-like protein (GLP), mRNA	H.sapiens ART4 gene	601194440F1 NIH_MGC_7 Homo saplens cDNA, clone IMAGE:3538425 5'	no26c07.s1 NCI_CGAP_Pr1 Homo sapiens cDNA clone IMAGE:1009284 similar to contains element L1	repentive element;	Homo sapiens chromosome 12 open reading frame 3 (C12OKF3), mKNA	yd35f07.r1 Soares fetal liver spleen 1NFLS Homo saplens cDNA clone IMAGE:110245 5	yd35f07.r1 Soares fetal liver spleen 1NFLS Homo saplens cDNA clone IMAGE:110245 51	Mus musculus dynein, axon, heavy chain 11 (Dnahc11), mRNA	Mus musculus dynein, axon, heavy chain 11 (Dnahc11), mRNA	AV723976 HTB Homo sepiens cDNA clone HTBAAG01 5'	Homo sapiens golgi autoantigen, golgin subfamily a, 2 (GOLGA2) mRNA	Homo saplens chromosome 21 segment HS21C027	Homo sapiens chromosome 21 segment HS21C027	H. sapiens DNA for endogenous retroviral like element	Homo sapiens chromosome 21 segment HS21C018	Homo saplens partial 5-HT4 receptor gene, excns 2 to 5
Top Hit Datebase Source	EST_HUMAN	i ·		EST_HUMAN	EST HUMAN	Not III	1			-N						IN	EST_HUMAN		HOMAN			EST HUMAN	NT		EST_HUMAN		LN	NT	IN	NT	NT
Top Hit Acession No.	6.0E-45 AW157570.1	11418213 NT	5.0E-45 AL163203.2	5.0E-45 BF333627.1	5.0E-45 AI523766.1	00 45 0 0 40 0 4 10 4 4	T		1.	5.0E-45 AB022318.1	11496268 NT	11496268 NT	11418704 NT	4759223 NT	8923698	4.0E-45 X95826.1	4.0E-45 BE265622.1		4.0E-45 AA226220.1	11435947 NT	3.0E-45 T71480.1	3.0E-45 T71480.1	6753651 NT	6753651 NT	3.0E-45 AV723976.1	4758451 NT	3.0E-45 AL163227.2	3.0E-45 AL163227.2	3.0E-45 X89211.1		2.0E-45 AJ243213.1
Most Similar (Top) Hit BLAST E Value	6.0E-45	6.0E-45	5.0E-45	5.0E-45	5.0E-45	20 30	5.0E-45	5.0E-45	5.0E-45	5.0E-45	5.0E-45	5.0E-45	5.0E-45	5.0E-45	5.0E-45	4.0E-45	4.0E-45		4.0E-45	4.0E-45	3.0E-45	3.0E-45	3.0E-45	3.0E-45	3.0E-45	3.0E-45	3.0E-45	3.0E-45	3.0E-45	2.0E-45	2.0E-45
Expression Signal	3.77	1.80	1.71	4.42	287	200	4 00	1.09	0.92	0.92	0.87	0.87	1.12	1.45	25	6.3	2,15		0.81	1.36	0.93	1.03	1.34	1.34	1.76	4.31	7.52	7.52	3.45	3.12	0.92
ORF SEQ ID NO:				28313	29477		16016 73068	32665						35861		27385				31659			32895								29287
Exon SEQ ID NO:	17242	26154	14090	15199	16455	1	10023	ì	1	19366		1.	21552	1	24982	14330	15496		_		16580	16580		19536	1	ŀ	23550	Į į	ı	15697	16273
Probe SEQ ID NO:	4087	12911	915	2058	3281	000	8700	6143	6190	6190	6318	6318	8471	9241	11997	1167	2365		9157	12166	3411	4199	9929	6366	8645	8994	10515	10515	13040	2572	3097

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			7	7	- 1		т	$\neg$	Т	7	Т	Т	7	_	7	Т	7	Т	1	Т	Т	Т	7	Т	_[	-,	1	ı	-1	1	1
Тор Hit Descriptor	Human eosinophil Charcot Leyden crystal (CLC) protein (lysophospholipase) gene, promoter and exon 1	601467793F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3870838 5	RCO-LT0001-150200-032-d11 LT0001 Homo saplens cDNA	ts56a01.x1 NCI_CGAP_Kid8 Homo septens cDNA clone IMAGE:2232552.3	MR0-HT0923-190800-201-e02 HT0923 Homo capiens cDNA	aa87712.r1 Stratagene fetal retina 937202 Homo sapiens cDNA clone IMAGE:838319 5' similar to TR:G1144569 G1144669 R-SLY1.;	xp72a03.x1 NCI_CGAP_Dv40 Homo sepiens cDNA clone IMAGE:2745868 3'	xp72a03.x1 NCI_CGAP_Ov40 Homo saplens cDNA clone IMAGE:2745868 3'	Homo sapiens calcium channel, voltage-dependent, alpha 11 subunit (CACNA11), mRNA	601284360F1 NIH_MGC_44 Homo sapiens oDNA clone IMAGE:3806183 5	601284360F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3506183 5	Homo sapiens RAP1A, member of RAS oncogene family (RAP1A), mRNA	Homo saplens Langerhans cell specific c-type lectin (LANGERIN), mRNA	Human pro-a2 chain of collegen type XI (COL11A2) gene, complete cds	Homo sapiens chromosome 21 open reading frame 1 (C21orf4), mRNA	Homo saplens mRNA for KIAA1591 protein, partial cds	601289116F1 NIH_MGC_8 Homo saplens cDNA clone IMAGE;3619803 5	yr05b02.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:204363 5	Homo sapiens niban protein (NIBAN), mRNA	Homo sapiens peroxisomal blogenesis factor 14 (PEX14), mRNA	Homo sapiens peroxisomal biogenesis factor 14 (PEX14), mRNA	Homo sapiens DNA for amyloid precursor protein, complete cds	601511228F1 NIH_MGC_71 Homo saplens cDNA clone IMAGE:3912535 57	Human mRNA for KIAA0299 gene, partial cds	Homo sapions protein kinase C, alpha blinding protein (PRKCABP), mRNA	Homo sapiens hypothetical protein FLJ20454 (FLJ20454), mRNA	Homo saplens Ran GTPase activating protein 1 (RANGAP1), mRNA	Homo sapiens calclum channel, voltage-dependent, alpha 11 subunit (CACNA1), mRNA	Mus musculus keratin complex 2, gene 6g (Krt2-6g), mRNA	Homo sapiens chromosome 21 segment HS21C009	2822449.5prime NIH_MGC_7 Homo saplens cDNA clone IMAGE:2822449 5
Top Hit Database Source	TN	EST_HUMAN	EST HUMAN	EST_HUMAN	EST_HUMAN	EST HUMAN	EST_HUMAN	EST_HUMAN	Ę	EST_HUMAN	EST_HUMAN	NT	L	NT	N.	Ę	EST_HUMAN	EST_HUMAN	Ę	ΕN	NT	TN	EST_HUMAN	NT	LN L	N	LN.	IN	NT	N	EST_HUMAN
Top Hit Acession No.	01665.1	2.0E-45 BE782184.1	2.0E-45 AW834834.1	2.0E-45 AI636786.1	2.0E-45 BE934350.1	2.0E-46 AA458770.1	2.0E-45 AW270280.1	2.0E-45 AW270280.1	11418157 NT	1.0E-45 BE389855.1	1.0E-45 BE389855.1	4506412 NT	7657290 NT	J32169.1	8659558 NT	1.0E-45 AB046811.1	1.0E-45 BE396633.1	1.0E-45 H57443.1	11545796 NT		11422236 NT	1.0E-45 D87675.1	1.0E-45 BE887843.1	1.0E-45 AB002297.1	11418099 NT	11526291 NT	11418177 NT	11418157 NT	9910293 NT	9.0E-46 AL163209.2	9.0E-46 AW246964.1
Most Similar (Top) Hit. BLAST E Vatue	2.0E-45 L01665.1	2.0E-45	2.0E-45	2.0E-45	2.0E-45	2.0E-46	2.0E-45	2.0E-45	2.0E-45	1.0E-45	1.0E-45	1.0E-45	1.0E-45	1.0E-45 U32169.	1.0E-45	1.0E-45	1.0E-45	1.0E-45	1.0E-45	1.0E-45	1.0E-45	1.0E-45	1.0E-45	1.0E-45		1.0E-45		1.0E-45	9.0E-46	9.0E-46	9.0E-46
Expression Signal	5.45	1.1	0.91	0.51	12.66	2.71	3.35	3.35	2.73	1.22	1.99	1.02	1.66	. 10.41	0.85	0.69	6.4	1.05	1.56	0.7	0.7	6.0	3.92	66.0	3.5	19.43	6.42	4.02	2.71	6.82	6.80
ORF SEQ ID NO:	33198					38177		38482				26714	ĺ	L	'	l			31181	L	34823	35425	35950	L		L		31963			37335
Exan SEQ ID NO:	19810	20842	١.	1	1	24510	24784	24784	25710	13617	13617	ı		1	1	1	1	1	i .	1	21302	1	1	L		L	1_		L	L	Ц
Probe SEQ ID NO:	6651	7786	8610	9784	11042	11450	11794	11794	13087	126	422	485	129	3172	3581	3664	4599	4848	5081	8220	8220	8806	9321	9722	12369	12562	12568	13047	8423	8835	10697

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										T		Г		xx42e04.x1 NCI_CGAP_Ut1 Homo sapiens cDNA clone IMAGE:2706654 3' similar to gb:L08069 DNAJ				Homo sapiens chromosome 21 segment HS21C010	Г	Г	Г		П	Г	Г	no54e09.s1 NCI_CGAP_SS1 Homo sapiens cDNA clone IMAGE:1104520 3' similar to gb:X53741_rna1_ MAN   FIBULIN-1_ISOFORM A PRECURSOR (HUMAN);	T	hi896c03.x1 NCJ_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3008836 3' similar to gb:X14008_ma1   LYSOZYME C PRECURSOR (HUMAN);contains element MER37 repetitive element;
Top Hit Datebase Source	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	ΙN	EST_HUMAN	۲	NAME OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY	MOL ISS	EST_HUMAN		EST_HUMAN		EST_HUMAN	EST_HUMAN	EST_HUMAN	<u>F</u>	EST_HUMAN	EST_HUMAN		EST_HUMAN	EST_HUMAN	EST_HUMAN	EST HUMAN	NAMI H		EST_HUMAN
Top Hit Acession No.	8.0E-46 AI433261.1	8.0E-46 AI433261.1	8.0E-46 BE167244.1	7.0E-46 BE388165.1	7.0E-46 BE064386.1	8922708 NT	7.0E-46 BF105845.1	7.0E-46 AL163246.2	7 7007 4014	6.0E-40 A1804301.1	6.0E-46 Al884381.1		6.0E-46 AI635448.1		6.0E-46 AW513244.1	8.0E-46 BF509740.1	6.0E-46 BE784971.1	6.0E-46 AL163210.2	5.0E-46 BE677194.1	5.0E-46 BE677194.1		5.0E-46 BF590442.1	5.0E-46 BF347229.1	5.0E-46 AW582253.1	5.0E-46 BE549744.1	4 OF 48 AABO1143 1		4.0E-46 AW770544.1
Most Similar (Top) Hit BLAST E Value	8.0E-46	8.0E-46	8.0E-46	7.0E-46	7.0E-46	7.0E-46	7.0E-46	7.0E-46	100	6.0E-40	6.0E-46		6.0E-46		6.0E-48	8.0E-46	6.0E-46	6.0E-46	5.0E-46	5.0E-48		5.0E-46	5.0E-46	5.0E-46	5.0E-46	4 OF 48	2	
Expression Signal	7.67	7.67	2.72	4.79	1.33	4	1.8	2.6	0	0.8/	6.87		11.57		66.0	0.67	2.14	5.31	1.17	1.17		1.52	3.69	0.75	0.59	20.6	200	2.89
ORF SEQ ID NO:	28760						33171	L		7808Z	29038		32778		33807				29796	L	L	33436		L		Ŀ		27981
Exen SEQ ID NO:	15639	ı	1	ı	l .	19343	19783	25469	ļ	9ZRCL	15926	ı	19431	1	20445	L_	١	L	16781	16781		20026	L	1	l	ł	L.	14889
Probe SEQ ID NO:	2513	2513	8244	4703	4928	6167	6623	12706		2812	2812		6257		7366	7541	11673	289	3617	3617		6874	7080	7244	7544	999	3	1740

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Top Hit Descriptor	hIB6c03.x1 NCI_CGAP_Lu24 Homo sapiens cDNA cione IMAGE:3008836 3' similar to gb:X14008_rna1 LYSOZYME C PRECURSOR (HUMAN);contains element MER37 repetitive element ;	Human endogenous retrovirus RTVL-H2	Human Ig germline gamma-3 heavy-chain gene V region, partial cds	Human Ig germline gamma-3 heavy-chain gene V region, partial cds	Homo saplens DNA for Human P2XM, complete cds	Homo sapiens acidic 82 kDa protein mRNA (HSU15552), mRNA	Homo sepiens mitogen-activated protein kinase kinase kinase kinase 3 (MAP4K3), mRNA	H. sapiens Ig lambda light chain variable region gene (7c.11.2) germline; ig-Light-Lambda; VL.ambda	H. sepiens Ig lambda light chain variable rogion gene (7c.11.2) germiine, ig-Light-Lambda; VI.ambda	wi49c04.x1 NCI_CGAP_Lu19 Homo sapiens cDNA clone IMAGE:2406150 3' similar to contains THR.b2 THR remaitive element :	Human AD amyord mRNA complete orts	Thinks AD an injude in way, complete out	Human AD amyloid minny, complete cas	Human mRNA for KIAA0061 gene, partial cds	ne06a09.s1 NCI_CGAP_Co3 Homo sapiens cDNA clone IMAGE:880408 3' similar to contains THK.b2 THK in repetitive element :	227a11.s1 Soares_feta_Jiver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:431996 3'	Homo sapiens Bruton's tyrosine kinase (BTK), alpha-D-galactosidase A (GLA), L44-like ribosomal protein [1.44] and FTP3 (FTP3) cenes, comploite cds	759e02 rt Soares testis NHT Homo sabiens cDNA done IMAGE:726650 5 similar to SW:RSP1 MOUSE	Q01730 RSP-1 PROTEIN.	Mus musculus sperm tall associated protein (Stap), mRNA	801445137F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3849297 5	Homo sapiens small acidic protein (IMAGE145052), mRNA	601765225F1 NIH_MGC_53 Homo saplens cDNA clone IMAGE:3997326 5'	y/32d01.r1 Soares fetal liver spleen 1NFLS Homo sapions cDNA clone IMAGE:206977 5'	zh84f12.r1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:428015 5	xq78h03.x1 NCI_CGAP_Lu34 Homo saptens cDNA clone IMAGE:2756789 31	Homo sapiens cell division cycle 10 (homologous to CDC10 of S. cerevisiae) (CDC10) mRNA	EST390625 MAGE resequences, MAGP Homo sapiens cDNA
Top Hit Database Source	EST_HUMAN	IN	NT	NT	NT	TN	ŇT	TN	뉟	H HAAN	TIV	2	-N	N	NAM H TOTA	EST HUMAN	<u> </u>		EST_HUMAN	N.	EST_HUMAN	IN.	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	LNI	EST_HUMAN
Top Hit Acession No.	4.0E-46 AW 770544.1	4.0E-46 M18048.1	4.0E-46 M36852.1	4.0E-46 M36852.1	4.0E-46 AB002059.1	7657203 NT	4506376 NT	3.0E-46 Z73660.1	3.0E-46 Z73660.1	9 OF 46 A 1921 462 4	A1001 402.1	3.0E-46 L08850.1	3.0E-46 L08850.1	3.0E-46 D31765.1	2 DE-46 4 4 4 6 8 6 4 6 1	2.0E-46 AA678248.1	2 OF 48   178027 1	117010	2.0E-46 AA399286.1	9910569 NT	2.0E-46 BE869151.1	7857233 NT	2.0E-46 BF028854.1	2.0E-46 H48391.1	2.0E-46 AA001786.1	2.0E-46 AW 277214.1	4502694 NT	1.0E-46 AW978516.1
Most Similar (Top) Hit BLAST E Value	4.0E-46	4.0E-46	4.0E-46	4.0E-46	4.0E-46	3.0E-46	3.0E-48	3.0E-46	3.0E-46	97 110 6	S.OF 10	3.0E-46	3.0E-46	3.0E-46	2 NE.46	2.0E-46	20 10	200.2	2.0E-46	2.0E-46	2.0E-46	2.0E-48	2.0E-46	2.0E-46	2.0E-46	2.0E-46	1.0E-46	П
Expression Signal	299	7.4	2.1	2.1	1.36	9.0 28.0	1.21	1.11	1.11	47.75	12.43	0.61	0.61	1.78	79 CL	3.78	2	20.0	1.26	7.1	1.29	1.82	1,4	1.57	3.31	4.26	4.31	4.88
ORF SEQ ID NO:	27982	29021		31787	31989	28620		31015	31016	0999	1	1		38556	00026		27008		31188	L						31864	27483	
. Exen SEQ ID NO:	14889	15913	l_		25565	1	L	18028	18028	•	П	22284		24861	14027	L	<u> </u>	┸	18217	Ĺ	L	L	i	(	1	(	1	1
Probe SEQ ID NO:	1740	2798	5553	5553	12851	2359	4513	4898	4898	9	6460	9206	9208	11873	080	1593	4674	Š	5089	7653	8260	11524	12294	12555	12596	12934	1261	2356

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	Top Hit Descriptor	EST48b095 WATM1 Homo sapiens cDNA done 48b095	np78b02.s1.NCI_CGAP_Pr2 Homo sepiens cDNA clone IMAGE:1132395 similar to gb:X76717 H.seplens MT-11 mRNA. (HUMAN);	Homo sepiens mRNA for KIAA0980 protein, partial cds	7e92b01 x1 NCI_CGAP_Ov18 Home saplens cDNA clone IMAGE:3643705 3'	Homo saplens centaurin-alpha 2 protein (HSA272195), mRNA	Homo saplens centautin-alpha 2 protein (HSA272195), mRNA	Th48e07.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3567862 3' similar to contains element. MER27 repetitive element:	7692b01x1 NCI CGAP Ov18 Homo sapiens cDNA clone IMACE:3643705 3'	Homo sapiens CTL2 gene	502072284F1 NCI CGAP Bm67 Homo sapiens cDNA clone IMAGE:4215398 5	602072264F1 NCJ_CGAP_Brn67 Homo sepiens cDNA clone IMAGE:4215398 5	AV715377 DCB Homo sapiens cDNA clone DCBAIE03 5	Homo sapiens Xq pseudoautosomal region; segment 1/2	higaeo4.x1 NCI_CGAP_Lu24 Home sapiens cDNA clone INAGE:3009534.3' similar to TR:O75703 O75703 HAPOTHETICAL 12.4 KD PROTEIN :	Home conjune and fines nardein ZNE288 (ZNE288) mRNA	Hallo opposite and importance in a contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of	Homo saptens straitar to addo-Keto reductase tamily 1, member b1 (addose l'eductase) (n. saptens) (LOC63093), mRNA	Homo sapiens SEC14 (S. cerevisiae)-like 2 (SEC14L2), mRNA	Homo sapiens HLA-C gene, exon 5, individual 19323	Hamo sapiens HLA-C gene, exon 5, individual 19323	Homo saplens protein phosphatase 2, regulatory subunit B (B56), epsilon isoform (PPP2R5E) mRNA	Hano sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22, segment 3/3	Homo sapiens mRNA for GCK family kinase MINK-2, complete cds	Homo sapiens mRNA for GCK family kinase MINK-2, complete cds	AV683284 GKC Homo sapiens cDNA clane GKCASH11 5'	Homo sapiens chromosome 21 segment HS210046	HSU77054 Human Homo saplens cDNA clone N7	LE98h02 x1 NCI_CGAP_Kid11 Homo saplens cDNA clone IMAGE:2296659 3'	Homo sapiens RECQL5 beta mRNA for DNA helicase recQ5 beta, complete cds	Homo sapiens RECQL6 beta mRNA for UNA helicase recub beta, complete cas
	Top Hit Database Source	EST_HUMAN	EST_HUMAN	TN	EST HUMAN	LN.	NT	NAMI III TOB	FST HUMAN	L	EST HUMAN	EST HUMAN	EST HUMAN	E	NO FOLLOWING		Z	Ľ,	LN L	TN	TN	Ä	L'N	N-	N F	EST_HUMAN	TN	EST_HUMAN	EST HUMAN	NT	LN
	Top Hit Acession No.	97330.1	1.0E-46 AA631912.1	1.0E-46 AB023197.1	1.0E-46 BF194707.1	8923762 NT	8923762 NT	4 OF 48 DE408247 4	1.0E-46 BF194707 1	1 0F 46 A 1245621 1	1 0F-46 RF531102.1	1.0E-46 BF531102.1	1.0E-46 AV715377.1	9.0E-47 AJ271735.1	47 AM 77 AM 7 AM 7 AM 7 AM 7 AM 7 AM 7 A	44401400	N 8545241	11432209 NT	11417966 NT	718536.1	Y18536.1	5453955 NT	8.0E-47 AJ229043.1	8.0E-47 AB041926.1	8.0E-47 AB041926.1	7.0E-47 AV683284.1	6.0E-47 AL163246.2	6.0E-47 U77054.1	6.0E-47 AI695189.1	6.0E-47 AB042824.1	6.0E-47 AB042824.1
	Most Similar (Top) Hit BLAST E Value	1.0E-46 H97330.1	1.0E-46 A	1.0E-46	1.0E-46	1.0E-46	1.0E-46	4 01 48 5	1.0E-46.F	1 0F 46 /	1 0F 46 F	1.0E-461	1.0E-46/	9.0E-47 /	100	8.0E 47	9.0E-4/	9.0E-47	9.0E-47	8.0E-47 Y18536.1	8.0E-47 Y18536.1	8.0E-47	8.0E-47	8.0E-47	8.0E-47	7.0E-47					
	Expression Signel	3.53	2.12	3.13	5.89	5.34	5.34	0	3 72	184	6	1.39	180	3.7	30.0	3.03	0.80	4.1			32.2	1.5	2.04		    -		3.04				0.69
	ORF SEQ ID NO:	28725			32313		32610		33280	38136	3010E					Ì	33039	38110		28100		20062			29882		28851				36539
	Exon SEQ ID NO:	15600	i	1	ı	١.	25818		19902	Н	1			L		- 1	19672	24449	<u></u>	1	┖	15897	1	1	L	1	1	١.	l	ŧΙ	22953
	Probe SEQ ID NO:	2473	3321	4995	5817	8609	6098		6/40	44440	12222	12323	13178	787		304	8208	11388	12874	1851	1851	2784	3089	3715	3715	12962	2613	8890	9478	9913	9913

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Table 4
Single Exon Probes Expressed in Placenta

Top Hit Descriptor	Homo sapiens CDC37 (cell division cycle 37, S. cerevisiae, homolog) (CDC37), mRNA	EST00738 Fetal brain, Stratagene (cat#936206) Homo sapiens cUNA cione HFBCFU/	Homo sapiens E1A binding protein p300 (EP300) mRNA	MR4-TN0108-280800-201-dn4 TN0108 Homo saplens cDNA	601280486F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:36/2437 5	601280486F1 NIH_MGC_39 Homo capient cDNA clone IMAGE:3622437 5	RC3-BN0034-220300-015-f05 BN0034 Homo sapiens cUNA	xx66b07.x1 NCI_CGAP_Lym12 Homo sapiens cDNA clone IMAGE:2848597 3' similar to SW:IN16_MOUSE. Q84252 VIRAL INTEGRATION SITE PROTEIN INT-8: [1]:	601497639F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3899721 5	601497639F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3899721 5	yy64b04,s1 Soares_multiple_sclerosis_ZNbHMSP Homo sapiens cUNA crone IMAGE:277327.3	Homo sapiens chromosome 21 segment HS21C084	Homo sapiens glutamate receptor, ionotropic, kalnate 1 (GRIK1) mRNA	Homo sapiens nuclear dual-specificity phosphatase (SBF1) mRNA, partial cds	Human T-cell receptor active alpha-chain mRNA from JM cell line, complete cds	UI-HF-BM0-adx-d-07-0-UI.r1 NIH_MGC_38 Homo sapiens cDNA clone (MAGE:3063203 5	UI-HF-BM0-adx-d-07-0-UI.r1 NIH MGC 38 Homo sapiens cDNA clone IMAGE:3063205 3	qh04c07.x1 Scares_NFL_1_GBC_S1 Homo sapiens cDNA clone IMAGE:1843/10.3	w/11h08.x1 NCI_CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2402559 3	w/11h08.x1 NCI_CGAP_Kid12 Homo sapiens cLINA clone IMAGE:2402559 3	EST375869 MAGE resequences, MAGH Homo sapiens cDNA	EST375869 MAGE resequences, MAGH Hamo sapiens cDNA	Homo sapiens myosin phosphatase, target subunit 2 (MYP 1.2), mRNA	Homo sapiens chromosome 21 segment HS21C009	Homo sapiens chromosome 21 segment HS21C009	wq96b02.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2479851 3/	Homo sapiens KIAA0428 gene product (KIAA0428), mRNA	ng43h12.s1 NCI_CGAP_Co3 Homo sepiens cDNA clone IMAGE:9376073	Homo saplens ring finger protein (C3HC4 type) 8 (RNF8), mRNA	nf23g07.s1 NCI_CGAP_Pr1 Homo sapiens cDNA clone IMAGE:914652	nf23g07.s1 NCI_CGAP_Pr1 Homo sapiens cDNA clone IMAGE:914652	Homo sapiens RevIRex activation domain binding protein-related (RAB-R) mKNA	EST377239 MAGE resequences, MAGI Homo sapiens cDNA
Top Hit Database Source	NT	EST_HUMAN	NT	EST_HUMAN	EST HUMAN	EST HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST HUMAN	EST_HUMAN	NT	LN	NT	NT	EST_HUMAN	EST HUMAN	EST_HUMAN	EST_HUMAN	EST HUMAN	EST_HUMAN	EST_HUMAN	토	N.	LN.	EST_HUMAN	FN.	EST_HUMAN	N	EST_HUMAN	EST_HUMAN	NT	EST_HUMAN
Top Hit Acession No.	11423972 NT		4557556 NT	.0E-47 BE938896.1	0E-47 BE616483.1	.0E-47 BE616483.1	.0E-47 AW993777.1	.0E-47 AW515509.1	3.0E-47 BE907634.1	3E907634.1	V57483.1	3.0E-47 AL163284.2	4504116 NT	J93181.1	3.0E-47 M12959.1	4W408800.1	3.0E-47 AW408800.1	3.0E-47 AI222413.1	3.0E-47 AI819755.1	3.0E-47 AI819755.1	3.0E-47 AW963796.1	3.0E-47 AW963796.1	4505318 NT	AL163209.2	2.0E-47 AL163209.2	2.0E-47 AI969279.1	7662109 NT	2.0E-47 AA524514.1	4504866 NT	2.0E-47 AA569592.1	2.0E-47 AA569592.1	5174648 NT	2.0E-47 AW965168.1
Most Similar (Top) Hit BLAST E Value	5.0E-47	5.0E-47 M78590.1	4.0E-47	4.0E-47	4.0E-47	4.0E-47	4.0E-47	4.0E-47	3.0E-47	3.0E-47	3.0E-47	3.0E-47	3.0E-47	3.0E-47	3.0E-47	3.0E-47	3.0E-47	3.0E-47	3.0E-47	3.0E-47	3.0E-47	3.0E-47	2.0E-47	2.0E-47	2.0E-47	2.0E-47	2.0E-47	2.0E-47	2.0E-47	2.0E-47	2.0E-47		
Expression Signal	5.73	5.58	7.03	0.82	2.22	2.22	0.83	1.98	209	2.09	3.99	10.04	0.97	6.61	1.14	4.68	4.68	1.71	0.88	0.88	0.77	0.77	1.21	2.45	2.45	0.95				1.67		2.14	
ORF SEQ ID NO:	33255		27660		35292		35436		26778	28779	Ĺ	L	29562	L		1	32655		34089		35654	L	26409					27952	Ļ	30628	L	L	L
Exan SEQ ID NO:	19865	ı		١.	1	1	ı	l	1	L	1_	14141	L		L	l	1	19852	ì.	l	ı	ı	13377	L	Ĺ	1		1		1	1	1	1
Probe SEQ ID NO:	6707	11035	1432	6971	8677	8677	8818	11936	558	558	841	898	3376	4073	4482	6136	6136	6694	7540	7540	9033	9033	152	86	66	1598	1623	1712	4467	4503	4503	4628	4933

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Top Hit Descriptor	ov61h03,x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1641845.3'	Homo sapiens regulator of G-protein signaling 6 variant form (RGS6) mRNA, complete ods	601463932F1 NIH_MGC_67 Homo saplens cDNA clone IMAGE:3867487 5	601463932F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3867487 5	Homo sapiens 5-hydroxytryptamine 1D receptor pseudogene with an Alu repeat insertion	Homo sapiens DNA for amyloid precursor protein, complete cds	Homo sapiens DNA for amyloid precursor protein, complete cds	Homo sepiens SPH-binding factor mRNA, partial cds	Homo sepiens BTG family, member 3 (BTG3), mRNA	yr82e08.s1 Soares infant brain 1NIB Homo saplens cDNA clone IMAGE:29966 3' similar to contains OFR	repatitive element;	Homo sapiens chramosome 21 cogment H521 C009	qp99h03.x1 Soares_fetal_lung_NbHL19W Homo sapiens cDNA clone IMAGE:1831189 3	601155321F1 NIH_MGC_21 Hamo saplens cDNA clone IMAGE::3138893 5/	601155321F1 NIH_MGC_21 Hamo sapiens cDNA clone IMAGE:3138893 51	RC3-ST0197-130400-017-h02 ST0197 Homo sapiens cDNA	ari 9e06.x1 Barstead aorta HPLRB6 Homo sapiens cDNA done IMAGE:2355586 3' similar to gb:M22995	RAS-RELATED PROTEIN RAP-1A (HUMAN);	hi84a11.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2978972.3' similar to gb:MZ6326   KERATIN, TYPE I CYTOSKELETAL 18 (HUMAN);	Т	1	spliced	CM2-MT0100-310700-290-f05 MT0100 Homo saplens cDNA	601511714F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3913106 5	601511714F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3913106 5	at/35h09.x1 Barstead colon HPLRB7 Homo sapiens cDNA clone IMAGE:2377889 3' similar to TR:060844 Ageneral Domesta DOME DE PAT ZVANGEN GRANUI E MEMBRANE PROTEIN	1		╗	Homo sapiens aminoacylase 1 (ACY1), mRNA	Homo saplens aminoacylase 1 (ACY1), mRNA	hk6tbc6.x1 NCI_CGAP_Lym12 Homo eaplens cDNA clone IMAGE:3001133 3' similar to gb:X64707 BREAST BASIC CONSERVED PROTEIN 1 (HUMAN);
Top Hit Database Source	EST_HUMAN	LN	EST_HUMAN	EST_HUMAN	ΤN	뒫	Į,	IN	IN		EST HUMAN	LN L	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN		EST HUMAN	EST HUMAN	L		ž	EST_HUMAN	EST_HUMAN	EST_HUMAN		ES L'HOMAN	EST_HUMAN	EST_HUMAN	TN.	N F	EST_HUMAN
Top Hit Acession No.	2.0E-47 AI041128.1	2.0E-47 AF073921.1	2.0E-47 BE778475.1	2.0E-47 BE778475.1	L09731.1	2.0E-47 D87675.1	2.0E-47 D87675.1	2.0E-47 AF071771.1	11526138 NT		2.0E-47 R42423.1	2.0E-47 AL163209.2	1.0E-47 A1333429.1	1.0E-47 BE280477.1	1.0E-47 BE280477.1	1.0E-47 AW813906.1		1.0E-47 AI880886.1	1 0F-47 AW664648 1	ĺ		9.0E-48 AF223391.1	9.0E-48 BF359947.1	9.0E-48 BE888196.1	9.0E-48 BE888196.1	, 00,000	9.0E-48 AI833168.1	9.0E-48 AU123240.1	9.0E-48 BE393813.1	TN 0081094	4501900 NT	8.0E-48 AW 768477.1
 Most Similar (Top) Hit BLAST E Value	2.0E-47	2.0E-47	2.0E-47	2.0E-47	2.0E-47	2.0E-47	2.0E-47	2.0E-47	2.0E-47		2.0E-47	2.0E-47	1.0E-47	1.0E-47	1.0E-47	1.0E-47		1.0E-47	1 0F-47	1 0F-47		9.0E-48	9.0E-48	9.0E-48	9.0E-48		9.0E-48	- 1		8.0E-48	8.0E-48	
Expression Signal	0.77	8.0	1.32	1.32	1.34	1.96	1.96	1.76	1.27		3.36	1.87	5.42	1.1	1.1	2.4		10.78	4 24	2.28		3.84	0.73	1.1	1.1		0.57	0.71	3.08	1.75	1.65	5.72
ORF:SEQ (D NO:		32407	1		١	34753		35533	l		31653		27663					33464		37205		27879			32291				38098			29390
SEQ ID NO:	18366	L		L	١.	1	1	ı	1	[ _	26073		14590	L	ł	1	1	20054		上	L	14795	ł	ł	1	١		19625	24439	L	L	)
Probe SEO ID NO:	5245	5904	6097	6097	7876	8151	8151	8915	9690		12357	12394	1437	3926	3926	5187		7189	Gaco	10564		1643	3646	5797	5797		6226	6355	11378	1279	1280	3205

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Top Hit Descriptor	hk61b03.x1 NCI_CGAP_Lym12 Homo sapiens cDNA clone IMAGE:3001133 3' sImilar to gb:X64707 BREAST BASIC CONSERVED PROTEIN 1 (HUMAN);	Homo saplens glutamate receptor, ionotropic, kainate 1 (GRIK1) mRNA	Homo sapiens mRNA for KIAA1209 protein, partial cds	Homo saplens mRNA for KIAA1209 protein, partial cds	Homo sapiens tousled-like kinase 1 (TLK1), mRNA	Homo saplens SET domain and mariner transposase fusion gene (SETMAR) mRNA	Homo sapiens histidyl-tRNA synthetase (HARS), mRNA	yg37b02.r1 Soares Infant brain 1NIB Homo sapiens cDNA clone IMAGE:34747 5	wi69h03.x1 NCI_CGAP_Kid12 Hamo saplens cDNA clane IMAGE:2398613 3'	Homo sapiens mRNA for AIE-75, complete cds	Homo sapiens BMX non-receptor tyrosine kinase (BMX), mRNA	Homo saplens mRNA for KIAA1624 protein, partial cds	Homo sapiens mRNA for KIAA1624 protein, pertial cds	Homo sapiens putative oncogene protein mRNA, partial cds	Homo sapiens hypothetical protein FLJ11006 (FLJ11006), mRNA	zq45b08.s1 Stratagene hNT neuron (#937233) Homo sapiens cDNA clone IMAGE:632627 3' similar to	contains Alu repetitive element;	Homo sapiens phosphodiesterase 1A, calmodulin-dependent (PDE1A) mRNA	RC4-BT0311-141199-011-h06 BT0311 Homo saplens cDNA	Ha140-f Adult heart, Clontech Homo sapiens cDNA clone a140-f	tu47a02.x1 NCI_CGAP_Pr28 Homo sapiens cDNA clone IMAGE:2254154 3'	RC4-BT0311-141199-011-h06 BT0311 Homo sapiens cDNA	AV690964 GKC Homo sapiens cDNA clone GKCDRE12 5'	Homo sapiens chromosome X open reading frame 6 (CXORF6) mRNA	Homo sapiens chromosome X open reading frame 6 (CXORF6) mRNA	Hamo sapiens opioid growth factor receptor mRNA, complete cds	hI14b12.x1 NCI_CGAP_GU1 Homo sepiens cDNA done IMAGE:2972255 3' similar to SW:DCRB_HUMAN P58555 DOWN SYNDROME CRITICAL REGION PROTEIN B. ;	204g03.r1 Sogres_feta_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:429844 5'	MR4-BT0657-060400-201-e10 BT0657 Homo saplens cDNA	Human endogenous retrovirus HERV-P-T47D	nv03f05.s1 NCI_CGAP_Pr22 Homo saplens cDNA clone IMAGE:1219137 3' similar to contains PTR5.b1 PTR5 repetitive element;
Top Hit Database Source	EST_HUMAN B	,		1 LN					EST_HUMAN v	IN TN							EST_HUMAN o		EST_HUMAN F	EST HUMAN	Г		EST_HUMAN /		-		EST HUMAN	Γ	Т	Z	
Top Hit Acession No.	8.0E-48 AW 768477.1	4504116 NT	7.0E-48 AB033035.1	7.0E-48 AB033035.1	6912719 NT	5730038 NT	1416831		6.0E-48 AI761111.1	6.0E-48 AB006955.1	11420995 NT	6.0E-48 AB046844.1	6.0E-48 AB046844.1	6.0E-48 AF026816.1	11427428 NT		6.0E-48 AA189080.1	4826891 NT	5.0E-48 BE064410.1	4,0E-48 R45715.1	-	4.0E-48 BE064410.1	3.0E-48 AV690984.1	4885170 NT	4885170 NT	3.0E-48 AF172453.1	3 0E-48 AW 664531.1	3.0E-48 AA009541.1	ŀ		} }
Most Similar (Top) Hit BLAST E Velue	8.0E-48	8.0E-48	7.0E-48	7.0E-48	7.0E-48	7.0E-48	7.0E-48	7.0E-48 R19623.1	6.0E-48	6.0E-48	6.0E-48	6.0E-48	6.0E-48	6.0E-48	6.0E-48		6.0E-48	5.0E-48	5.0E-48	4.0E-48	4.0E-48	4.0E-48	3.0E-48	3.0E-48	3.0E-48	3.0E-48		ļ			) }
Expression Signal	5.72	99.0	2.58	18.69	1.96	6.39	24.01	2.98	0.88	0.84	0.93	0.78	0.78	1.57	1.87		2.84	1.48	1.04	1.02	3.11	1.75	1.91	31.61	31.61	0.93					
ORF SEQ ID NO:	29391	30208			27761		33233	L	29858			l				١.	36514	29569	35395	29053			L	28282					32516	L	
Exon SEQ ID NO:	16380	17197	13698	13698	ı	14819	19843	\_	L	19359	i .	1			1		22830	18465	1	l	ı	ı		i .	1	1	ı	L	L	L	1 1
Probe SEQ (D NO:	3205	4041	503	504	1527	1667	9899	12125	3687	6183	6924	7628	7628	9323	9741		0686	3384	8774	2829	11200	12050	1416	2032	2032	3505	37.24	4382	6015	74.59	8585

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Top Hit Descriptor	UHH-BW1-ani-a-10-0-Ui.s1 NCI_CGAP_Sub7 Homo sapiens cDNA clone IMAGE:3082267 3'	zx80c03.r1 Soares ovary fumor NbHOT Homo sapiens cDNA clone IMAGE:810052 5'	fmfc7 Regional genomic DNA specific cDNA library Homo sapiens cDNA clone CR17-26	TCBAP1D3842 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA Homo sapiens cDNA clone TCBAP3842	no18g01.s1 NCI_CGAP_Phe1 Homo sepiens cDNA clone IMAGE:1101072.3'	no18g01.s1 NCI_CGAP_Phe1 Homo saplen's cDNA clone IMAGE:1101072.31	Homo saplens mRNA for KIAA1501 protein, partial cds	Homo sapiens mRNA for KIAA1501 protein, partial cds	Homo espiens v-rel avian reticuloendothellosis viral oncogene homolog A (nuclear factor of kappa light polypeptide gene enhancer in B-cells 3 (p55)) (RELA), mRNA	AV743451 CB Hamo sapiems aDNA clone CBCCGG10 5'	UI-H-Bi2-agi-b-11-0-UI.s1 NCI_CGAP_Sub4 Homo sepiens cDNA clone IMAGE:2724453 3'	2x80c03.r1 Scares overy tumor NbHOT Homo septens cDNA clone IMAGE:810052 5'	601305064F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3639782 5'	Homo sapiens cisplatin resistance-associated overexpressed protein (LOC51747), mRNA	Homo sapiens amyloid beta (A4) precursor protein (protesse nexin-II, Alzheimer disease) (APP), mRNA	Homo sapiens EBNA-2 co-activator (100kD) (p100), mRNA	Homo sapiens EBNA-2 co-activator (100kD) (p100), mRNA	Homo sapiens RNA binding motif protein 6 (RBM6) mRNA	Hamo sepiens chramosome 21 segmant HS21C102	Homo sapiens chromosome 21 segment HS21C046	Human endogenous retroviral DNA (4-1), complete retroviral segment	kd17c01 x1 NCI_CGAP_Co16 Homo sapiens cDNA clone IMAGE:2075904 3' similar to TR:O14588 O14588 SIMILARITY TO U73941;	td17c01.x1 NCI_CGAP_Co16 Hamo saplens cDNA clone IMAGE:2075904 3' similar to TR:O14588 O14588 CIA4888		Homo septems NF2 gene	Homo sapiens mRNA for KIAA1071 protein, partial cds	Homo sapiens mRNA for KIAA1071 protein, partial cds	Homo sapiens hunlingtin (Huntington disease) (HD) mRNA	Homo sapiens mitogen-activated protein kinase kinase kinase 13 (MAP3K13), mKNA	Homo sapiens mitogen-activated protein kinase kinase kinase 13 (MAP3K13), mKNA
Top Hit Database Source		EST_HUMAN	EST_HUMAN	EST HUMAN	EST HUMAN	EST_HUMAN	LN.	LN	Į.	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST HUMAN	LN	NT	LN	NT	NT	N	NT	LN	EST HUMAN		ESI HUMAIN	¥	NT	NT	NT	Ę	닐
Top Hit Acession No.	3.0E-48 BF514170.1	4A465007.1	A631940.1	3E246085.1	2.0E-48 AA613171.1	4A613171.1	AB040934.1	AB040934.1	11496238 NT	2.0E-48 AV743451.1	4W291799.1	AA465007.1	2.0E-48 BE737154.1	7706534 NT	4502166 NT	7657430 NT	7657430 NT	5032032 NT	.0E-48 AL163302.2	.0E-48 AL163246.2	.0E-48 M10976.1	0F-48 AI889077.1	1 2 2 2 2 2	.0E-48 AIBBS077.1	.0E-48 Y18000.1	.0E-48 AB028994.1	.0E-48 AB028994.1	4755137 NT		4758695 NT
Most Similar (Top) Hit BLAST E Value	3.0E-48	2.0E-48	2.0E-48	2.05-48	2.0E-48	2.0E-48	2.0E-48	2.0E-48	2.0E-48	2.0E-48	2.0E-48	2.0E-48	2.0E-48	1.0E-48	1.0E-48	1.0E-48	1.0E-48	-	1	1.0E-48	1.0E-48	1.0F.48		١	1	l	1			1.0E-48
Expression Signal	8.1	99'0	1.7	0.60	0.64	0.64	3.99	3.99	3.54	1.13	1.38	2.98	1.25	2.33	4.67	1.52	1.52	4.01	13.8	0.94	1.1	1.24			0.87		69.0			
ORF SEQ ID NO:	1					32434		34237				26245		26311	27137		L		L	29759		32948		32949		33274	33275			
Exan SEQ ID NO:	1_	13244	13285		1	1_	1		1	21631		1	)	1	14072		14266	1	15111	16742		19686	<u> </u>		Ĺ	19883	19883	<u> </u>	22110	
Probe SEQ ID NO:	11114	2	46	4654	5935	5935	7688	7688	7703	8550	12109	12320	12674	57	896	1101	1101	1324	1968	3577	5240	6417		817	6628	6727	6727	7407	9031	9031

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hd44e02xt Soares\_NFL\_T\_GBC\_S1 Homo saplens cDNA clone IMAGE:2912378 3' similar to TR:095636 095636 CAMP-REGULATED GUANINE NUCLEOTIDE EXCHANGE FACTOR II.;
AU140742 PLACE4 Homo saplens cDNA clone PLACE4000148 5' ba55g05.x1 NIH\_MGC\_10 Homo sepiens cDNA clone IMAGE:2800504 3' similar to gb:X17206 40S RIBOSOMAL PROTEIN S4 (HUMAN); gb:M20632 Mouse LLRep3 protein mRNA from a repetitive element. DKFZp762C033\_s1 762 (synonym: hmel2) Homo sepiens cDNA clone DKFZp762C033\_3' wf25h04.x1 Soares\_NFL\_T\_GBC\_S1 Homo sepiens cDNA clone IMAGE:23566633 3' similar to TR:O54923 ts38d12.x1 NCI\_CGAP\_Ut4 Homo septens cDNA clone IMAGE:2230871 S' similar to contains Alu repetitive #25h04.x1 Soares\_NFL\_T\_GBC\_S1 Homo sapiens cDNA clone IMAGE:2356663 3' similar to TR:054923 Homo sapiens proteasome (prosome, macropain) 26S subunit, ATPase, 4 (PSMC4) mRNA Homo sapiens proteasome (prosome, macropain) 26S subunit, ATPase, 4 (PSMC4) mRNA Homo sapiens proteasome (prosome, macropain) 26S subunit, ATPase, 4 (PSMC4) mRNA Homo sapiens proteasome (prosome, macropain) 26S subunit, ATPase, 4 (PSMC4) mRNA Homo sapiens proteasome (prosome, macropain) 26S subunit, ATPase, 4 (PSMC4) mRNA Homo sapiens proteasome (prosome, macropain) 26S subunit, ATPase, 4 (PSMC4) mRNA Homo sapiens proteasome (prosome, macropain) 26S subunit, ATPase, 4 (PSMC4) mRNA Homo sapiens proteasome (prosome, macropain) 26S subunit, ATPase, 4 (PSMC4) mRNA DKFZp761A138\_s1 761 (s/monym: hamy2) Homo saplens cDNA clone DKFZp761A138 3 15d6 Human retina cDNA randomly primed sublibrary Homo sapiens cDNA Mus musculus MysPDZ mRNA for myosin containing PDZ domain, complete cds 5578a08 s1 NCI\_CGAP\_GCB1 Homo sapiens cDNA clone IMAGE:1337462 3' Homo sapiens mRNA for KIAA1245 protein, partial ods 601888036F1 NIH\_MGC\_17 Homo sapiens oDNA clone IMAGE:4122110 5' Homo sapiens B cell linker protein (SLP65), mRNA Homo sapiens B cell linker protein (SLP65), mRNA Human mositol 1,4,5 trisphosphate receptor type 1 mRNA, partial cds rop HIt Descriptor domo saplens gene for activin receptor type IIB, complete cds Homo sapiens Chediak-Higashi syndrome 1 (CHS1) mRNA domo sapiens chromosome 21 segment HS21C084 element contains element PTR5 repetitive element; HYPOTHETICAL PROTEIN DJ845024.3 Mus musculus T-box 20 (Tbx20), mRNA Mus musculus T-box 20 (Tbx20), mRNA complete (MOUSE); 054923 RSEC15. 054923 RSEC15. **EST HUMAN** EST HUMAN EST\_HUMAN EST HUMAN EST\_HUMAN EST HUMAN EST\_HUMAN HUMAN EST\_HUMAN SWISSPROT EST\_HUMAN HUMAN Top Hit Database Source 5729990 NT 11429808 10048417 10048417 Top Hit Acession 8.0E-49 123850.1 8.0E-49 123850.1 8.0E-49 AB008681.1 6.0E-49 AW731740.1 6.0E-49 AL162091.1 6.0E-49 AW511225.1 6.0E-49 AU140742.1 1.0E-48 W26785.1 8.0E-49 AB026497.1 AL163284.2 7.0E-49 AI807191.1 7.0E-49 AL120937.1 7.0E-49 AI807191.1 8.0E-49 AAB72183. 1.0E-48 BF304683.1 8.0E-49 AI623722.1 ģ 7.0E-49 7.0E-49 1.0E-48 1.0E-48 7.0E-49 8.0E-49 .0E-49 1.0E-48 (Top) Hit BLAST E Value Most Similar 1.27 20.33 2.33 0.79 3.65 2.08 6.79 4.74 4.23 1.41 3.07 3.09 0.93 Expression Signal 32456 31815 30367 26638 26637 26638 27469 30890 31815 37804 38785 26637 26638 26637 36053 36399 37221 37222 32702 35109 ORF SEQ Ö Q 19140 19734 18771 18771 17378 Exon SEQ ID 22821 23616 21572 24169 13602 13602 19354 26014 19354 ÿ 5954 5926 405 202 12282 2064 6178 6178 11096 405 406 406 248 5576 ន្ទ 8491 12097 142 Probe SEQ ID 9414 9468 9781 10581

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Table 4
Single Exon Probes Expressed in Placenta

Top Hit Descriptor	UI-H-Bi3-alo-a-05-0-UI.s1 NCI_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:3068048 3'	EST77525 Pancreas tumor III Homo sapiens cDNA 5' end	EST77525 Pancreas fumor III Homo sapiens cDNA 5' end	zj29c08.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:451694.3'	Homo sapiens chromosome 21 segment HS21C010	Homo sapiens chromosome 21 segment HS21C010	zp29c07.r1 Stratagens neuroepithelium (#937231) Homo sapiens cDNA clone IMAGE:610860 5' similar to TR:G233226 G233226 RTVL-H PROTEIN. ;contains LTR7.t3 LTR7 LTR7 repetitive element;	Homo sapiens putative tumor suppressor ST13 (ST13) mRNA, complete cds	Homo caplens cimilar to ribosomal protein S27 (metallopenstimulin 1) (H. sapiens) (LOC63362), mRNA	x108b01.x1 NCI_CGAP_Ut4 Homo sapiens cDNA clone IMAGE:2675593 3' cimilar to WP:B0350.2B CE06703 ;	Homo sapiens mRNA for ankyrin B (440 kDa)	Homo sapiens mRNA for ankyrin B (440 kDa)	Homo sapiens UDP-N-acetyl-aipha-D-galactosamine:polypeptide N-acetylgalactoseminyltransferase 8 (GaINAc-T8) (GALNT8), mRNA	Homo saplens UDP-N-acetyl-apha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 8 (GalNac-T8) (GALNT8): mRNA	Homo sapiens KIAA0823 gene product (KIAA0823), mRNA	Homo saplens copine III (CPNE3), mRNA	Homo sapiens copine III (CPNE3), mRNA	zr90f05.r1 NCI_CGAP_GCB1 Homo saplens cDNA clone IMAGE:682977 5'	Homo saplens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds	H.sapiens mRNA for acetyl-CoA carboxylase	ze31c05,r1 Scares retina N2b4HR Homo saplens cDNA clone IMAGE:360584 5' similar to contains L1.t3 L1	repetitive element;	Human type IV callagen (CUL4Ab) gene, exan 40	EST25e12 WATM1 Homo septens cDNA clone 25e12	EST42572 Endometrial tumor Homo sapiens cDNA 5' end	MR3-HT0487-150200-113-g01 HT0487 Homo saplens cDNA	yx23d06,r1 Soares melanocyte 2NbHM Homo saplens cDNA clone IMAGE:262571 5
Top Hit Database Source	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	NT	NT	EST_HUMAN	NT	Ā	EST HUMAN	NT	N.	IN TN	F	NT	PN	NT	EST_HUMAN	LΝ	L		EST HOMAN	Ę	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN
Top Hit Acession No.	AW452218.1	4A366556.1	4A366556.1	4A707567.1	AL163210.2	5.0E-49 AL163210.2	AA172121.1	5.0E-49 U17714.1	11436355 NT	0E-49 AW189533.1	4.0E-49 Z28634.2	.0E-49 Z26634.2	11525737 NT	14525737 NT	7662209INT	11425374 NT	11425374 NT	.0E-49 AA210798.1	4.0E-49 AF240786.1	3.0E-49 X68968.1		3.0E-49 AA016131.1		3.0E-49 H39479.1		2.0E-49 BE165980,1	2.0E-49 N26448.1
Most Similar (Top) Hit BLAST E Value	6.0E-49	6.0E-49	6.0E-49	6.0E-49	5.0E-49	5.0E-49	5.0E-49	5.0E-49	5.0E-49	4.0E-49	4.0E-49	4.0E-49	4.0E-49	A 0F. 40	4.0E-49	4.0E-49	4.0E-49	4.0E-49	4.0E-49	3.0E-49	1	3.0E-49	3.0E-49	3.0E-49	3.0E-49		
Expression Signal	3.39	2.48	2.48	10.54	5.84	5.84	10.18	7.1	7.59	28.39	0.96	0.98	0.68	0.68	0.69	0.47	0.47	2.74	2.93	0.91		2.73	2.68	9.83	1.41	1.93	1.15
ORF SEQ ID NO:	38291		38651			28952		29032	29533	26754		33940								26789		.		34127	38316		29487
Exan SEQ ID NO:	24612	24946	24946	_	L	13912	14983	15922	16519	13731	1	1	1	1	I.	i	22144	l	25413	ł	ļ			20649	24636		16468
Probe SEQ ID NO:	11557	11961	11961	12670	730	730	1836	2808	3346	538	7395	7395	7422	7422	7997	9065	9065	12514	12615	574		2713	5098	7577	11582	678	3294

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Top Hit Descriptor	Homo saplens RNA binding protein II (RBMII) gene, complete cds	AV717938 DCB Homo serpiens cDNA clone DCBALB01 5	EST02558 Estal hain Strategiene (cet#936706) Homo septens cDNA clone HFBCY50	O 102000 1 state printing the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the	Homo sapiens SNCA isotorm (SNCA) gene, compilere cus, arientawery spinous	601458531F1 NIH_MGC 66 Homo sapiens cunn dane IMAGE. Joozyoo 3	Homo sapiens keratin 18 (KR i 18) mKNA	601115769F1 NIH_MGC_16 Homo sapiens cDNA cione IMAGE:3330273 3	601820053F1 NIH_MGC_58 Home sapiens culva clone IMAGE:4452452 5	yn48h04.r1 Soares adult brain N2b5HB55Y Homo septens cUNA done liw4dE:17703 5 sinning 10. SP;GBG1_HUMAN Q08447 GUANINE NUCLEOTIDE-BINDING PROTEIN G(T) GAMMA-1 SUBUNIT;	EST376713 MAGE resequences, MAGH Homo sapiens dDNA	601290330F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3620863 5	601290330F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3620863 5'	w78g12.s1 Soares_placenta_8to9weeks_ZNbHP8to9W Homo sapiens cDNA clone IMAGE:258406 3 similar to qb:X65873 KINESIN HEAVY CHAIN (HUMAN);	w/78412 s1 Scarces placenta Bboweets 2NbHP8bbW Home sapiens cDNA clone IMAGE:258406 3'	similar to gb:X65873 KINESIN HEAVY CHAIN (HUMAN);	Homo sapiens RNA binding motif protein 7 (LOC51120), mRNA	601300992F1 NIH MGC_21 Homo sapiens cDNA clone IMAGE:3635386 3	DKFZp434D2423_r1 434 (synonym: htes3) Homo sapiens cDNA cione DNr 2p434D2423 3	AV751477 NPD Home sapiens cDNA clone NPDAWE04 3	Homo sapiens brefeldin A-inhibited guanthe nucleatide-exchange protein 1 (DICH), minne	MR0-HT0407-010200-006-102 H 10407 Homo sapiens CLINA	Homo sapiens cacherin EGFLAG seven-bass G-type receptor 1 (CELSAT), IIINNA	Homo sapiens glycine N-methytransferase (GNM I) gene, compilere cus	601176250F1 NIH_MGC_17 Homo sapiens cUNA clone IMAGE:3331369 3	Homo sapiens chromosome 21 segment HS21 C002	Homo sapiens mRNA for VIP receptor 2	Homo saplens mRNA for VIP receptor 2	Homo sapiens actinin, elpha 1 (ACTN1) mRNA	Homo sapiens p47 (LOC51674), mRNA	Homo sapiens p47 (LOC51674), mRNA	Homo sapiens capping protein (actin filament) muscle Z-line, beta (CAPZE), mKNA	Hamo sapiens hepatocyte growth ractor( n'Gr.) gene, exon 16
Top Hit Database Source	Z	T HIMAN	144	HOME	$\exists$	T_HUMAN		╗	EST_HUMAN	EST_HUMAN	EST HUMAN		EST_HUMAN	EST HUMAN	Т	EST_HUMAN	LN	EST HUMAN	EST_HUMAN	EST HUMAN		EST_HUMAN	LN	LN	EST_HUMAN	NT	NT	NT	LN	TN	ΤN	LN	LN.
Top Hit Acession No.	2 0F-49 AF026564.1	Ī				0E-49 BF035327.1	4557887 NT	1.0E-49 BE255216.1	0E-49 BF131007.1	0E-49 H18291.1	0E-49 AW964640.1	0E-49 BE398110.1	.0E-49 BE398110.1	OE-40 N258841	1200ct	.0E-49 N25884.1	9994184 NT	.0E-49 BE 409340.1	.0E-49 AL043129.2	.0E-49 AV751477.1	11427366 NT	.0E-49 BE169343.1	11418322 NT	- 1	9.0E-50 BE295758.1		X95097.2	X95097.2	8.0E-50 4501890 NT	7706394 NT	7706394 NT	4826658 NT	8.0E-50 D90334.1
Most Similar (Top) Hit BLAST E Value	2 OF 49 /	7 07 30 6	2.05-48	2.0E-49	2.0E-49 /	1.0E-49	1.0E-49	1.0E-49	1.0E-49	1.0E-49	1.0E-49	1.0E-49	1.0E-49	1 OF 40		1.0E-49	1.0E-49	1.0E-49	1.0E-49	1.0E-49	1.0E-49	1.0E-49	1.0E-49	9.0E-50	9.0E-50		_				8.0E-50		
Expression Signal	880	3	¥ 1	1.87	2.69	9.1	73.58	2.93	4.68	0.85	1.09	2.78	2.78	00.0	202	2.09	0.71	1.48		1.32	2.91	1.26	1.82	0.92	0.63	4.18		1.92			1.05		2.67
ORF SEQ ID NO:	2002		33437							32728			33916			34004		35809	L	L	38325					26426		26960			L		
Exan SEQ (D NO:	16977	7	2002/	21373	26008	14097	14736		18674	19377		1		1	2000	20530		22271	1	ı	1	25119	25349	L	26215	L	L		1_	(	1	(	15160
Probe SEQ ID NO:	2650	200	6875	82	12626	922	1584	1844	5475	6202	6208	7372	7372	92.7	/453	7453	8874	9193	10331	11304	11590	12148	12508	5109	6534	174	737	737	1803	2552	2552	2764	2891

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Top Hit Descriptor	QV0-BT0703-280400-211-e08 BT0703 Homo sapiens cDNA				Г	Г		Г		Т	Г	nu45h10.s1 NCI_CGAP_Pr4 Homo sapiens cDNA clone IMAGE:1043683 similar to contains PTR5.t3 PTR5		Z162b01.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:726889 5' similar to TR:G1335769 (G1335769 GAG-POL POLYPROTEIN.;	no54e09.s1 NCI_CGAP_SS1 Homo septens cDNA done IMAGE:1104520 3' shriller to gb:X53741_ma1 FBULIN-1. ISOFORM A PRECURSOR (HUMAN);	Т	Homo capiens cysteinyl-tRNA synthetase (CARS), mRNA	QV1-BT0681-280300-127-f12 BT0681 Homo sapiens cDNA	П		CMYAS Human cardiac muscle expression library Homo saplens cDNA clone 4151935 similar to CMYAS	Т	Tight is suppose broad through the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the c	Homo eapiens protein tyrosine phosphatase, non-receptor type 12 (r. 1.14 12), minny	Homo saptens similar to sema domain, immunoglobulin domain (1g), snort basic domain, secreted, (semaphorin) 3A (H. saptens) (LOC63232), mRNA	Homo sapiens FYVE domain-containing dual specificity protein phosphatase FYVE-DSP1a mRNA, complete	SDS	Homo sapiens FYVE domain-containing dual specificity protein phosphatase FYVE-USP1a mKNA, complete cds
Top Hit Database Source	EST HUMAN	EST_HUMAN	EST HUMAN	EST HUMAN	EST HUMAN	EST_HUMAN	EST HUMAN	EST_HUMAN	EST HUMAN	EST_HUMAN	EST HUMAN		EST_HUMAN	EST HUMAN	NAMIN TRE	Σ	F	EST HUMAN	TN	EST HUMAN	MATERIA TOTAL		Z	ĮN,	 		N	TN
Top Hit Acession No.	7.0E-50 BE089591.1	7.0E-50 BF091922.1	7.0E-50 BF091922.1	7.0E-50 AA627822.1	7.0E-50 AI872137.1	6.0E-50 BE794381.1	6.0E-50 BE044076.1	8.0E-50 AA312079.1	6.0E-50 AA312079.1	5.0E-50 BF332838.1	5.0E-50 BF332838.1		5.0E-50 AA557683.1	5 0F-50 AA403053 1	4 0E-50 4 AB01143 1	AL 163248.2	4.0E-50 11440683 NT	4.0E-50 BE087536.1	3.0E-50 M18048.1	3.0E-50 AA746142.1	A Managed A	AW /55		11419317 NT	11421514 NT		3.0E-50 AF233436.2	3.0E-50 AF233436.2
Most Similar (Top) Hit BLAST E Value	7.0E-50	7.0E-50 I	7.0E-50	7.0E-50	7.0E-50	6.0E-50	6.0E-50	8.0E-50	6.0E-50	5.0E-50	5.0E-50		5.0E-50	5.05	4 OF 50	4.0E-50	4.0E-50	4.0E-50	3.0E-50	3.0E-50	ŀ	1		3.0E-50	3.0E-50		3.0E-50	
Expression Signal	1.07	67.0	67.0	0.74	23.18	0.67	3.28	3.32	3.32	1.34	1.34		5.27	178	284		0.92							0.89	1.71		5	5
ORF SEQ ID NO:	26843	<u> </u>						37765	1	l	28081			28777		29712		33924		29557			ļ	33375	33648		34376	34377
Excn SEQ ID NO:	13819		_	1	1.	17602	1	1		1		•	22370		1_	L	1_	1	1	l	l	-		19968	20219	1_	20877	20877
Probe SEQ ID NO:	634	6923	6923	7457	10993	4462	8408	11053	11053	1835	1835		9294	12000	8	3536	9	7383	1992	3371		3846	6815	6815	6904		7822	7822

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	7	7	$\neg$	7	7	-,	т	7	7	7	7	т	7	7	7	7	7	7	7	Т	7	3	٦		Т		7			
Тор Hit Descriptor	Homo sapiens ankyrin-like with transmembrane domains 1 (ANKTM1), mRNA	Homo saplens mRNA for KIAA1598 protein, partial cds	Homo sapiens t-complex 10 (a murine top homolog) (TCP10), mRNA	Human mRNA for KIAA0299 gene, partial cds	Homo saplens Grb2-associated binder 2 (KIAA0571), mRNA	Homo sapiens CTL2 gene	Homo saplens gene for AF-8, complete ods	Homo sapiens MHC class 1 reglon	Homo sapiens midline 1 (Opitz/BBB syndrome) (MID1) mRNA	Homo sapiens decorin D mRNA, complete cds, alternatively spliced	Mus musculus mRNA for high-suffur keratin protein, partial cds	Homo sapiens mRNA for KIAA0776 protein, partial cds	AU124065 NTZRM2 Hamo sepiens cDNA clone NTZRM2001609 5'	Homo sapiens TFF gene cluster for trefoil factor, complete cds	Homo sapiens TFF gene cluster for trefoil factor, complete cds	Human HALPHA44 gene for alphe-tubulin, exons 1-3	Human HALPHA44 gene for alpha-tubutin, exons 1-3	Mus musculus keratin complex 2, gene 6g (Krt2-6g), mRNA	Mus musculus keretin complex 2, gene 6g (Krt2-6g), mRNA	Macaca mulatta cyclophilin A mRNA, complete cds	Homo sapiens chromosome 21 segment HS21C009	Homo sapiens Xq pseudoautosomal region; segment 1/2	Homo sapiens RGH2 gene, retrovirus-like element	hd44e02.xf Soares_NFL_T_GBC_S1 Homo sepiens cDNA done IMAGE:2912378 3' similer to TR:095636 095636 CAMP-REGULATED GUANINE NUCLEOTIDE EXCHANGE FACTOR II. ;	ny67h03.s1 NCI_CGAP_GCB1 Hamo sapiens cDNA clane IMAGE:1283381 3'	ab23g04.x5 Strategene lung (#837210) Homo sepiens cDNA clone IMAGE:841686 3' sImilar to SW :PSM_HUMAN Q04609 PROSTATE-SPECIFIC MEMBRANE ANTIGEN;	zk51c09.r1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA done IMAGE:486352 5'	abz3g04.x5 Stratagene lung (#937210) Homo sapiens cDNA clone IMAGE:841686 3' cimilar to SW:PSM_HUMAN Q04609 PROSTATE-SPECIFIC MEMBRANE ANTIGEN ;	abz3g04.x5 Stratagene lung (#837210) Homo sapiens cDNA clone IMAGE:841686 3' similar to SW. PSM_HUMAN Q04609 PROSTATE-SPECIFIC MEMBRANE ANTIGEN ;	yw24g06.r1 Morton Fetal Cochlea Homo sapiens cDNA clone IMAGE::253210 5
Top Hit Database Source				NT	N	NT	NT	NT	NT	NT .	NT	NT	EST_HUMAN	NT	. TN	Ł	NT	NT	NT	TN	IN	IN	LN	EST HUMAN	EST HUMAN	EST HUMAN	EST HUMAN	EST HUMAN	EST HUMAN	EST_HUMAN
Top Hit Acessian No.	F001589 NT	3.0E-50 AB046818.1	18514	3.0E-50 AB002297.1	11436955 NT	3.0E-50 AJ245621.1		2.0E-50 AF055056.1	4557752 NT	2.0E-50 AF138303.1	386424.1	2.0E-50 AB018319.1	2.0E-50 AU124065.1	2.0E-50 AB038162.1	2.1		K06956.1	9910293 NT	TN 5910293 NT	20E-50 AF023861.1	1.0E-50 AL163209.2	1.0E-50 AJ271735.1	1.0E-50 D11078.1	9.0E-51 AW511225.1	9.0E-61 AA744837.1	9.0E-51 AI791154.1	9.0E-51 AA043738.1	9.0E-51 AI79/154.1	9.0E-51 A 791154.1	9.0E-51 H89078.1
Most Similar (Top) Hit BLAST E Value	3.0E-50	3.0E-50	3.0E-50	3.0E-50 /	3.0E-50	3.0E-50/	3.0E-50/	2.0E-50 /	2.0E-50	2.0E-50 /	2.0E-50 D86424.1	2.0E-50	2.0E-50/	2.0E-50 /	2.0E-50/	2.0E-50 X06956.1	2.0E-50 X06956.1	2.0E-50	2.0E-50	2.0E-50	1.0E-50	1.0E-50	1.0E-50	9.0E-51	9.0E-61					
Expression Signal	99.0	1.08	1.03	1.04	1.51	8.19	1.35	7.94	6.16	33.77	0.75	1.37	0.61	1.03	1.03	7.21	7.21	1.6	1.6	1.39	2.17	10.11	1.65	1.04	0.58	0.7	1.29	0.68		
ORF SEQ ID NO:	35404	36657	36670	37380	38080	37564	31922		27327	27713	30499	31412	33562	35126	Ì	35268		36728			26701		37038	32617		<u> </u>		<u> </u>		
Exan SEQ ID NO:	21861	23061	23070	23770	24425	23938	25792	13978	14269	14627	17519	18442	20143	21592	21592	1	1	L	23126	24945	13669		1	1	1	)	1	1	ļ	1 1
Probe SEQ ID NO:	8782	10023	10032	10737	11364	11752	13217	799	1104	1474	4376	5329	7007	8511	8511	8650	8650	10088	10088	11960	474	2438	10396	8104	6354	8872	9525	9700	0020	11764

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Top Hit Descriptor	yw24g06.r1 Morton Fetal Cochlea Homo sapiens cDNA clone IMAGE:253210 5'	am10h02.s1 Soares_NFL_T_GBC_S1 Homo sepiens cDNA clone IMAGE:1466451 3' similer to SW:CAYP_CANFA P10463 CALCYPHOSINE;	Homo sapiens glycine amidinotransferase (L-arginine:glycine amidinotransferase) (GATM) mRNA	Homo sapiens glycine amidinotransferase (L-arginine:glycine amidinotransferase) (GATM) mRNA	np98e09.s1 NCI_CGAP_Lu1 Homo sapiens cDNA clone IMAGE:1142440 3' similar to gb:X12671_ma1 HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN A1 (HUMAN);	Homo sapiens very long-chain acyl-CoA synthetase homolog 1 mRNA, complete cds	Homo seplens PDZ-73 protein (PDZ-73/NY-CO-38), mRNA	AU138590 PLACE1 Homa sepiens cDNA clane PLACE1008887 5'	QV4-NT0028-200400-180-d05 NT0028 Homo sapiens cDNA	xn34a03.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2695564 3' similar to TR:Q9Z340 Q9Z340 ATYPICAL PKC SPECIFIC BINDING PROTEIN.;	DKFZp434B2229_r1 434 (synonym: htes3) Homo saplens cDNA clone DKFZp434B2229 5'	DKFZp434B2229_r1 434 (synonym: htes3) Homo saplens cDNA clone DKFZp434B2229 5	Homo seplens immunoglobulin superfamily, member 3 (IGSF3), mRNA	UI-H-BW0-aip-b-05-0-UI.s1 NCI_CGAP_Sub6 Homo sapiens cDNA clone IMAGE:2729817 3'	Homo sapiens HSPC331 mRNA, partial cds	Homo sapiens putetive DNA binding protein (M96), mRNA	Homo sapiens KIAA0929 protein Msx2 interacting nuclear target (MINT) homolog (KIAA0929), mRNA	Homo sepiens KIAA0929 protein Msx2 interacting nuclear target (MiNT) homolog (KIAA0929), mRNA	Homo saplens solute carrier family 2 (facilitated glucose transporter), member 9 (SLC2A9), mRNA	Homo saplens solute carrier family 2 (facilitated glucose transporter), member 9 (SLC2A9), mRNA	Human haptoglobin related (Hpr) gene exon 3	Homo sapiens mitogen-activated protein kinase kinase 1 (MKK4) gene, exon 4	Homo sapiens mitogen-activated protein kinase kinase 1 (MKK4) gene, exon 4	Homo sapiens ribosomal protain S6 kinase, 70kD, polypeptide 1 (RPS6KB1) mRNA	Homo sapiens non-kinase Cdc42 effector protein SPEC2 (LOC56990), mRNA	Homo sapiens cerebral cell adhesion molecule (LOC51148), mRNA	Homo sapiens hypothetical protein FLJ11042 (FLJ11042), mRNA	Homo sapiens hypothetical protein FLJ11042 (FLJ11042), mRNA	Homo sapiens B9 protein (B9), mRNA
Top Hit Datebase Source	EST HUMAN IN	al 14.1 EST_HUMAN S		Т	EST_HUMAN H	TN		EST_HUMAN A	EST_HUMAN C	EST HUMAN C	_	EST_HUMAN D		EST_HUMAN L							TN.	IN.	TN T						
Top Hit Acession No.	.0E-51 H89078.1	9.0E-51 AA885514.1	4503932	4503932 NT	.0E-51 AA610842.1	8.0E-51 AF064254.1	11439587 NT	8.0E-51 AU138590.1			7.0E-51 AL079623.1	7.0E-51 AL079628.1	11421595 NT	7.0E-51 AW295603.1	7.0E-51 AF161449.1	F678763 NT	7657266 NT	7657266 NT	5910553 NT	9910553 NT		6,0E-51 AF070083.1		4506736 NT	11416751 NT	11429665 NT	11428525 NT	11428525 NT	7661535 NT
Most Similar (Top) Hit BLAST E Value	9.0E-51	9.0E-51	8.0E-51	8.0E-51	8.0E-51	8.0E-51	8.0E-51	8.0E-51	7.0E-51	7.0E-51	7.0E-51 /	7.0E-51	7.0E-51	7.0E-51	7.0E-51	6.0E-51	6.0E51	6.0E-51	6.0E-51	6.0E-51	6.0E-51	6.0E-51	6.0E-51	6.0E-51	6.0E-51	6.0E-61	6.0E-51	6.0E-51	6.0E-51
Expression	1.97	1.84	1.11	1.11	5.38	0.71	211	1.05	1.27	0.82	1.37	1.37	1.18	1.44	1.36	0.94	5.93	14.65	99'0	0.66	1.48	8.16	8.16	0.93	0.82	2.15	0.69	0.69	2.05
ORF SEQ ID NO:	37580	<u> </u>		30678			34387		29541								28287	29743			L	32642		_		31486	35965		36509
Exan SEQ ID NO:	23950	ì	ł	l	17825	ł	ı	l	ł		L	17427	17518	17611	24970	ı	15177	16727	17566	L	L	19303		20215	<u> </u>	18531	22413		
Probe SEQ ID NO:	11764	12069	4529	4559	4690	7321	7830	9964	3354	3447	4282	4282	4375	4471	11985	1657	2036	3562	4426	4426	6113	6124	6124	0069	7032	7104	9337	9337	9885

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Top Hit Descriptor	Human ankyrin (ANK1) gene, exon 2	Homo sapiens interleukin 17 receptor (IL17R), mRNA	Homo sapiens chromosome 21 segment HS21C003	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA	Novel human gene mapping to chomosome X	Homo sapiens 26S proteasome associated pad1 homolog (POH1) mRNA	Homo sapiens mRNA for nucleoporin 155	Human Ku (p70/p80) subunit mRNA, complete cds	Human Ku (p70/p80) subunit mRNA, complete cds	Homo septens mRNA for KIAA1411 protein, partial cds	Homo saplens RNA bInding motif protein 3 (RBM3), mRNA	tr81c09.xt NCI_CGAP_Pen1 Homo sapiens cDNA clone IMAGE:2224720 3' similar to gb:M26326 KERATIN, TYPE I CYTOSKELETAL 18 (HUMAN);	It81c08.x1 NCI_C6AP_Part Homo sapiens cDNA clone IMAGE:2224720 3' sImiliar to gb:M26326 izebatin type i cytoskej ETAI 48 (HUMAN):	CENTIN, III ELICITORIUM (MESTACONIII 1977)	zq87g01.s1 Stratagene hN I neuron (#937233) Homo sapiens cunA cione imAGE. 049000 3	Novel human gene mapping to chomosome 22	ya47c08.r1 Soares Infant brain 1NIB Homo sapiens cDNA clone IMAGE:63233 5' similar to gb:M14123_cds4 RETROVIRUS-RELATED POL POLYPROTEIN (HUMAN);contains LTR3 repetitive element ;	Human hnRNP C2 protein mRNA	ia04d06.у1 Human Pancreatic Islets Homo caplens cDNA 6'	Homo sapiens X-linked anhidrolic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions	Homo sapiens ubiquitin protein ligase E3A (human papilloma virus E6-associated protein, Angelman	syndrome) (UBE3A) mRNA	601285694F1 NIH_MGC_44 Homo saplens cDNA clone IMAGE:3607463 5	601285694F1 NIH MGC 44 Homo sapiens cDNA clone IMAGE:3607463 5	z/30a05.r1 Stratagene NT2 neuronal precursor 937230 Homo septiens cDNA clone IMAGE:664880 5 similar to TR:6233226 G233226 RTVL-H PROTEIN. ;contains LTR7.t3 LTR7 repetitive element;	ti27g03.x1 NCI_CGAP_Kid11 Homo saplens cDNA clone IMAGE:2131732 3'	UI-H-BI1-adj-d-02-0-UI.s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2716831 3	te76c08.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2092622 3' similar to TR:Pe31u7 P93107 PF20.;
Top Hit Database Source	NT				NT			IN				EST_HUMAN		Т	EST_HUMAN	NT	EST_HUMAN	Ę	EST HUMAN	\ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \			EST HUMAN		EST HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN
Top Hit Acessian No.	U50093.1	11526289 NT	5.0E-51 AL163203.2	4507500 NT	5.0E-51 AL133204.1	5031980 NT	5.0E-51 AJ007558.1	5.0E-51 M30938.1	5.0E-51 M30938.1	5.0E-51 AB037832.1	5803136 NT	3.0E-51 AI587348.1		١		3.0E-51 AL159142.1	3.0E-51 R15914.1		3.0E-51 AW583777.1	3 OF-51 AF003528 1		4507798 NT	2.0E-51 BE391063.1	2.0E-51 BE391063.1	2.0E-51 AA233352.1	2.0E-51 Al492415.1	2.0E-51 AW 137826.1	2.0E-51 Al381520.1
Most Similar (Top) Hit BLAST E Value	6.0E-51	6.0E-51	5.0E-51	5.0E-51	5.0E-51	5.0E-51	5.0E-51	5.0E-51	5.0E-51	5.0E-51	5.0E-51	3.0E-51		3.05-51	3.0E-51	3.0E-51	3.0E-51	3.0E-51	3.0E-51	3.05-51		2.0E-51	2.0E-51	2.0E-51			2.0E-51	2.0E-51
Expression Signal	0.79	1.84	6.22	1.7.1	2.39	1.14	10.38	1.31	1.31	1.04	3.8	14.26		48.14	1.38	1.85	23	3.85	0.61	A.		1.98	0.89	0.89	16.76	3.05	1.21	0.66
ORF SEQ ID NO:	36598	38265	27047	27061	27247	27875	28894	30221	30222		38292	Ì				30567		l				26619	L	١_		29990	L	
Exon SEQ ID NO:	23003	24590	13993	14004	16028	14790	1	1	17211	18305	24613	13363		14365	15119	17586	20813	22/19	26227	1	ı	13585	1	Į.	1		١	i i
Probe SEQ ID NO:	9964	11534	814	826	1016	1638	2658	4055	4055	5183	11558	137		1203	1976	4446	7753	9040	8900	1,206.7	100	377	708	200	1723	3827	4616	5326

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Top Hit Descriptor	601470446F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3873563 5'	Homo sapiens diacylglycerol kinase iota (DGKI) gene, exon 23	Homo sapiens celi recognition molecule Caspr2 (KIAA0863), mRNA	601676787F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3959613 5'	601676787F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3959613 51	Homo sapiens disrupted in schizophrenia 1 (DISC1), mRNA	is74e07.x1 NCJ_CGAP_GC8 Homo sapiens cDNA clone IMAGE:2236980 3' similar to SW:TRKC_HUMAN  Q16288 NT-3 GROW TH FACTOR RECEPTOR PRECURSOR;	MR3-HT0487-150200-113-g01 HT0487 Homo saplens cDNA	Homo saplens mRNA for KIAA0457 protein, partial cds	AV682474 GKB Homo sapiens cDNA clone GKBAGF05 5	EST91296 Synovial sercoma Homo capiens cDNA 5' end	obs4f09.x5 NCI_CGAP_Kid5 Homo sapiens cDNA clone IMAGE:1325609 3' similar to SW.1NME1_MOUSE   P35436 GLUTAMATE [NMDA] RECEPTOR SUBUNIT EPSILON 1 PRECURSOR;	ob34f09.x5 NCI_CGAP_Kld5 Homo sepiens cDNA cbne IMAGE:1325609 3' similar to SW:NME1_MOUSE   P35436 GLUTAMATE [NMDA] RECEPTOR SUBUNIT EPSILON 1 PRECURSOR;	Homo sapiens myeloid/fymphoid or mixed-lineage leukernia (trithorax (Drosophila) homolog); translocated to, 4 (MLLT4), mRNA	Homo sapiens eukaryotic translation initiation factor 4A, isoform 1 (EIF4A1) mRNA	AV742248 CB Hamo sapiens cDNA clane CBFBCC12 5'	Homo sapiens serine palmitoyl transferase, subunit II gene, complete cds; and unknown genes	b12056t Testis 1 Homo sapiens cDNA clone b12056	te39g02.x1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:2089106 3'	7096b02.x1 NCI_CGAP_Ov18 Homo sapiens cDNA clone IMAGE:3644091 3' similar to TR:P87892 P87892 PROTEASE ;	AV760590 MDS Homo sapiens cDNA done MDSCBB02 5'	285e07.s1 Soeres_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:448500 3' similar to contains THR.t3 THR.t3 THR repetitive element;	INVZ1902.61 NCI_CGAP_GCB0 Homo sapiens cDNA done IMAGE:1241138 3' similar to contains THR.t3 THR recettive element:	H.sapiens mRNA for laminin-5, alpha3b chain	Homo sapiens hypothetical protein FLJ13556 similar to N-myc downstream regulated 3 (FLJ13556), mRNA
Top Hit Database Source	EST_HUMAN	LN	٦	EST_HUMAN	EST_HUMAN	Ę	EST HUMAN	EST_HUMAN	ĮZ	EST HUMAN	EST HUMAN	EST_HUMAN	EST_HUMAN	FN	LN LN	EST_HUMAN	IN	EST_HUMAN	EST HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST HIMAN	NT	NT
Top Hit Acession No.	2.0E-51 BE782015.1	2.0E-51 AF219927.1	7662349 NT	2.0E-51 BE901994.1	2.0E-51 BE901994.1	11037064 NT	2.0E-51 Al917078.1	2.0E-51 BE165980.1	2.0E-51 AB007926.1	2.0E-51 AV682474.1	2.0E-51 AA378559.1	2.0E-61 Al732861.1	2.0E-51 Al732851.1	11419159 NT	4503528 NT	1.0E-51 AV742248.1	1.0E-51 AF111168.2	1.0E-51 T18862.1	1.0E-51 AI572532.1	1.0E-51 BF434359.1	1.0E-51 AV760590.1	9.0E-52 AA777621.1	8 0F-52 AA720574 1	8.0E-52 X84900.1	11968028 NT
Most Similar (Top) Hit BLAST E Velue	2.0E-51	2.0E-51	2.0E-51	2.0E-51	2.0E-51	2.0E-51	2.0E-51	2.0E-51	2.0E-51	2.0E-51	2.0E-51	2.0E-61	2.0E-51	2.0E-51	1.0E-51	1.0E-51	1.0E-51	1.0E-51	1.0E-51	1.0E-51	1.0E-51	9.0E-52	8.015.52	8.0E-52	
Expression Signal	3.54	67.0	1,29	1.61	1.61	1.03	1.76	4.86	69'0	1.58	1.07	5.82	5.82	1.62	10.94	37.16	0.82	3.7	1.03	0.51	1.97	9.43	11.42	2.39	2.85
ORF SEQ ID NO:	32658		34161	35512	35513	35854	36347	36420	36438	37283	37329	31789	31790	31992	_		31036	31720	34384	34684			26412	1	27922
Exon SEQ ID NO:	19317	20537	20685	21975	21975	22312	7777	22843	ı	ı	23723	18752	18752	25571	13348	14676	18048	18704	20882	21169	26232	25409	13381	L	14838
Probe SEQ ID NO:	6139	7462	7615	8896	8896	9235	9712	9803	9818	10648	10690	11610	11610	12860	117	1523	4918	5505	7827	8087	12076	12610	158	1526	1686

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	Top Hit Descriptor	Homo saplens hypothetical protein FLJ13556 similar to N-myc downstream regulated 3 (FLJ13556), mRNA	Homo capieno hypothetical protein FLJ13556 similar to N-myc downstream regulated 3 (FLJ13556), mRNA	Homo saplens hypothetical protein FLJ13556 similar to N-myc downstream regulated 3 (FLJ13556), mRNA	Homo saplens transforming growin factor, beta-induced, 68kD (TGFBI), mRNA	Homo septens utansionning grown record, both John Replace CONA clone IMAGE:326578 5 similar to	contains Alu repotitive elements are a contained to the contains Alu repotitive elements.	QV3-BT0537-27/1299-049-00/ BT0537 Harito septembly Colors and S171 dene.	Homo saplens S164 gene, partrai cds, FS1 arta rypoureucal process, compress of partrai cds	qg44f04.x1 Soares_testis_NHT Homo saplens cDNA clone IMAGE:1836047.3	tz46h04.y1 NCI_CGAP_Bm52 Homo septens cDNA clone IMAGE:229161/1 5 stimust to swypersement of the september of the specific HEPARAN SULFATE.	PROTEOGLYCAN CORE PROTEIN TRECORSON,	H. sapiens flow-sorted critications and a filling in against, coopered in the filling of the filling in the filling of the filling in the filling of the filling of the filling of the filling of the filling of the filling of the filling of the filling of the filling of the filling of the filling of the filling of the filling of the filling of the filling of the filling of the filling of the filling of the filling of the filling of the filling of the filling of the filling of the filling of the filling of the filling of the filling of the filling of the filling of the filling of the filling of the filling of the filling of the filling of the filling of the filling of the filling of the filling of the filling of the filling of the filling of the filling of the filling of the filling of the filling of the filling of the filling of the filling of the filling of the filling of the filling of the filling of the filling of the filling of the filling of the 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	Most Similar (Top) Hit BLAST E Value	8.0E-52	8.0E-52	8.0E-52	8.0E-52	8.0E-52	7.0E-52	6.0E-52	6.0E-52	6.0E-52		9	9			4	4.0E-52	4	4			4	4	4	4	_		ł	- [
	Expression Signal	2.85	6.75			0.76	1.86	0.63	7.1			2.36											3.44	12.79	1.3				1.18
	ORF SEQ ID NO:	27923	27922			34233	35836		27970			38214							31574			35347		č	-			8 26791	
	SEQ ID NO:	14838	14838	14838	20751	20751	22293	1	Į	1	1	24543	L	22647	ı	14977	17193		18603	l					25741	17353	l _l		15211
	Probe SEQ ID NO:	1688	4101	4101	7686	7686	9215	1214	47.90	5845	3	11484	4562	9592	1695	1829	4037	4862	5401	5401	8228	8731	12429	12987	13141	4204	576	576	2071

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Top Hit Descriptor	bb88b07.yr NIH_MGC_9 Homo sepiens cDNA clone IMAGE:3030421 5' similar to gb:X18493 M.musculus mRNA for Zpf-1 zino finger protein (MOUSE);	802084710F1 NIH_MGC_83 Homo sapiens oDNA clone IMAGE:4248891 5'	Novel human gene mapping to chromosome 20, similar to membrane transporters	qa56e05.s1 Soares_NhHMPu_S1 Homo saplens cDNA done IMAGE:1690784 3'	qa56e05.s1 Scares_NhHMPu_S1 Homo sapiens cDNA done IMAGE:1690784 3'	L3-CT0214-231299-053-E12 CT0214 Homo sapiens cDNA	Homo sapiens interleukin 21 receptor (IL21R), mRNA	Homo sapiens mRNA for KIAA1081 protein, partial cds	os45d12,y5 NCI_CGAP_Br2 Homo sapiens cDNA clone IMAGE:1608311 5'	Homo sapiens transducin (beta)-like 1 (TBL1) mRNA	Homo sapiens transducin (beta)-like 1 (TBL1) mRNA	Macaca mulatta beta-tubulin mRNA, complete ods	2/45g05.s1 Soares_fetal_liver_spleen_INFLS_S1 Homo sapiens cDNA clone IMAGE:453272.3'	Homo sapiens NADH dehydrogenase (ubiquinone) Fe-S protein 5 (15kD) (NADH-coenzyme Q reductase)	(NDUFS5) mRMA	Homo saplens SET domain and mariner transposase fusion gene (SETMAR) mRNA	Homo sapiens SET domain and mariner transposase fusion gene (SETMAR) mRNA	wid9c04x1 NC_CGAP_Lu19 Homo sapiens cDNA clone IMAGE:2406150 3' similar to contains THR.b2	I HR repetitive element ;	wj49c04.x1 NCI_CGAP_Lu19 Homo sapiens cDNA clone IMAGE:2406150 3' similar to contains THR.b2 THR reneitive element:	AV715377 DCB Homo sapiens cDNA clone DCBAIEC3 6	zd49g12.r1 Soares_fetal_heart_NbHH19W Homo sapiens oDNA clone IMAGE:344038 5'	Homo sapiens LIM domain kinase 2 (LIMK2), mRNA	xn72e07 x1 NCI_CGAP_CML1 Homo saplens cDNA clone IMAGE:2700036 3' similar to contains Alu	repetitive element contains element LTR2 repetitive element ;	wf67d05.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2360649 3' similar to TR:Q16859	Q16859 CARBOXYLESTERASE;	zu75h12.s1 Soares_testis_NHT Homo saplens cDNA done IMAGE:743879 3'	Homo sapiens glutamate-ammonia ligase (glutamine synthase) (GLUL) mRNA	Homo saplens arylsulfatase D (ARSD), transcript variant 1, mRNA	pol=reverse transcriptase homolog {retroviral element} [human, endogenous retroviral element RTVL-Hp1, Genomic, 660 nt]
Top Hit Database Source	EST_HUMAN	EST_HUMAN	ΙN	EST_HUMAN	Г	EST_HUMAN	۲N	٦	EST_HUMAN	٦	F	Į	EST_HUMAN		۲	NT	۲		EST_HUMAN	ECT HIMAN	T				EST_HUMAN		EST_HUMAN	<b>EST_HUMAN</b>	LN LN	ĽZ	FN
Top Hit Acession No.	2.0E-52 BE207575.1	2.0E-52 BF677892.1	2.0E-52 AL137188.3	2.0E-52 Al141802.1	2.0E-52 Al141802.1	2.0E-52 AW848041.1	11141868 NT	2.0E-52 AB029004.1	AI792146.1	2.0E-52 5032158	5032158 NT	2.0E-52 AF147880.1	2.0E-52 AA778795.1		4758789 NT	5730038 NT	5730038 NT		2.0E-52 AI831462.1	2 OF 82 6 1831 482 1	2.0E-52 AV715377.1	2.0E-52 W70260.1	11417990 NT		2.0E-52 AW 236297.1		2.0E-52 Al808985.1	1.0E-52 AA634445.1	4504028 NT	4502238 NT	1.0E-52 S61070.1
Most Similar (Top) Hit BLAST E Value	2.0E-52	2.0E-52	2.0E-52	2.0E-52	2.0E-52	2.0E-52	2.0E-52	2.0E-52	2.0E-52	2.0E-52	2.0E-52	2.0E-52	2.0E-52		2.0E-52	2.0E-52	2.0E-52		2.0E-52	200	2.0E-52	2.0E-52	2.0E-52		2.0E-52		2.0E-52	1.0E-52	1.0E-52	1.0E-62	1.0E-52
Expression Signal	5.1	11.46	3.41	1.4	1.4	3.24	1.98	0.96	0.76	69'0	0.69	8.71	96.0		-	4.6	4.6		3.14	24.6	2.52	1.46	3.25		6.6		5.72	1.89	18.76	1.86	2.6
ORF SEQ ID NO:	28818		31190						ļ		34559		35759			36965			38209	05000					31541				27630		29315
Exan SEQ ID NO:	15693	15911	18220	18251	1	1	19663	L	L	ŀ	ļ	L	22215	L	22642	23356	L		24540	OFFIC	1	ļ.,	<u>L</u> .	1	26194		25437	13739	I _	L.	1 1
Probe SEQ ID NO:	2568	2796	5092	5126	5126	5821	6497	6853	7081	9662	7996	8854	9136		0896	10321	10321		11481	41/04	11401	11634	11918		12234		12658	546	1402	2800	3126

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Top Hit Descriptor	Human P-giycoprotein (MDR1) gene, exon 4	Human PMS2 related (hPMSR2) gene, complete cds	Human aidolase C gene for fructose-1,6-bisphosphate aldolese	Homo sapiens basic transcription factor 2 p44 (btf2p44) gene, partial cds, neuronal apoplosis inhibitory	protein (naip) and survival motor neuron protein (smn) genes, complete cos	Homo saplens chromosome 21 segment HS21C027	Rattus norvegicus putative four tepeat ion channel mRNA, complete cds	of08g05.y1 Morton Fetal Cochlea Homo sapiens cDNA clone IMAGE:2483145 o	Homo sapiens chromosome 21 segment HS21C002	Homo sapiens protein tyrosine phosphatase PTPCAAX1 (nPTPCAAX1) mKNA, complete cos	Homo sapiens proteasome (prosome, macropain) subunit, beta type, 2 (PSMB2), mKNA	Homo sapiens 5'-3' exaribonuclease 2 (XRN2), mRNA	Homo sapiens 5'-3' excriboruclease 2 (XRN2), mRNA	Homo sapiens protein kinase, cAMP-dependent, regulatory, type II, beta (PRKARZB) mRNA	Homo sapiens core binding factor alpha1 subunit (CBFA1) gene, exon 3	601904771F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4132793 5	### THR.trl NOI_CGAP_Brn23 Homo sapiens cDNA clone IMAGE:2099077 3' similar to contains THR.trl	1 Control of the Control of the Control of the Control of Control of Control of Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control 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TO	601810969F1 NIH_MGC_48 Home sapiens cDNA cione IMAGE:405597 / 5	Homo saplens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORC1L4 genes,	complete cds)	Wzzzcoz xr Soares_Dieckgraefe_colon_NHCD Homo sapiens cDNA clone IMAGE: 2508799 3	IL2-UM0081-240300-055-D03 UM0081 Homo saplens cDNA	Homo sapiens 26S protessome subunit 9 mRNA, complete cds	Homo saplens MIL1 protein (MIL1), mRNA	QV1-HT0412-280300-123-c04 HT0412 Homo sapiens cDNA
Top Hit Database Source	L	ΙN	LN LN		Z	NT	NT	EST_HUMAN	NT	NT	NT	TN	TN	LN	TN	EST_HUMAN	MAARI IN TOO	NAMOR I SE	Z	TOT	NAMOR 122	- L	14 4 4 4 1 E C	TOT TOTAL	ES HOMAN	EST HUMAN	EST_HUMAN		NT	EST_HUMAN	EST_HUMAN	F	LN	EST_HUMAN
Top Hit Acession No.	A29426.1	J38964.1	(07292.1		J80017.1	1.0E-52 AL163227.2	1.0E-52 AF078779.1	1.0E-52 AW020370.1	1.0E-52 AL163202.2	J48296.1	11426321 NT	11421401 NT	11421401 N	4506064 NT	9.0E-53 AF001446.1	7.0E-53 BF238465.1	7 00000	7.0E-53 A1421/82.1	5.0E-53 4758543 NT	AL 103202.2	5.0E-53 AW 813003.1	AL 100200.2	4.0E-53 AL.103283.4	4.0E-63 A(613037.1	4.0E-53 F13080.1	4.0E-53 BF128701.1	4.0E-53 BF128701.1		3.0E-53 AB026898.1	3.0E-63 AW050836.1	3.0E-53 AW 803563.1	3.0E-53 AF001212.1	11526297 NT	3.0E-53 BE160025.1
Most Similar (Top) Hit BLAST E Value	1.0E-62 M29426.1	1.0E-52 U38964.1	1.0E-52 X07292.1		1.0E-52 U80017.1	1.0E-52	1.0E-52	1.0E-52	1.0E-52	1.0E-52 U48296.1	1.0E-52	1.0E-52	1.0E-62	9.0E-53	9.0E-53	7.0E-53	1	/.OE-03/	5.0E-53	3.00.0	3.0E-33	4.05-30	4.05-53	4.0E-53	4.0E-53	4.0E-53	4.0E-53		3.0E-53	3.0E-63	3,0E-53	3.0E-53	3.0E-63	
Expression	4.43	233	2.07		0.59	1.18	0.77	0.68	1.06	2.12	1.72	1.31	1.31	0.69	3.3	8.65		90./	4.46	0.92	1.93	2.07	2.07	0.67	0.94	2.99	2.99		2.34	1.18	0.75	26.0		
ORF SEQ ID NO:	31628				34576		36029			37720		38819			L				30351				26302		- 1		38222		28965		L			L
Exon SEQ ID NO:	18648	1	L	1	21064	21740	22465	23837	23847	24083	24150	L	1	1	17650	25332	ł	-	Į	- 1	- 1	$\perp$	- 1	- 1		24548	1	L	15844	L	L	L	1	}
Probe SEQ ID NO:	5448	6523	7588		8014	8660	9390	10804	10814	11004	11075	12135	12135	3891	4511	12480		12958	4214	5233	12528	2	8	9616	8966	11489	11489		2726	3825	4713	5541	5743	6323

Page 320 of 550 Table 4 Single Exon Probes Expressed in Placenta

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Top Hit Descriptor	H.sapiens graf gene	H.sapiens graf gene	GIF-growth inhibitory factor [human, brain, Genomic, 2015 nt]	Homo sapiens bane morphogenetic protein 5 (BMP5), mRNA	Homo sapiens FGFR1 oncogene partner (FOP), mRNA	Homo sapienc acetyl-Coenzyme A carboxylase alpha (ACACA), mRNA	EST77525 Pancreas tumor III Homo sapiens cDNA 5' end	Homo saplens hyaluronic acid receptor (HAR), mRNA	Homo saplens Bruton's tyrosine kinase (BTK), apha-D-galactosidase A (GLA), L44-like ribosomal protein	(L44L) and F1F3 (F1F3) games, complete cas	Homo sapiens ATPase, H+ transporting, lysosomal (vacuolar proton pump) 31kD; Vacuolar proton-ATPase, subunit E; V-ATPase, subunit E (ATP6E), mRNA	Homo saplens leucine aminopoptidase (LOC51056), mRNA	Homo saplens dihydropyridine receptor alpha 2 subunit (CACNA2D1) gene, exon 8	Human Krueppel-related DNA-binding protein (TF34) gene, partial cds	PM1-CT0396-170800-001-903 CT0396 Homo sapiens cDNA	PM1-CT0396-170800-001-g03 CT0396 Homo sapiens cDNA	EST387707 MAGE resequences, MAGN Homo sapiens cDNA	5429 seq.F Human fetal heart, Lambda ZAP Express Homo capiens cDNA 5'	2822665,5prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2822665 5	7550b02.x1 NCI_CGAP_Lu24 Homo sapiens cDNA done INAGE:3231627 3' stmilar to TR:Q04009 Q04009	Homo saplens Xa aseudoautosomal region: segment 2/2	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes,	complete cds)	601176725F1 NIH_MGC_17 Homo saplens cDNA done IMAGE:3531919 5'	CM4-NN 1029-150800-543-e02 NN 1029 Hamo saplens cDNA	RC5-BN1058-270400-031-D01 BN1058 Homo sapiens cDNA	19571.seq.F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA 5	H.sapiens mRNA for hnRNPcore protein A1	2822943.3prime NIH_MGC_7 Homo sapiens cDNA clane IMAGE:2822943 3'	Homo sapiens glutamate receptor, lonotropic, kainate 1 (GRIK1) mRNA	Homo sapiens IQ motif conteining GTPase activating protein 1 (IQGAP1) mRNA	601272863F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3614031 5'
Top Hit Database Source	LZ	NT	TN	Ę	N-	NT	EST HUMAN	NT	<u>+</u>	Z	¥	Z.	E	LN L	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN		LA TOWN		NT	EST_HUMAN	EST_HUMAN	EST HUMAN	EST HUMAN	FZ	EST HUMAN	L		EST HUMAN
Top Hit Acesslon No.	3.0E-53 Y10388.3	3.0E-53 Y10388.3		10835090 NT	5901953 NT	11426423 NT	2.0E-53 AA36656.1	7705394 NT	1 70007	J/802/.1	4502316 NT	7705687 NT	2.0E-53 AF083822.1	2.0E-53 M61873.1	2.0E-53 BF334740.1	2.0E-53 BF334740.1	2.0E-53 AW975598.1	2.0E-53 AA095652.1	2.0E-53 AW 245676.1	2 00 00 00 00 00 0				1.0E-53 BE296386.1	1.0E-53 BF364201.1	1.0E-53 BE012071.1	1.0E-53 AA249072.1		1.0E-53 AW 245422.1	4504116 NT	96786	8.0E-54 BE386785.1
Most Similar (Top) Hit BLAST E Value	3.0E-53	3.0E-53	3.0E-53 S72043.1	3.0E-53	3.0E-53	3.0E-53	2.0E-53 /	2.0E-53	200	Z.UE-53 U/80Z/.1	2.0E-53	2.0E-53	2.0E-53	2.0E-53	2.0€-53	2.0E-53	2.0E-53	2.0E-53 /	2.0€-53 /	2000	1.0E-53		1.0E-53	1.0E-53	1.0E-53	1.0E-53	1.0E-53	1.0E-53 X79536.1	1.0E-53	9.0E-54	9.0E-54	8.0E-54
Expression Signal	0.76	0.76	10.97	0.85	9.77	1.18	11.25	3.29	90	0.20	12.68	62.0	1.29	2.59	2.46	2.46	1.01	0.48	3.47	0	222		2.99	1.06	1.5	0.87	9.0	4.73	1.47	0.61	5.86	1.23
ORF SEQ ID NO:	33776		35116					28325		70007		29483	29508		31756		34658			27847				31178	33392	33942		35915	38345			26465
Exen SEQ ID NO:	20330	20330		i i	22334		13665	15209		13333	15725		16490	L	18739			21278	22663	30000	Ĺ			18208	19984	20475	21202		25176			13435
Probe SEQ ID NO:	7247	7247	8499	9060	9257	12361	470	2068	7070	\$	2601	3280	3317	4170	5542	5542	8055	8196	9608	10987	1477		3496	5078	6831	7397	8120	9280	12228	3324	5417	212

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Top Hit Descriptor	Homo sapiens insulin-like growth factor 2 receptor (IGF2R) mRNA	Homo sapiens ATP-binding cassette, sub-family A (ABC1), member 8 (ABCAB), mKNA	af9c12.s.1 Scares_testis_NHT Homo saplens cDNA clone 1377046.3 similar to contains MEK30.t3 MEK30 repetitive element;	Homo sapiens mRNA for monocyte chemotactic protein-2	yw68d12.s1 Soares_placenta_8to9weeks_ZNbHP8to9W Homo sepiens cDNA clone inAcE.257.359 s similar to contains LTR7.b3 LTR7 repetitive element;	Homo sapiens similar to nuclear factor related to kappa B binding protein (H. sapiens) (LOC63182), mRNA	Homo sapiens golgin-like protein (GLP), mRNA	Homo sapiens golgin-like protein (GLP), mKNA	qb67g03.x1 Soares_fetal_heart_NbHH19W Homo caplens cDNA clons IMAGE:1705204 3 similar to contains OFR.t1 OFR repetitive element;	Homo sapiens DNA for MICB, exon 4, 5 and partial cds	Homo sapiens hypothetical protein DKFZp434M035 (DKFZp434M035), mRNA	Homo sepiens hypothetical protein DKFZp434M035 (UKFZp434M035), mKnA	Homo sapiens hypothetical protein DKFZp434M035 (DKFZp434M035), mKNA	Homo sapiens chloride charmel 6 (CLCN6) mRNA	AV754746 TP Homo sepiens cDNA clone I PGAACTU 5	Homo sapiens phosphatidylinositol 4-kinase, catalytic, alpha polypeptide (PIN4CA) micha	H. capiens sho pseudogene, p66 Isotom	H sepiens sha pseudogene, p66 Isotorm	RC3-ST0197-151099-011-708 ST0197 Homo sapiens c.DNA	ZING FINGER PROTEIN 84 (ZING FINGER PROTEIN FIFTZ)	Tupata betangen beta actin mRNA, parital cds	EST177696 Jurkat T-cells VI Homo sapiens cDNA 5 end similar to glyceration yae-5-pi lospitate	dehydrogenase	Human mRNA for KIAA0077 gene, partial cds	Human mRNA for KIAA0077 gene, partial cds	wd26d11.x1 Soares_NFL_T_GBC_S1 Homo saptens cDNA clone IMAGE:2329269 3' similar to 1R:002711	002711 PRO-POL-DUTPASE POLYPROTEIN;	EST185371 Colon cardinoma (HCC) cell line from sapiens cunk o ellu	hd87g08.x1 NCI_CGAP_GC8 Homo saplens cUNA clone IMAGE::2910342 3	UKFZp434E0/31_r1 434 (synonym. ntess) numo squique curva cione cur processione
Top Hit Database Source			EST HUMAN		EST_HUMAN		LN		EST HUMAN	N <sub>1</sub>	L	NT	NT	NT	EST_HUMAN	INT	۲	NT	EST_HUMAN	SWISSPROT	N		EST HUMAN	NT	IN		EST_HUMAN	EST HUMAN	EST HUMAN	EST_HUMAN
Top Hit Acession No.	4504610 NT	E005700	7.0E-54 AA812537.1	Y16645.1	7.0E-54 N27177.1	11417222 NT	8923698 NT	8923698 NT	7.0E-54.A(160189.1	6.0E-54 AB003618.1	8922148 NT	8922148 NT	8922148 NT	4502872 NT	6.0E-54 AV754748.1	4505806 NT	5.0E-54 Y09846.1	6.0E-54 Y09846.1	6.0E-54 AW813557.1	5.0E-54 P51523	4.0E-54 AF110103.1		4.0E-54 AA306764.1	4.0E-54 D38521.1	4.0E-54 D38521.1		4.0E-54 AI935086.1	3.0E-54 AA313487.1	3.0E-54 AW 515742.1	3.0E-54 AL110383.1
Most Similar (Top) Hit BLAST E Value	8.0E-54	8.0E-54	7.0E-54	7.0E-54 Y16645.1	7.0E-54	7.0E-54	7.0E-54	7.0E-54	7.0E-54	6.0E-54	6.0E-54	6.0E-54	6.0E-54	6.0E-54	6.0E-54	6.0E-54	5.0E-54	6.0E-54	6.0E-54	5.0E-54										
Expression Signal	2.08	23.39	1.35	2.23	2.63	2.1	4.1	1.4	3.40	0.84	0.77	0.77	0.72	22.75	1.09	2.15	2.04	3.31	1.52	1.94	56.19		14.58		3.26		1.85	8.12	96.0	1.19
ORF SEQ ID NO:	28133		]	28128						28285					30704				37552	28483			27211		28097			26358		3 28872
Exas SEQ ID NO:	15026	19239	13632	15021			1	24426	L.	1		.1_	1	1_	L	L	1	18125	<u> </u>	15352	L	L		14894	Ł	L	16448	ı	1	15758
Probe SEQ ID NO:	1882	6057	305	1877	2278	10333	11365	11365	44670	20,5	396	396	3355	4111	4584	4988	4986	5115	11741	2218	187		978	1848	1848	Š	3274	96	1604	2635

Page 322 of 550 Table 4 Single Exon Probes Expressed in Placenta

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	Top Hit Descriptor	Homo saniens BMX non-receptor brosine kinase (BMX) mRNA	Constant Species negethered human NbHPA Homo sablens oDNA clone IMAGE:1386270 3	BISCOOS STOOM STOOM STOOM STOOM STOOM STOOM STOOM STOOM STOOM STOOM STOOM STOOM STOOM STOOM STOOM STOOM STOOM STOOM STOOM STOOM STOOM STOOM STOOM STOOM STOOM STOOM STOOM STOOM STOOM STOOM STOOM STOOM STOOM STOOM STOOM STOOM STOOM STOOM STOOM STOOM STOOM STOOM STOOM STOOM STOOM STOOM STOOM STOOM STOOM STOOM STOOM STOOM STOOM STOOM STOOM STOOM STOOM STOOM STOOM STOOM STOOM STOOM STOOM STOOM STOOM STOOM STOOM STOOM STOOM STOOM STOOM STOOM STOOM STOOM STOOM STOOM STOOM STOOM STOOM STOOM STOOM STOOM STOOM STOOM STOOM STOOM STOOM STOOM STOOM STOOM STOOM STOOM STOOM STOOM STOOM STOOM STOOM STOOM STOOM STOOM STOOM STOOM STOOM STOOM STOOM STOOM STOOM STOOM STOOM STOOM STOOM STOOM STOOM STOOM STOOM STOOM STOOM STOOM STOOM STOOM STOOM STOOM STOOM STOOM STOOM STOOM STOOM STOOM STOOM STOOM STOOM STOOM STOOM STOOM STOOM STOOM STOOM STOOM STOOM 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homefor mRNA complete cds	Truin separation Evin annuage and the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the 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Homo sapiens mRNA for brain ryanodine receptor, complete cds	Homo sapiens Janus kinase 2 (a protein tyrosine kinase) (JAKZ), mKNA	Homo sepiens serologically defined colon cancer antigen 10 (SDCCACIV), minute	
	Top Hit Database Source	1	1	EST HOMAN	EST_HUMAN	ΝΤ	EST HUMAN	EST HUMAN	EST_HUMAN	EST_HUMAN	FZ	LN L	EST_HUMAN	NT	MALAI TO T	ESI HOMAN	Z	EST_HUMAN	뉟	LZ.	ı۱	EST TOWAR	Z	N.	2	- !	LN	¥	Į.	NT	TN.	NT	
,	Top Hit Acession No.	10000	12434			11434806 NT	.0E-54 BF345600.1		_		5031900 NT	4507164 NT	2.0E-54 AW163175.1	2.0E-54 AL163210.2		2.0E-54 AW057524.1	2.0E-54 AJ278314.1	2.0E-54 AA532925.1	4502642 NT	2.0E-54 AF208161.1	2.0E-54 4759069 NT	3E047864.1	1142665/ NI	2.0E-54 AB046811.1	2.0E-54 AB046811.1	2.0E-54 AF008915.1	2.0E-54 AB023212.1	2.0E-54 AB023212.1	11426544	2 DE-54 AB001025.1	11429127 NT	11416762 NT	
	Most Similar (Top) Hit T BLAST E Value		3.0E-54	3.0E-54 AA844061.1	3.0E-54 AA844061.1	3.0E-54	3.0E-54 B	3.0E.54.4	3.0E-54 A	3.0E-54 A	2.0E-54	2.0E-54	2.0E-54.A	2.0E-54 A		2.0E-54 A	2.0E-54 P	2.0E-54	2.0E-54	2.0E-54 /	2.0E-54	2.0E-54	2.0E-54	2.0E-54 /	2.0E-54 /	2.0E-54 /	2.0E-54						
	Expression Signal	1	1.36	1.34	1.34	1.77	4.01	800	1.32	3.16	17.67	1.54	1.25				9.0	6.1	1.74	7.1						1.63	0.68	0.68	0				
	ORF SEQ ID NO:		32527	34096	34097		38053	70,00	32110		26871	İ	l		_		29577									33351	33701		1	33010			1
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Top Hit Descriptor	Homo sapiens serologically defined colon cancer antigen 10 (SDCCAG10), mRNA	Homo sapiens mRNA for KIAA0462 protein, partial cds	Homo sapiens EVI5 homolog mRNA, complete cds	Homo capiens pescadillo (zebrafish) homolog 1, containing BRCT domain (PES1), mRNA	Homo saplens period (Drosophila) homolog 3 (PER3), mRNA	601899230F1 NIH_MGC_19 Homo saplens oDNA clone IMAGE:4128535 5	Homo sepiens similar to nuclear factor related to kappa B binding protein (H. sapiens) (LOC63182), mRNA	2u10e09.r1 Soares_testis_NHT Homo sepiens cDNA clone IMAGE:731464 5	zu/0e09.r1 Scares_testis_NHT Homo saplens cDNA clone IMAGE:731464 5	AU077341 Sugano cDNA library Homo saplens cDNA clone ZN6C880 similar to 6'-end region of Human gamma-glutamy transpeptidese mRNA, 5 end	QV2-BT0635-160400-143-h12 BT0635 Homo sapiens cDNA	Homo sapiens RFB30 gene for RING finger protein	Homo saplens RFB30 gene for RING finger protein	fh02a02.x1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:2960907 5'	xd76c02.x1 Soares_NFL_T_GBC_S1 Homo sepiens cDNA clone IMACE:2803522 3' similar to TR:O80365 O80365 FOS39564_1;	ak28a11.s1 Scares_tests_NHT Homo sepiens cDNA clone IMAGE:1407260 3'	AU139909 PLACE1 Homo saplens cDNA clone PLACE1011576 5'	tq29f09.x1 NCI_CGAP_Ut1 Homo saplens cDNA clone IMAGE:2210249 3'	tq29f09x1 NCI_CGAP_Utf Homo sapiens cDNA clone IMAGE:2210249 3'	7637c01.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3284640 3'	ym57g07.r1 Soares Infant brain 1NIB Homo sapiens cDNA clone IMAGE:52444 5'	Homo sapiens mRNA for KIAA1501 protein, partial cds	zj95b09.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo saplens cDNA clone IMAGE:462617 3'	295b09.sf Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:4626173'	JI-H-BI1-efy-g-09-0-UI.s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2723536 3'	Homo sapiens anysulfatase E (chondrodysplasia punctate 1) (ARSE), mRNA	Homo sapiens arysulfatase E (chondrodysplasia punctala 1) (ARSE), mRNA	Homo saplens paraoxonase 2 (PON2) mRNA, and translated products	Homo sapiens paracconase 2 (PON2) mRNA, and translated products	Homo saplens Rho GTPase activating protein 6 (ARHGAP6), transcript variant 5, mRNA	Homo saplens speckle-type POZ protein (SPOP), mRNA
Top Hit Database Source	TN	ĮN.	IN	NT	LN LN	EST_HUMAN	TN	EST HUMAN	EST_HUMAN	EST HUMAN	EST HUMAN	L	NT.	EST_HUMAN	EST_HUMAN	EST HUMAN	EST_HUMAN	EST_HUMAN		EST_HUMAN	EST_HUMAN	ΙN	EST_HUMAN			TN	ΙN	LN	TN	TN	
Top Hit Acession No.	11416762 NT	2.0E-54 AB007931.1	2.0E-54 AF008915.1	7657454 NT	8567387 NT	1.0E-54 BF315418.1	11417222 NT	1.0E-54 AA412409.1	1.0E-54 AA412409.1	1.0E-54 AU077341.1	9.0E-55 BE081469.1	8.0E-55 Y07829.2	8.0E-55 Y07829.2	8.0E-55 AW 409714.1	7.0E-55 AW103839.1	7.0E-55 AA889581.1	7.0E-55 AU139909.1	7.0E-55 AI561036.1	7.0E-55 AI561056.1	7.0E-55 BE670608.1	7.0E-55 H23396.1		5.0E-55 AA704971.1	5.0E-55 AA704971.1	5.0E-55 AW 206021.1	4502240 NT	4502240 NT	4505952 NT	4505952 NT	7382477 NT	11434422 NT
Most Similar (Top) Hit BLAST E Value	2.0E-54	2.0E-54	2.0E-54	2.0E-54	2.0E-54	1.0E-54	1.0E-54	1.0E-54	1.0E-54	1.0E-54	9.0E-55	8.0E-55	8.0E-55	8.0E-55	7.0E-55	7.0E-55	7.0E-55	7.0E-55	7.0E-55	7.0E-55	7.0E-55	6.0E-55	5.0E-55	5.0E-55	5.0E-55	5.0E-55	5.0E-55	5.0E-55	5.0E-55	5.0E-55	5.0E-55
Expression Signal	0.76	0.46	1.46	1.72	4.36	1.65	0.5	0.52	0.52	2.33	1.02	1.59	2.77	1.83	0.48	1.28	1.71	80.8	808	1.18	6.37	1.96	1.21	1.21	1.51	1.49	1.49	1.08	1.08	1.03	0.72
ORF SEQ ID NO:	36972				31970		35545	37105	37106		37208	-				36021		38215		31860			28051								33996
Exon SEQ ID NO:	23361	П		L	25591	17724	22006	23494	23494	25709	23603	14500	14503	24530	22083	22458	22490	24544					. 1						25833		20523
Probe SEQ.1D NO:	10326	10841	11275	12027	12893	4587	8927	10459	10459	13086	10568	1344	1348	11471	9004	9383	9416	11485	11485	12726	13050	11804	1810	1810	4894	6670	6670	6805	6805	7182	7446

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	Top Hit Descriptor	Homo sapiens protein tyrosine phosphatase, receptor type, alpha polypeptide (PTPKA) mKNA	RC4-BT0310-110300-015-110 B10310 Home superis curva	Homo sapiens mRNA for KIAA0611 protein, partial cds	Homo sapiens mRNA for KIAA0611 protein, partial cds	Homo seplens nel (chioken) like 2 (NELL2), mRNA	Home carlens SIKAP55 homologue (SKAP-HOM), mRNA	Promo september 19 (SKAP-HOM), mRNA	Transcription September (PES1), mRNA	FIGURE September Committee Committee Committee Committee Committee Committee Committee Committee Committee Committee Committee Committee Committee Committee Committee Committee Committee Committee Committee Committee Committee Committee Committee Committee Committee Committee Committee Committee Committee Committee Committee Committee Committee Committee Committee Committee Committee Committee Committee Committee Committee Committee Committee Committee Committee Committee Committee Committee Committee Committee Committee Committee Committee Committee Committee Committee Committee Committee Committee Committee Committee Committee Committee Committee Committee Committee Committee Committee Committee Committee Committee Committee Committee Committee Committee Committee Committee Committee Committee Committee Committee Committee Committee Committee Committee Committee Committee Committee Committee Committee Committee Committee Committee Committee Committee Committee Committee Committee Committee Committee Committee Committee Committee Committee Committee Committee Committee Committee Committee Committee Committee Committee Committee Committee Committee Committee Committee Committee Committee Committee Committee Committee Committee Committee Committee Committee Committee Committee Committee Committee Committee Committee Committee Committee Committee Committee Committee Committee Committee Committee Committee Committee Committee Committee Committee Committee Committee Committee Committee Committee Committee Committee Committee Committee Committee Committee Committee Committee Committee Committee Committee Committee Committee Committee Committee Committee Committee Committee Committee Committee Committee Committee Committee Committee Committee Committee Committee Committee Committee Committee Committee Committee Committee Committee Committee Committee Committee Committee Committee Committee Committee Committee Committee Committee Committee Committee Committee Committee Committee Committee Committee Committee Committee	E313/0004 MACE Indian mofile protein. Y chromosome, family 1, member A1 (RBMY1A1) mRNA	Homo septems now billion in the property (SS3786), mRNA	Fromo sapiens predicted concentration (SS3786), mRNA	Homo sapiens predicted usicultiast process (2014) The Sapiens and Active MAGE:3390043 3' similar to	7j52b10.X1 Soares_NST_ro_sw_O1_ro_j	Homo sapiens proteasome (prosome, macropain) subunit, aipha type, z (1 Gwrz) micro.	omo sapiens proteasome (prosome, madupani) subuni, apia sipia sipia sipia sipia sipia sipia sipia sipia sipia sipia sipia sipia sipia sipia sipia sipia sipia sipia sipia sipia sipia sipia sipia sipia sipia sipia sipia sipia sipia sipia sipia sipia sipia sipia sipia sipia sipia sipia sipia sipia sipia sipia sipia sipia sipia sipia sipia sipia sipia sipia sipia sipia sipia sipia sipia sipia sipia sipia sipia sipia sipia sipia sipia sipia sipia sipia sipia sipia sipia sipia sipia sipia sipia sipia sipia sipia sipia sipia sipia sipia sipia sipia sipia sipia sipia sipia sipia sipia sipia sipia sipia sipia sipia sipia sipia sipia sipia sipia sipia sipia sipia sipia sipia sipia sipia sipia sipia sipia sipia sipia sipia sipia sipia sipia sipia sipia sipia sipia sipia sipia sipia sipia sipia sipia sipia sipia sipia sipia sipia sipia sipia sipia sipia sipia sipia sipia sipia sipia sipia sipia sipia sipia sipia sipia sipia sipia sipia sipia sipia sipia sipia sipia sipia sipia sipia sipia sipia sipia sipia sipia sipia sipia sipia sipia sipia sipia sipia sipia sipia sipia sipia sipia sipia sipia sipia sipia sipia sipia sipia sipia sipia sipia sipia sipia sipia sipia sipia sipia sipia sipia sipia sipia sipia sipia sipia sipia sipia sipia sipia sipia sipia sipia sipia sipia sipia sipia sipia sipia sipia sipia sipia sipia sipia sipia sipia sipia sipia sipia sipia sipia sipia sipia sipia sipia sipia sipia sipia sipia sipia sipia sipia sipia sipia sipia sipia sipia sipia sipia sipia sipia sipia sipia sipia sipia sipia sipia sipia sipia sipia sipia sipia sipia sipia sipia sipia sipia sipia sipia sipia sipia sipia sipia sipia sipia sipia sipia sipia sipia sipia sipia sipia sipia sipia sipia sipia sipia sipia sipia sipia sipia sipia sipia sipia sipia sipia sipia sipia sipia sipia sipia sipia sipia sipia sipia sipia sipia sipia sipia sipia sipia sipia sipia sipia sipia sipia sipia sipia sipia sipia sipia sipia sipia sipia sipia sipia sipia sipia sipia sipia sipia sipia sipia sipia sipia sipia sipia sipia sipia sipia sipia sipia sipi	Homo sapiens diacyglycerol kinase, garrina (soku) (Lokus)	Homo saplens diacylglycerol kinase, gamma (90kD) (DGKG) mkny timediac parame E2 variant 1 (UBE2V1) mRNA	Homo sapiens upriquimin-dujuganing enzymo La carrent	Homo sapiens criticinoscine za segmenta recessoralizations apiens cDNA	A305 Hullian Four Barrier 17 Home septens cDNA clone IMAGE:4120338 5	20 180031 St. Chromosome 7 Felial Brain cDNA Library Homo sapiens cDNA clone 7B09A09	PM41-HT0603-090300-001-q08 HT0603 Homo saplens cDNA	Homo saniens chromosome 21 segment HS21C084	Uman endonemonis retrovirus oHE.1 (ERV9)	Human and oceanous retroviral DNA (4-1), complete retroviral segment	Home saniens syntaxin-binding protein 1 (STXBP1) mRNA, and translated products	Home content through notein lease E34 (human papilloma virus E6-associated protein, Angelman	Syndrome) (UBE3A) mRNA Lama content CINA	CMM-H108/6-130800-337-gus H108/9 hours septems con IMAGE:3078275 5	UHRIT-DNU-RIS-1-302-301. TNII Julia Saplens CDNA clone IMAGE:3134463 3'	h-76h08 x1 NCI CGAP Kid11 Homo saplens cDNA clone IMAGE:3134463 3	
and in love and income	Top Hit Database Source		EST_HUMAN R	Г							HUMAN				EST_HUMAN O						$\neg$	7	T	TOT TOWAN	Т		Z				$\neg$	Т	FOT LIMAN	7
olgino  -	Top Hit Acession No.	4506302 NT	5 0E-55 BE064386.1	Γ	Γ	2765	COLORGO	11421649 IN	11421649 NT	972	4.0E-55 AW957994.1	4826973 NT	7661713 NT	7661713 NT	4 0E-55 BF061411.1	4506180 NT	4506180 NT	4503314 NT		4507794 NT	4.0E-55 AL163210.2	4.0E-55 W 28189.1	4.0E-56 BF303941.1	3.0E-55 AA077156.1	3.0E-55 BE1/8519.1	3.0E-55 AL 163284.2	2.0E-55 X57147.1	M10976.	4507296 NI	4507798 NT	2.0E-55 BE719986.1	2.0E-55 AW 501988.1	2.0E-55 BF224452.1	2.0E-55 BF224452.1
	Most Similar (Top) Hit BLAST E Value	5.0E-55	5.0E-55.B	5 OF-55 A	8 OE 55 A	0.00-30.0	3.UE-33	5.0E-55	5.0E-55	5.0E-55	4.0E-55/	4.0E-55	4.0E-55	4.0E-55	4 0F-55	4.0E-55	4.0E-55	4 0F-55	4.0E-55	4.0E-55	4.0E-55	4.0E-55	4.0E-55	3.0E-55	3.0E-55	3.0E-55	2.0E-55		2.0E-55	2.0E-66	2.0E-55			
ţ	Expression Signal	23	0.91	153	3	20.	1.13	1.3	1.3	1.73	2.24	32.17	2.15	2.15	4.72	2.19	2.19	8.38	8.36	3.02	9.85	2.31	1.82	99:0	4.18	3.53	1.69		3.98	0.89	3.51			0.48
	ORF SEQ ID NO:	35865		046970	300/2	36873	37069	38236	38237		26310	26906		_		28341	28342	2000	$\perp$			-		33279			26830		26880	29222				2 35893
	SEQ ID	10000	1000	02077	282/8	- 1		24560	l .	25298	16004	L	L	1_	1	15221	15001	2003	1	1_	_	24563	25244			3 25719	13594	5 13757	3 13852	16199		1	L	5 22342
	Probe SEQ ID NO:	100	37,0	9520	10243	10243	10427	11502	11502	12421	28	689	1472	1472	1	1344	2000	200	2151	2384	8539	11605	12337	6731	12273	13103	388	566	999	3023	489	7673	9265	926

Page 325 of 550 Table 4 Single Exon Probes Expressed in Placenta

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Top Hit Descriptor	am98h05.s1 Strategene schizzo brain S11 Homo sapiens cDNA clone IMAGE:1684185 3 similar to contains THR.b2 THR repetitive element;	QVG-BN0147-280400-213-g06 BN0147 Homo saptens cLNA	AU119344 HEMBA1 Homo sapiens cDNA clone HEMBA1005583 3	Homo sapiens ubiquitin protein ligese E3A (human papilloma virus E6-associated protein, Argeiman syndrome) (UBE3A) mRNA	Homo sapiens mannose-8-phosphate receptor (cation dependent) (Morric) michael	Oryctologus cuntculus New Zealand white elongation factor 1 apha (Raberlac) mRNA, complete ods	ov85g09.x1 Scares_testis_NHI Home sapiens conva citine imAGE. 1044100 3	Homo sapiens mRNA for KIAA0903 protein, partial cos	601120118F1 NIH MGC 20 Homo sapiens curva didne investigated a	601120116F1 NIH MGC 20 Homo sapiens oDNA clone IMAGE:2397027 5	Homo saptens SMA3 (SMA3), mRNA	Homo sapiens testis-specific Testis Transcript Y 1 (111Y1) mKNA, partial cus	Human mRNA for HLA-A11E, a MHC class I malecule (major nistocon paticina) complex)	Homo sapiens mRNA for KIAA0406 protein, partial cds	Homo sapiens mRNA for KIAA0406 protein, partial cos	Homo sapiens CLP mRNA, pertial cds	Homo sapiens mRNA for KIAA1219 protein, partial cds	43c5 Human retina cDNA randomly primed sublibrary nome sapiens conva	Homo saplens chromosome 21 segment HSZ1CUO/	Homo sapiens chromosome 21 segment HSZTCO10	yv44g03.r1 Soares fetal liver spieen 1N*LS homo sapiens con a cione inin on 12-17-02.5	Homo sapiens DSCR5b mKNA, complete cds	Homo saplens DSCK5b mKNA, complete cus	Homo saplens PRO1851 mik/NA, compliere cas	Homo sapiens hect domain and RLD 2(HERC2), mRNA	Homo sapiens hect domain and RLD 2 (HERC2), mRNA	Homo sapiens discs, large (Drosophila) homolog 2 (chaps/m-110) (DLCZ), mKNA	Homo sapiens discs, large (Drosophila) homolog 2 (chapsyn-110) (DLG2), micro	Homo sapiens SKAP55 homologue (SKAP-HOM), mKNA	Homo saplens phospholipid scramblase 1 gene, complete cds	Homo sepiens phospholipid scramblase 1 gene, comprendus
Top Hit Database Source	EST_HUMAN	EST_HUMAN	EST_HUMAN	F	ĻΝ	NT	EST_HUMAN	IN	EST_HUMAN	EST HUMAN	TN	. LN	NT	TN	LZ	LΝ	1 1	EST HUMAN	NT	LΝ	EST_HUMAN	NT	N <sub>T</sub>	LN	Ŋ	FN	NT	LN.	NT	NT	N
Top Hit Acesslon No.	0E-55 A1002836.1			96776	4505060 NT			.0E-55 AB020710.1	.0E-55 BE277861.1	.0E-55 BE277861.1	5803174 NT	.0E-55 AF000990.1	.0E-55 X13111.1	.0E-55 AB007866.2	.0E-55 AB007868.2	.0E-55 L54057.1	I.0E-55 AB033045.1	.0E-55 W 28189.1	.0E-55 AL163267.2	.0E-55 AL163210.2	1.0E-65 N77261.1	.0E-55 AB037163.1	.0E-55 AB037163.1	.0E-55 AF119856.1	11433046 NT	11433046 NT	11432994 NT	11432994 NT	11421649 NT	1.0E-55 AF224492.1	1.0E-55 AF224492.1
Most Similar (Top) Hit T BLAST E Value	2.0E-55 A	2.0E-55 B	2.0E-55 AU119344.1	2.0E-55	1.0E-55	1.0E-55 U09823.1	1.0E-55 A	1.0E-55	1.0E-55	1.0E-55	1.0E-55	1.0E-55	1.0E-55.>	1.0E-55	1.0E-55	1.0E-55	1.0E-55			1.0E-55	1.0E-55	-	-	_	1.0E-55	Ĺ	1.0E-55	1.0E-55			
Expression Signal	4.33	0.67	2.35	1.34	1.62	40.5	1.38	3.92		2.33				5.51		3.37				1.1	96.0	1.15	1.15	0.65			1.7	1.7	0.49		0.93
ORF SEQ ID NO:			37897			<u> </u>	L			28252		28673	L	28857			L					31054		31876							
Exon SEQ ID NO:	22436	22518	24761	1	1	13417	ľ	ł	ı	L	L	ı	1	ı	ı	1		1	i.	1	L	L	L	L	L	1	1.	١.	1_	1	1 1
Probe SEQ ID NO:	936	0447	11102	13477	66	194	588	1173	2008	2006	2401	2415	2588	2620	2620	2677	2850	3495	4097	4409	4853	4949	4949	5614	8401	840	8478	8478	8266	8273	8273

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Top Hit Descriptor	Homo saplens chromosome 21 segment HS21C010	Homo sapiens chromosome 21 segment HS210010	Human infant brain unknown product mRNA, complete cds	Seq1576 b4HB3MA Cot8-HAP-Ft Homo sapiens cDNA clone b4HB3MA-COT8-HAP-Ft61 5' similar to similar	to Chirtese namster Unity-coamplined protein myty-	Homo saplens hypothetical protein FLJ10891 (FLJ10891), mRNA	Homo saplens DNA-binding protein (LOC56242), mRNA	601237702F1 NIH_MGC_44 Homo saptens cDNA clone IMAGE:3609552 5'	Homo sapiens chromosome 21 segment HS21 0009	yn62g03.r1 Soares adult brein N2b5HB55Y Homo sapiens cDNA clone IMAGE:173044 5' similar to contains	I HK repetitive etement ;	RC1-CT0252-231099-013-b07 CT0252 Homo sepiens cDNA	RC1-CT0252-231099-013-b07 CT0252 Homo sapiens cDNA	RC3-BN0053-170200-011-h01 BN0053 Homo sapiens cDNA	UI-H-Bl0p-aau-a-05-0-UI.s1 NCI_CGAP_Sub2 Homo sapiens cDNA clone IMAGE:2710544 3'	43c5 Human retina cDNA randomly primed sublibrary Homo sapiens cDNA	CHR220038 Chromosome 22 exon Homo sapiens cDNA clone C22_55 5'	Homo sapiens beta-tubulin mRNA, complete cds	Homo sapiens bete-tubulin mRNA, complete cds	Homo sapiens tubulin, beta polypeptide (TUBB) mRNA	Homo sapiens tubulin, beta polypeptide (TUBB) mRNA	Homo sapiens X-linked antidrollic ectodermal dysplasia prolein gene (EDA), exon 2 and flanking repeat	Homo seplens uncharacterized bone marrow protein BM031 mRNA, complete cds	Homo sapiens uncharacterized bone marrow protein BM031 mRNA, complete cds	Homo sapiens lymphocyte specific protein 1 (LSP1) gene, LSP1-7 allele, partial cds	tm65g12.x1 NCI_CGAP_Brn25 Homo septens cDNA clone IMAGE:2163046 3'	tm65g12.x1 NCI_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2163046 3'	Homo sapiens hypothetical protein PRO1304 (PRO1304), mRNA	Homo sapiens 5-3' excribonuclease 2 (XRN2), mRNA	Homo sapiens oncogene TC21 (TC21), mRNA	EST28889 Cerebellum II Homo saplens cDNA 5' end	EST28889 Cerebellum II Homo sapiens cDNA 5' end	Homo sapiens MHC class 1 region
Top Hit Database Source	Ł	Į.	닏		ES HOMAN	LN	٦	EST HUMAN	Į.	1	EST HOMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	TN	TN	IN	۲	<u>L</u>	Z L	Ā	N F	EST_HUMAN	EST_HUMAN	F	Ę	NT	EST HUMAN	EST HUMAN	Ę
Top Hit Acession No.	1.0E-55 AL163210.2	1.0E-55 AL163210.2	1.0E-55 U50950.1		10045.1	8922743 NT	10567821 NT	9.0E-56 BE379074.1	8.0E-56 AL163209.2		7.0E-56 H19934.1	7.0E-56 AW361213.1	7.0E-56 AW361213.1	5.0E-56 AW997712.1	5.0E-56 AW015507.1	5.0E-56 W 28189.1	5.0E-56 H55099.1	4.0E-56 AF141349.1	4.0E-56 AF141349.1	4507728 NT	4507728 NT	4 OF GR ATTOOR 20 4	4.0E-56 AF217508.1	4.0E-58 AF217508.1	4.0E-56 AF043349.1	4.0E-58 A1498066.1	4.0E-56 Al498066.1	8924029 NT	6912743 NT	6912697 NT	3.0E-56 AA325826.1	3.0E-56 AA325826.1	3.0E-56 AF055066.1
Most Similar (Top) Hit BLAST E Value	1.0E-55 /	1.0E-55/	1.0E-55	i i	1.0E-55   10045.1	1.0E-55	1.0E-55			İ	7.0E-56	7.0E-56	7.0E-56	5.0E-56	5.0E-56	5.0E-56	5.0E-56	4.0E-56	4.0E-56	4.0E-56	4.0E-56	20 10 4	4.0E-56	4.0E-58	4.0E-56	4.0E-58	4.0E-56	3.0E-56	3.0E-56	3.0E-56	3.0E-56	3.0E-56 /	3.0E-56
Expression Signal	2.41	2.41	1.86				1.78	1.85	1.34	1	7.08	1.93	1.93	2.7	0.71	1,35	2.47	8.64	8.64	3.61	3.61	- 8	4	<u>4</u> .	1.68	7.73	7.73	2.69	1.84	1.6	1.67	1.67	2.81
ORF SEQ ID NO:	37851	37852	37544		3/30/	38476	38560		38277		]		j	27968	35995						28999	98786	32915	32216	37384	37863	37864		28047		29376		
Exon SEQ ID NO:	24223	24223	l	ļ	- 1	- 1	24864	١.			- 1	- (		14877	1.	23634				15888	15888	49790	19556	19556	23757	24234	24234	14527	L		16370	16370	17098
Probe SEQ ID NO:	11152	11152	11733		1/00	11789	11876	7522	11545		2793	7818	7818	1727	9362	10599	12513	28	28	2773	27.73	2072	6387	6387	10724	11163	11163	1372	1804	2217	3195	3185	3939

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					aigi (iC	Siligie Exult Flores Expressed	
Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
4507	17648	30634	0.67	3.0E-56	7657042 NT		Homo sapiens Down syndrome candidate region 1 (DSCR1), mRNA
4544	L			3.0E-56		NT	Homo sapiens chromosome 21 segment HS21 C068
4695	1_			3.0E-56	3.0E-56 5902085 NT		Homo sapiens superkiller viralicidic activity 2 (S. cerevisiae nomolog) Fine (SNIVZE), IIINVA
5801	<u>l</u>	32283	1.5	3.0E-56	4759163 NT		Homo sapiens sparc/osteorectin, cwcv and kazal-like domains proteoglycan (testican) (SPOCK) mRNA
5801			70		TN 89163/14		Home saplens sparc/osteonectin, cwcv and kazzi-like domains proteoglycan (testican) (SPOCK) mRNA
7014	L			<u> </u>	3.0E-56 11421124 NT		Homo sapiens lysosomal-associated membrane protein 2 (LAMP2), mrnA
7476		L	2.07	3.0E-56	4504970 NT		Homo sapiens LIM binding domain 2 (LDb2) mixing
7476	<u>ا</u>	34024		_	4504970 NT		Homo sapiens LIM binding domain 2 (LUB2) mKNA
9016	1_				11418704 NT		Homo sapiens bone morphogenetic protein 5 (Bivir 5), mixiva
10018	1_	36852					Homo sapiens mRNA for KIAA0145 protein, partial cas
10698	L.		1.39		926		Homo sapiens KIAA0317 gene product (NJAA0317), minka
10980	L		2.62		AB042556.1		Home sapiens mikina, similar to rat myoringalin, comprements.
11594	L				5902013 NT		Homo sapiens nuclear pore complex meracung protein (** 1. /), minos
11594	L	38331			5902013 NT		Homo sapiens nuclear pore complex interacting protein (thr in ), tim vis
12377	L.	<u> </u>			11434876 NT	N	Homo sapiens caveoin 3 (CAVS), mrvvA
12377	L_	32076		<b>!</b>	3.0E-56 11434876 NT	L'A	Homo sapiens caveolin 3 (CAV3), mKNA
537	L				AA199818.1	EST HUMAN	zdozava. si okranagene neurocpurrellurii (#80/2010) romo supremo ozna i ozna i ozna i ozna i ozna i ozna i ozna
751	16021	26975	1.18		ĺ	EST_HUMAN	RC4-B10310-110300-019-710 B10310 nonio sepienis convo
751	16021				1	EST_HUMAN	RC4-BT0310-11030C-015-110 BT0310 notice september 500 No.
3053	16229					Ę	Homo sabiens mining to NAA1++ promise one
3391	L					뉟	Homo sapiens gene for activin receptor type ito, curliplete cus
3624	┖	29805			AV70318	EST_HUMAN	AV703184 ADB Home sapiens convacione ADDCT C10 5
7239	1	L	1.39	Ţ	5730038 NT	N <sub>1</sub>	Homo sapiens of i domain and mariner dailsposase tosted gene (of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant
1003	1	L	3.01		1.0E-56 AF190930.1	M	Macaca fascicularis protein tyrosine prospinerase (Fru-1) inny. Company.
3765	1	29928		٢	.0E-56 AW 589833.1	EST_HUMAN	hg23c11.x1 NCL CGAP GC6 Homo sapiens cUNA clone INALELEMENTS
3765	١.		1.84	-	.0E-56 AW589833.1	EST_HUMAN	hg23c11.x1 NC_CGAP_GC8 Homo sepiens cDNA dione invAGE: 2340432.3
5145	L				1.0E-56 A1905162.1	EST_HUMAN	QV-BT077-130199-079 BT077 Homo sapiens curvA
10161	上				1.0E-56 AL163203.2	Z	Homo sapiens chromosome 21 segment HSZ1 cuus
10264	L	36886			1.0E-56 AW845987.1	EST_HUMAN	RC2-CT0163-220999-001-E02 CT0163 Hamo sapiens CDNA
645	L	1	1.39		9.0E-57 AW880885.1	EST HUMAN	QVC-O10033-0/0300-152-mus O10055 mulio saprens convo
11494	4 24552	2 38227			9,0E-67 AF228497.1	LN L	Homo sapiens serine processe 17 (NLN4) garie, complete cus
11494	4 24552	38228	1.72	_	9.0E-57 AF228497.1	N	Homo sapiens senne protesse i / (nens) Berre, contros ous
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Top Hit Descriptor	Homo sapiens mRNA for cyclin B2, complete cds	Homo sapiens hypothetical protein FLJ20371 (FLJ20371), mRNA	QV4-ST0234-181199-037-705 ST0234 Hamo sepiens dDNA	x05d10.x1 NCI_CGAP_Brn53 Homo sapiens cDNA clone IMAGE:27592513' similar to gb:U05875 INTERFERON-GAMMA RECEPTOR BETA CHAIN PRECURSOR (HUMAN);	v zv51b12.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:757151 5'	Homo sapiens aconitase 2, mitochondrial (ACO2), mRNA	Homo sapiens mRNA for KJAA0898 protein, partial cds	Homo saplens mRNA for KIAA0960 protein, partial cds	Homo saplens mRNA for KIAA0900 protein, partial cds	Homo sapiens KIAA0716 gene product (KIAA0716), mRNA	Homo sapiens mRNA for KIAA0837 protein, partial ods	Homo saplens mRNA for K/AA0837 protein, partial cds	Homo saplens hypothetical protein FLJ20371 (FLJ20371), mRNA	Homo saplens ninein (LOC51199), mRNA	Homo saplens Ras suppressor protein 1 (RSU1), mRNA	Homo sapiens SH3-domain binding protein 1 (SH3BP1), mRNA	Homo sapiens SH3-domain binding protein 1 (SH3BP1), mRNA	Homo saplens GYS2 gene, exon 14	Homo sapiens smg GDS-ASSOCIATED PROTEIN (SMAP), mRNA	Homo saplens smg GDS-ASSOCIATED PROTEIN (SMAP), mRNA	Homo eaplens Kruppel-like factor 8 (KLF8), mRNA	Homo saplens phosphatidylinositol 4-kinase 230 (pi4K230) mRNA, complete cds	Homo sapiens phosphatidy/inositol 4-kinase 230 (pl4K230) mRNA, complete cds	Homo saplens Xq pseudoautosomal region; segment 1/2	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes,	complete cds)	Homo sapiens ublquitin protein ligase E3A (human papilloma virus E6-associated protein, Angelman	syndrome) (UBE3A) mRNA	Inc13f07.51 NG_CGAP_Pr1 Homo sapiens cDNA cione IMAGE:1008037 cimilar to SW:RS10_HUMAN P86783 40S RIBOSOMAL PROTEIN S10;	N EST54770 Hippocampus II Homo saplens cDNA 5' end	783b10x1 NCI_CGAP_CLL1 Homo saplens cDNA clone IMAGE:3286443 3' similar to WP:Y47H9C.2 N   CE20263;
Top Hit Database Source	TN	LΝ	EST_HUMAN	EST HUMAN	EST_HUMAN	IN	μN	IN	NT	۲	NT	NT	IN	NT	ΙN	N	NT	١	ĮN.	ΙN	IN	IN	INT	Į		¥		TN	EST HUMAN	EST HUMAN	EST_HUMAN
Top Hit Acessian No.	9.0E-57 AB020981.1	8923349 NT	8.0E-57 AW816405.1	8.0E-57 AW 264599.1		18185	8.0E-57 AB020705.1		8.0E-57 AB023177.1	7662263 NT	8.0E-57 AB020644.1	8.0E-57 AB020644.1	8923349 NT	11433356 NT	11431260 NT	11545732 NT	11545732 NT	7.0E-57 AJ003100.1	7657592 NT	7657592 NT	TN 6262009	7.0E-57 AF012872.1	7.0E-57 AF012872.1	5.0E-57 AJ271735.1		4.0E-57 AB026898.1		4507798 NT	3.0E-57 AA230279.1	3.0E-57 AA348335.1	3.0E-57 BE676622.1
Most Similar (Top) Hit BLAST E Vatue	9.0E-57	8.0E-57	8.0E-57	8.0E-57	8.0E-57	8.0E-57	8.0E-57	8.0E-57	8.0E-57	8.0E-57	8.0E-57	8.0E-57	8.0E-57	8.0E-57	8.0E-57	8.0E-67	8.0E-57	7.0E-57	7.0E-57	7.0E-57	7.0E-57	7.0E-57	7.0E-57	5.0E-57		4.0E-57		3.0E-57	3.0E-57	3.0E-57	3.0E-57
Expression Signal	2.2	1.02	2.83	7.49	1.45	1.92	0.91	12.82	12.82	0.62	1.54	1.54	3.51	1.74	1.53	1.67	1.94	0.88	76.0	16:0	0.81	3.14	3.14	3.99		6.03		0.64	12.47	1.12	1.03
ORF SEQ ID NO:	38500	26252	26558	Ż7147	28112	31679	33066	33138	33139	34152	34486	34487	26252	l					ŀ	28933	28982		30144			30010		27062		28716	
Exon SEQ ID NO:	L	13252	<u></u>	14082		26034	19636	19753	19753	20677	20977	20977	13252	26022	<u> </u>	L				15817	16517	17139	17139	26071		17009	L	14005	14516	15591	1 1
Probe SEQ ID NO:	11811	14	308	907	1859	5355	6259	6593	6593	7607	7927	7927	11768	12041	12102	12791	12808	1246	2698	2698	3344	3982	3982	13185		3849		827	1362	2464	2768

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Top Hit Descriptor	7733brio x1 NCI_CGAP_CLL1 Homo saplens cDNA clone IMAGE:3296443 3' similar to WP:Y47H9C.2 CE20283 ;	Homo sapiens cell-line tsA201a chloride ion current inducer protein I(Un) gene, complete cos	RC3-CT0254-110300-027-d10 CT0254 Homo sapiens cUNA	Homo sapiens angiotensin I converting enzyme (peptidyl-dipeptidase A) 2 (ACEZ), mKNA	601589898F1 NIH MGC 7 Homo sapiens cUNA clone IMAGE:3944302 3	426 Human retina cDNA randomly primed sublibrary Homo sapiens cDNA	Homo sapiens hypometical protein FLJ 11050 (FLJ 11050), mKNA	Homo sapiens hypothetical protein FLJ11656 (FLJ11656), mRNA	Homo sapiens KiAA0649 gene product (KIAA0649), mKNA	Human farnesyl pyrophosphete synthetase mrNA, complete cds	AU117659 HEMBA1 Hamo septens cDNA clone HEMBA1001910 5	Homo sepiens hypothetical protein FLJ11656 (FLJ11656), mRNA	Homo sapiens hypothetical protein FLJ11656 (FLJ11656), mRNA	2820473.5prime NIH_MGC_7 Homo saplens cDNA clone IMAGE;2820473 6	zb45d11.r1 Soares_fetal_lung_NbHL19W Homo sapiens cDNA clone IMAGE:306549 5	AJ003649 Selected chromosome 21 cDNA library Homo saplens cDNA done MPIph 0-1L1	Homo sapiens SNARE protein kinase SNAK mRNA, complete cds	Homo sapiens SNARE protein kinase SNAK mRNA, complete cds	ak02b02.s1 Soares_parathyroid_tumor_NbHPA Homo sapiens cDNA clone IMAGE:1404747 3' similar to contains Alu repetitive element;contains element MER2z repetitive element ;	Homo sapiens chromosome 21 segment HS21C004	ye98h01.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:125809 5'	ye98h01.r1 Soares fetal liver spleen 1NFLS Homo saplens cDNA clone IMAGE:125809 5	ze40c06.r1 Soares retina N2b4HR Homo sapiens cDNA done IMAGE:361460 6	ze40c06.r1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:361450 5'	Homo saplens chromosome 21 segment HS21C083	ze31c05.r1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:360584 5' similar to contains L1.t3 L1	repetitive element ;	7n80f04.X1 NC_CGAP_Ov18 Homo sapiens cDNA clone IMAGE:3570965 3' ofmital to contains. LANT.11	MERZZ repetitive dement;	Homo sapiens small inductorie cycakine subjetting A (Oys-Oys), inclinical Z (Oo Ozz-C), inclinical Z (Oo Ozz-C), inclinical Z (Oo Ozz-C), inclinical Z (Oo Ozz-C), inclinical Z (Oo Ozz-C), inclinical Z (Oo Ozz-C), inclinical Z (Oo Ozz-C), inclinical Z (Oo Ozz-C), inclinical Z (Oo Ozz-C), inclinical Z (Oo Ozz-C), inclinical Z (Oo Ozz-C), inclinical Z (Oo Ozz-C), inclinical Z (Oo Ozz-C), inclinical Z (Oo Ozz-C), inclinical Z (Oo Ozz-C), inclinical Z (Oo Ozz-C), inclinical Z (Oo Ozz-C), inclinical Z (Oo Ozz-C), inclinical Z (Oo Ozz-C), inclinical Z (Oo Ozz-C), inclinical Z (Oo Ozz-C), inclinical Z (Oo Ozz-C), inclinical Z (Oo Ozz-C), inclinical Z (Oo Ozz-C), inclinical Z (Oo Ozz-C), inclinical Z (Oo Ozz-C), inclinical Z (Oo Ozz-C), inclinical Z (Oo Ozz-C), inclinical Z (Oo Ozz-C), inclinical Z (Oo Ozz-C), inclinical Z (Oo Ozz-C), inclinical Z (Oo Ozz-C), inclinical Z (Oo Ozz-C), inclinical Z (Oo Ozz-C), inclinical Z (Oo Ozz-C), inclinical Z (Oo Ozz-C), inclinical Z (Oo Ozz-C), inclinical Z (Oo Ozz-C), inclinical Z (Oo Ozz-C), inclinical Z (Oo Ozz-C), inclinical Z (Oo Ozz-C), inclinical Z (Oo Ozz-C), inclinical Z (Oo Ozz-C), inclinical Z (Oo Ozz-C), inclinical Z (Oo Ozz-C), inclinical Z (Oo Ozz-C), inclinical Z (Oo Ozz-C), inclinical Z (Oo Ozz-C), inclinical Z (Oo Ozz-C), inclinical Z (Oo Ozz-C), inclinical Z (Oo Ozz-C), inclinical Z (Oo Ozz-C), inclinical Z (Oo Ozz-C), inclinical Z (Oo Ozz-C), inclinical Z (Oo Ozz-C), inclinical Z (Oo Ozz-C), inclinical Z (Oo Ozz-C), inclinical Z (Oo Ozz-C), inclinical Z (Oo Ozz-C), inclinical Z (Oo Ozz-C), inclinical Z (Oo Ozz-C), inclinical Z (Oo Ozz-C), inclinical Z (Oo Ozz-C), inclinical Z (Oo Ozz-C), inclinical Z (Oo Ozz-C), inclinical Z (Oo Ozz-C), inclinical Z (Oo Ozz-C), inclinical Z (Oo Ozz-C), inclinical Z (Oo Ozz-C), inclinical Z (Oo Ozz-C), inclinical Z (Oo Ozz-C), inclinical Z (Oo Ozz-C), inclinical Z (Oo Ozz-C), inclinical Z (Oo Ozz-C), inclinical Z (Oo Ozz-C), inclinical Z (Oo Ozz-C), inclinical Z (Oo Ozz-C), inclinical Z (Oo Ozz-C), inclinical Z (Oo Ozz-C), inclinic	Homo Sapiens cell-tine N.G.1 transcriptional regulatory protein port tinnyry, compress cas	Homo sapiens 17-beta-nydroxysteroid denydrogenase 19 (nob 1764) gene, exurs o gird 4
Top Hit Database Source	EST_HUMAN	NT	EST HUMAN	L	EST_HUMAN	EST HUMAN	NT	Z	Z	Z	EST HUMAN	TN	NT	EST HUMAN	EST HUMAN	<b>EST HUMAN</b>	IN	IN	EST HUMAN	F	EST HUMAN	EST_HUMAN	EST HUMAN	EST_HUMAN	E		EST_HUMAN		EST HUMAN	Į.	LZ.	NT.
Top Hit Acession No.			.0E-57 AW853964.1	11225608 NT	3.0E-57 BE796537.1	3.0E-57 W 28130.1	11545798	1 (545798)NT	11427757 NT	105262.1	3.0E-57 AU117659.1	11545798 NT	11545798 NT	3.0E-57 AW248374.1	3.0E-57 W 23871.1	3.0E-57 AJ003649.1		2.0E-57 AF246219.1	2.0E-57 AA845419.1	2.0E-57 AL163204.2	2.0E-57 R07702.1	2.0E-57 R07702.1	2.0E-57 AA018299.1	2.0E-57 AA018299.1		İ	2.0E-57 AA016131.1		2.0E-57 BF115266.1	11431281 NT	2.0E-57 AF045452.1	2.0E-57 AF057722.1
Most Similar (Top) Hit BLAST E Vatue	3.0E-57	3.0E-57	3.0E-57	3.0E-57	3.0E-57	3.0E-57	3.0E-57	3.0E-57	3.0E-57	3.0E-57 J05262.1	3.0E-57	3.0E-57	3.0E-57	3.0E-57	3.0E-57	3.0E-57				1												
Expression Signal	1.03	-	51.29	1.25			1.99	1.99			5.14		69'0		6.37			2.80			0.72				7.42		1.48		31.41			1.06
ORF SEQ ID NO:	28993	29827		32675		34945	34966	34967		L											29818						•		4	32813	35449	36891
Exen SEQ ID NO:	15883	16815	16949	١.	1		l	ı	ı	1	ì	22567	L	L	L		<u> </u>	L		1	1	L	L	L	L	1_	18977		19334	19461	21911	23089
Probe SEQ ID NO:	2768	3652	3788	6153	6251	8338	8363	8363	8476	8624	9050	9451	9451	11148	12384	12982	1530	1530	2790	3525	3841	3641	4304	4304	4632		6785		6158	6288	8832	10051

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							0 000	SUG 3	AGE & SIMILER TO SW.: P.N.C.Z. ACADA	Sec0074 E	25:320713				VW0-100001	עאוצווו (פייסבו)		/05040\ m DNA	יוראר ופן, וווראה				CK1), mKNA	4.11	ilex, O subunit (oligomycin sensiuvity		nt, Christmas disease, hemophilia B)			V-140-1-1	J. mcAy	37642.3	
Top Hit Descriptor	Homo sapiens syneptojanin 1 (SYNJ1), mRNA	RCA-NTOAS7-160600-016-b05 NT0057 Homo saplens cDNA	Cara Handa Sacon 127 -07 Illanda Home seriens CDNA	MS-UMUD45-Z-40300-1Z/	CM3-UM0043-240300-127-607 UM0043 Homo sapiens CUNA	CM3-UM0043-240300-12/-e0/ UM0043 Homo sapiens CUNA	CM3-UM0043-240300-127-e07 UM0043 Homo sapiens CLNA	ar98e07.s1NCI_CGAP_Lu5 Homo sapiens cUNA cione IMAGE: 1603906 3	ts89e07.x1 NCI_CGAP_GC6 Homo sapiens cDNA clane IMACE::2238495 3 similar to SW:FRUZ_ACACA P19984 PROFILIN II;	Homo sapiens placenta-specific 1 (PLAC1), mRNA	ym51h07.r1 Sogres infant brain 1NIB Homo sapiens CLIVA clone IMAGE: 32071 3	Homo sapiens chromosome 21 segment HS21C085	Homo saplens apical protein, Xenopus laevis-like (APXL), mRNA	Homo sapiens nibrin (NBS) mRNA, complete cds	Homo sapiens nibrin (NBS) mRNA, complete cds	Homo sapiens holocytochrome c synthase (cytochrome c nemeryase) (news) micha	Homo sapiens hypothetical protain FLJ10826 (FLJ10826), mKNA	Homo sapiens mRNA for KIAA1617 protein, partial cds	Homo sapiens pre-mRNA splicing factor similar to S. cerevisiae Prp 10 (P.M. 10), III.N.M.	Homo sapiens chromosome 21 segment HS210018	Homo capiens mRNA for KIAA0611 protein, partial cds	Homo sapiens mRNA for KIAA0611 protein, partial cds	Homo sapiens cat eye syndrome chromosome region, candidate 1 (CECK1), mixiyA	Homo sapiens acetyl-Coenzyrne A carboxylase alpna (ACACA), mixiva	Homo sapiens ATP synthase, H+ transporting, mitochondrial F1 complex, U subunit (oligomydin sersaravity conferring protein) (ATP50) mRNA	Homo sepiens interleukin 10 receptor, beta (IL10RB), mRNA	Homo sepiens coegulation factor IX (plasma thromboplastic component, Christmas disease, hemophilia B)	(F9) mRNA	Human beta-prime-adaptin (BAM22) gene, exon 3	Human mRNA, Xq terminal portion	Homo sapiens EGF-like repeats and discoldin I-like domains 3 (EL/IL3), mixiva	hy18a02.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:3197642.3	Homo sapiens E18-55kDa-associated protein o (E15-AF5), inche
Top Hit Database Source		T CIC MANNI	T	┪		EST HUMAN C	EST_HUMAN C	EST_HUMAN a	EST_HUMAN P		EST_HUMAN Y			H								NT										T HUMAN	
Top Hit Acession Na	4507334 NT	3	1			5.0E-58 AW 797948.1 E	5.0E-58 AW 797948.1 E	5.0E-58 AA988183.1 E		96282		5.0E-58 AL163285.2 N	11421330 NT	5.0E-58 AF051334.1		4885400 NT	8922693 NT	5.0E-58 AB046837.1	11430647 NT		5.0E-58 AB014511.1	5.0E-58 AB014511.1	11526293 NT	11426423 NT	4502302 NT	4504634 NT		4503648 NT		16470.1	5031660 NT	4.0E-58 BE463857.1	11424059NT
Most Similar (Top) Hit BLAST E Vatue	8 TO 5	3.0L-30	5.0E-58 BE/63984.1	5.0E-58 A	5.0E-58 A	5.0E-58 A	5.0E-58 A	5.0E-58 A	5.0E-58 A1636745.1	5.0E-58	5.0E-58 H23072.1	5.0E-58 A	5.0E-58	5.0E-59 A	5.0E-58 A	5.0E-58	5.0E-58	6.0E-58	5.0E-58	5.0E-58 A	5.0E-58	5.0E-58	5.0E-58	5.05-58	4 0F-58	4 0F-58		4.0E-58	4.0E-58 U36251.1	4.0E-58 D16470.1	4.0E-58	4.0E-58	4.0E-58
Expression Signal	30.8	3.00	96.9	2.9	2.9	2	2	4.09	0.93	1.91	6.55	0.79	1.03	9.0	9.0	0.71	80.6	99.0	96'0	1.8	0.65	0,65	4.5	1.47	1 71	1 87		1.24	212	1.41	-	0.68	7.44
ORF SEQ ID NO:	00200	nacaz	26950	27442	27443	27442	27443	29585			32834	33063	33148	33665	33666	L	L		L	36973		ŀ			26827			27731				ı	38366
Exan SEQ ID NO:	1030,	13527	13910	14382	14382	L		1_	.i	18938	19479	19688	19760	20232	20232	L	L	L	L	1	1	ł	26065	L	l	١.		14649	L.	١.	Į	1	1 1
Probe SEQ ID NO:		311	728	1221	1221	1222	1222	3400	4373	5746	6307	6524	9	6917	6917	7255	8156	8548	10061	10328	10612	10612	12362	12850	à	8 8	2	1496	2696	3402	3834	7995	11624

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Top Hit Descriptor	yg10e02.r1 Soares infant brain 1NIB Homo saplens cDNA clone IMAGE:31693 5	Homo sapiens peptide YY (PYY) mRNA	602/85789F1 NIH_MGC_45 Homo sapiens cDNA clone IMAGE:4309943 6'	602185789F1 NIH_MGC_45 Homo saplens cDNA clone IMAGE:4309943 5	QV0-BT0702-170400-194-f09 BT0702 Homo sapiens cDNA	HSC1TG081 normalized infant brain cDNA Homo sapiens cDNA clone c-1tg08	AV712977 DCA Homo sapiens cDNA clone DCAAZG04 6	Homo sapiens 5-aminolevulinate synthase 2 (ALAS2) gene, complete ods	ba08b07.y1 NIH_MGC_7 Homo septens cDNA clone IMAGE:2823733 5' similar to gb:X69391 60S	RIBOSOMAL PROTEIN L6 (HUMAN); gb:X81987 M.musoulus mKNA for TAX responsive element binding	xe08e09.x1 Source NFL T GBC S1 Homo sabiens cDNA clone IMAGE:2567704.3'	60149961F1 NIH MGC 70 Homo sepions cDNA clone IMAGE 3901911 5	601499961F1 NIH MGC 70 Homo sapiens cDNA clone IMAGE:3901911 5'	UI-H-BW1-ams-g-11-0-UI.s1 NCI_CGAP_Sub7 Homo sapiens cDNA clone IMAGE:3071060 3'	em57e02.x1 Johnston frontal cortex Homo sapiens cDNA clone IMAGE:1539674 3' similar to WP:ZK328.1	CE05065 UBIQUITIN CONJUGATING ENZYMEI; RECOVERIN SUBFAMILY OF EF-HAND CALCIUM	BINDING PROTEIN;	yq08h06.r1 Soares fetal liver spleen 1NFLS Hamo saplens cDNA clone IMAGE:196379 5'	qm84c01.x1 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1895424 3'	Homo sapiens endocytic receptor Endo180 (ENDO180) mRNA, complete cds	Homo sapiens endocytic receptor Endo180 (ENDO180) mRNA, complete cds	601890812F1 NIH_MGC_17 Homo saplens cDNA done IMAGE:4131891 5	hm25f08.x1 NCI_CGAP_Tny4 Homo sapiens cDNA clone IMAGE:3013671 3'	Human complement component C5 mRNA, 3'end	Homo saniens NADH dehtydroxnenase (ubiquinone) 1 beta subcompley 9 (22kD B22) (NDUFB9), mRNA	EST369252 MAGE resequences, MAGD Homo sapiens cDNA	EST369252 MAGE resequences, MAGD Homo sapiens cDNA	Homo saplens partial AF-4 gene, exons 2 to 7 and Alu repeat elements	hy10f08.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:3196935 3'	Homo sapiens uncharacterized bone marrow protein BM038 mRNA, complete cds	Homo sapiens sterol regulatory element binding transcription factor 2 (SREBF2) mRNA	Homo sapiens G protein-coupled receptor 69A (GPR69A) mRNA
Top Hit Database Source	EST_HUMAN		EST_HUMAN	EST_HUMAN	EST HUMAN	EST_HUMAN	EST_HUMAN	NT		TANA IN FOR	Т	Т	Т	Г									EST_HUMAN	ΓŽ	Ę	T HUMAN	Т	Z	EST_HUMAN			
Top Hit Acession No.	3.0E-58 R17879.1	4758981 NT	3.0E-58 BF569848.1	3.0E-58 BF569848.1	3.0E-58 BE089509.1	F07056.1	7.1	2.0E-58 AF068624.1		2 AE 50 DE 20053 4	AW074831 1	2.0E-58 BE907186.1	2.0E-58 BE907186.1	2.0E-58 BF513488.1			2.0E-58 AI124874.1		2.0E-58 AI291407.1				2.0E-58 AW872641.1	1.0E-58 M65134.1	6274549 NT	1.0E-58 AW957182.1	1.0E-58 AW957182.1	1.0E-58 AJ238093.1	1.0E-58 BE466132.1	1.0E-58 AF217514.1	4759169 NT	5174444 NT
Most Simitar (Top) Hit BLAST E Value	3.0E-58	3.05-58	3.05-58	3.0E-58	3.05-58	3.0E-58 F07056.1	3.0E-58	2.0E-58			2.0E-58	2.0E-58	2.0E-58	2.0E-58			2.0E-58	2.0E-58	2.0E-58	2.0E-58	2.0E-58	2.0E-58	2.0E-58	1.0E-58	1 OF.58	1.0E-58	1.0E-58	1.0E-58	1.0E-58	1.0E-58	1.0E-58	1.0E-58
Expression Signal	96.0	2.6	3.07	3.07	0.61	1.1	2.49	12.47		1	0.0	2.53	2,53	1.7			2.16	0.83	0.83	2.79	2.79	16.01	1.58	1.06	133	1.12	1.12	2.8	1.28	1.01	1.14	1.01
ORF SEQ ID NO:		27647			32918	33115	33329				31630		L						33533		33849	37692	37913	26962	27314		]_	27654	١.	L		28322
SEQ ID NO:	13556	14574	L	1	19559	19736	1	14136		14474	1	25805	25805	19358			19423		20119	20389	20389	24058	24276	13922	14258	<u></u>	L	14581	14849	15837		15206
Probe SEQ ID NO:	345	1420	3246	3246	9390	6574	6778	963		0,57	5451	5473	5473	6182			6249	6283	7066	7307	7307	10979	11207	740	1003	1358	1358	1427	1697	2719	2863	2892

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Exon Signal 16791         ORF SEQ Signal 2010         Expression PLASTE PLASTE PLASTE No.         Most Similar No.         Top Hit Acession Value PLASTE No.           16791         100.03         1.0E-58         4758081 N 4507628 N 4507628 N 4507628 N 4507601 N 45076 N 45076 N 45076 N 45076 N 45076 N 45076 N 45076 N 45076 N 45076 N 45076 N 45076 N 45076 N 45077 N 45076 N 45077 N 45076 N 45077 N 45076 N 45077 N 45076 N 45077 N 45076 N 45077 N 45077 N 45077 N 45077 N 45077 N 45077 N 45077 N 45077 N 45077 N 45077 N 45077 N 45077 N 45077 N 45077 N 45077 N 45077 N 45077 N 45077 N 45077 N 45077 N 45077 N 45077 N 45077 N 45077 N 45077 N 45077 N 45077 N 45077 N 45077 N 45077 N 45077 N 45077 N 45077 N 45077 N 45077 N 45077 N 45077 N 45077 N 45077 N 45077 N 45077 N 45077 N 45077 N 45077 N 45077 N 45077 N 45077 N 45077 N 45077 N 45077 N 45077 N 45077 N 45077 N 45077 N 45077 N 45077 N 45077 N 45077 N 45077 N 45077 N 45077 N 45077 N 45077 N 45077 N 45077 N 45077 N 45077 N 45077 N 45077 N 45077 N 45077 N 45077 N 45077 N 45077 N 45077 N 45077 N 45077 N 45077 N 45077 N 45077 N 45077 N 45077 N 45077 N 45077 N 45077 N 45077 N 45077 N 45077 N 45077 N 45077 N 45077 N 45077 N 45077 N 45077 N 45077 N 45077 N 45077 N 45077 N 45077 N 45077 N 45077 N 45077 N 45077 N 45077 N 45077 N 45077 N 45077 N 45077 N 45077 N 45077 N 45077 N 45077 N 45077 N 45077 N 45077 N 45077 N 45077 N 45077 N 45077 N 45077 N 45077 N 45077 N 45077 N 45077 N 45077 N 45077 N 45077 N 45077 N 45077 N 45077 N 45077 N 45077 N 45077 N 45077 N 45077 N 45077 N 45077 N 45077 N 45077 N 45077 N 45077 N 45077 N 45077 N 45077 N 45077 N 45077 N 45077 N 45077 N 45077 N 45077 N 45077 N 45077 N 45077 N 45077 N 45077 N 45077 N 45077 N 45077 N 45077 N 45077 N 45077 N 45077 N 45077 N 45077 N 45077 N 45077 N 45077 N 45077 N 45077 N 45077 N 45077 N 45077 N 45077 N 45077 N 45077 N 45077 N 45077 N 45077 N 45077 N 45077 N 45077 N 45077 N 45077 N 45077 N 45077 N 45077 N 45077 N				_			Γ	Γ	1			T	T	T	T	T		T	T	T	1		13732		E			2		Ī	1		,	8	
Exon NO:         ORF SEQ Signal         Expression (Top) Hit Value         Top Hit Acession Value         Top Hit Acession Value         Top Hit No.         Top Hit Source           16791         28809         0.93         1.0E-58         4758081 NT         House           16791         28810         0.63         1.0E-58         4758081 NT         House           16791         29877         0.66         1.0E-58         44505281 NT         House           18213         31486         7.13         1.0E-58         44505281 NT         House           20138         32465         0.63         1.0E-58         BE061880.1         EST HUMAN           21387         0.67         1.0E-58         BE061880.1         EST HUMAN           22248         35695         0.67         1.0E-58         BRO1761001.1         EST HUMAN           22358         35695         0.67         1.0E-58         BA412397.1         EST HUMAN           22358         35695         0.64         1.0E-58         AA412397.1         EST HUMAN           22358         35695         0.77         1.0E-58         AA412397.1         EST HUMAN           22060         38767         0.74         8.0E-59         AA332291.1         EST H		Top Hit Descriptor	ато sapiens chondrottin sulfate proteoglycan 2 (versican) (CSPG2) mRNA	nomo santena chondroitin sulfate proteoglycan 2 (versican) (CSPG2) mRNA	omo saplens transition protein 1 (during histone to protamine replacement) (TNP1) mRNA	Abund of Same Mathers, St Home santas cONA clone IMAGE: 1678129 3	ZASRIOLIXI SURIES INITIATINI DE L'ARRESTA DE SARIES CINA	ALIACA CASO DE CASO DE CASO DE CASO DE CASO DE CASO DE CASO DE CASO DE CASO DE CASO DE CASO DE CASO DE CASO DE CASO DE CASO DE CASO DE CASO DE CASO DE CASO DE CASO DE CASO DE CASO DE CASO DE CASO DE CASO DE CASO DE CASO DE CASO DE CASO DE CASO DE CASO DE CASO DE CASO DE CASO DE CASO DE CASO DE CASO DE CASO DE CASO DE CASO DE CASO DE CASO DE CASO DE CASO DE CASO DE CASO DE CASO DE CASO DE CASO DE CASO DE CASO DE CASO DE CASO 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nomotog z (criapsyn-110) (DLOZ), m. v.n.	i sapiens immunoglobulin kappa light chain variable region L14	Juman MSH3 gene, exon10	domo sapiens TATA box binding protein (1BP) mRNA	ST95683 Tests I Hamo seplens cDNA 5' end	EST95683 Testis I Homo seplens cDNA 5' end	vh50d06.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2384171 3	301458531F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3862088 51	water control CGAP Kirs Homo septens cDNA clone IMAGE:1553550 3' similar to TR:Q13732 C	SA GENE PRODUCT PRECURSOR;	:n06h02.y1 Normal Human Trabecular Bone Cells Homo sapiens cDNA clone NHTBC_cn06h02 rand	#f48c11.x1 Soares_NFL_T_GBC_S1 Homo septens cDNA clone IMAGE:2336636 3	H.sapiens DNA for ZNF80-linked ERV9 long terminal repeat	au68c07.xf Schnelder fetal brain 00004 Homo sapiens cDNA clone IMAGE:2/81228 3 Similar to come to the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the 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KIAA0184 gene, partial cds	Homo sapiens phosphatidylinositol-4-phosphate 5-kinase, type II, beta (PIPSKZB) mKNA, and translated	products
Exon NO: 16791         ORF SEQ Signel         Expression (Top) Hit PLAST E         Top Hit Acession Value           16791         29809         0.93         1.0E-58         4758081           16791         29877         0.66         1.0E-58         4758081           16791         29877         0.66         1.0E-58         4758081           16791         29877         0.66         1.0E-58         4758081           16791         23860         0.83         1.0E-58         4758081           16791         23860         0.83         1.0E-58         4758081           16791         33566         0.49         1.0E-58         4758081           20138         33560         0.49         1.0E-58         AV412337.1           21469         36695         0.62         1.0E-58         AV412337.1           22260         38802         0.77         1.0E-58         AV412397.1           22358         35908         0.64         1.0E-58         AV412397.1           22358         35907         0.65         1.0E-58         AV412397.1           20207         33635         0.74         8.0E-59         AV382291.1           20207         33636         0.74							╗	HOMAN		HUMAN		П	$\neg$	T HUMAN					T_HUMAN		Т	Т	Т			HUMAN			T_HUMAN		EST_HUMAN		LN.		<u> </u>
Exon NO:         ORF SEQ Signal         Expression Signal         (Top) Hit PLAST E           1679-1         28809         0.93         1.0E-58           1679-1         28810         0.93         1.0E-58           1679-1         28810         0.93         1.0E-58           1679-1         28977         0.66         1.0E-58           1679-1         28977         0.66         1.0E-58           22149         35569         0.49         1.0E-58           22149         35695         0.62         1.0E-58           22358         35907         0.64         1.0E-58           22358         35907         0.64         1.0E-58           22358         35907         0.64         1.0E-58           22358         35907         0.64         1.0E-58           22358         35907         0.64         1.0E-58           220507         33635         0.74         8.0E-59           20207         33635         0.74         8.0E-59           16006         1.0E-58         0.74         8.0E-59           16006         0.69         0.65         0.65           16006         0.74         8.0E-59		fop Hit Acession No.	4758081	1750004	47.0001	07070			2031		5314				11432994			4507378	4A382291.1		l		DI DOCULI.	AA962431.1	A1750970.1	Al807484.1	X83497.1		AW162		5.0E-59 AV762869.1	11434908 NT	4.0E-59 D80006.1		ASOSB1B NT
Exon SEQ ID ID NO: Signal NO: Signal NO: Signal NO: Signal NO: Signal NO: Signal NO: Signal NO: Signal NO: Signal NO: Signal NO: Signal NO: Signal NO: Signal NO: Signal NO: Signal NO: Signal NO: Signal NO: Signal NO: Signal NO: Signal NO: Signal NO: Signal NO: Signal NO: Signal NO: Signal NO: Signal NO: Signal NO: Signal NO: Signal NO: Signal NO: Signal NO: Signal NO: Signal NO: Signal NO: Signal NO: Signal NO: Signal NO: Signal NO: Signal NO: Signal NO: Signal NO: Signal NO: Signal NO: Signal NO: Signal NO: Signal NO: Signal NO: Signal NO: Signal NO: Signal NO: Signal NO: Signal NO: Signal NO: Signal NO: Signal NO: Signal NO: Signal NO: Signal NO: Signal NO: Signal NO: Signal NO: Signal NO: Signal NO: Signal NO: Signal NO: Signal NO: Signal NO: Signal NO: Signal NO: Signal NO: Signal NO: Signal NO: Signal NO: Signal NO: Signal NO: Signal NO: Signal NO: Signal NO: Signal NO: Signal NO: Signal NO: Signal NO: Signal NO: Signal NO: Signal NO: Signal NO: Signal NO: Signal NO: Signal NO: Signal NO: Signal NO: Signal NO: Signal NO: Signal NO: Signal NO: Signal NO: Signal NO: Signal NO: Signal NO: Signal NO: Signal NO: Signal NO: Signal NO: Signal NO: Signal NO: Signal NO: Signal NO: Signal NO: Signal NO: Signal NO: Signal NO: Signal NO: Signal NO: Signal NO: Signal NO: Signal NO: Signal NO: Signal NO: Signal NO: Signal NO: Signal NO: Signal NO: Signal NO: Signal NO: Signal NO: Signal NO: Signal NO: Signal NO: Signal NO: Signal NO: Signal NO: Signal NO: Signal NO: Signal NO: Signal NO: Signal NO: Signal NO: Signal NO: Signal NO: Signal NO: Signal NO: Signal NO: Signal NO: Signal NO: Signal NO: Signal NO: Signal NO: Signal NO: Signal NO: Signal NO: Signal NO: Signal NO: Signal NO: Signal NO: Signal NO: Signal NO: Signal NO: Signal NO: Signal NO: Signal NO: Signal NO: Signal NO: Signal NO: Signal NO: Signal NO: Signal NO: Signal NO: Signal NO: Signal NO: Signal NO: Signal NO: Signal NO: Signal NO: Signal NO: Signal NO: Signal NO: Signal NO: Signal NO: Signal NO: Signal NO: Signal NO: Signal NO: Signal NO: Signal NO: Sig	-		1 0F.58	3 5	1.05-58	1.0E-38	1.0E-58 A	1.0E-58 E	1.0E-58	1.0E-58 /	1.0E-58	1.0E-58	1.0E-58	1.0E-58	1.0E-58	1.0E-58	1.0E-58	8 0E-59	8.0E-59	8 OF 59	9 JE 50	8.75	0.00							L	L	5.0E-59			7 00 50
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		Exan SEQ ID NO:	40704	IR/91	16791	16974	18213	19150	20138	21387	22149	22260	22358	22358	1	1	1	1	- 1	1		L	16005		l						1_	١.	l_	$\perp$	
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Top Hit Descriptor	Horno sepiens phosphatidylinositol 4-phosphate 5-kinase, type II, beta (PIP5K2B) mRNA, and translated products	Homo sapiens ryanodine receptor 3 (RYR3) mRNA	Homo sapiens ryanodine receptor 3 (RYR3) mRNA	Homo sepiens caterin (cadhern-associated protein), delta 2 (neural plakophilin-related arm-repeat protein) (CTNND2); mRNA	Homo sapiens 17-beta-hydroxysteroid dehydrogenase IV (HSD17B4) gene, promoter region and exon 1	EST377582 MAGE resequences, MAGI Homo sepiens cDNA	Homo sapiens KIAA0680 gene product (KIAA0580), mRNA	Homo sapiens plasminogen activator, tissue (PLATa) mRNA	Homo sapiens plasminogen activator, tissue (PLATa) mRNA	Homo sapiens mRNA for KIAA1112 protein, partial cds	Homo sapiens mRNA for KIAA1112 protein, partial cds	h02017t Testis 1 Homo sapiens cDNA clone h02017 5' end	h02017t Testis 1 Homo sapiens cDNA clone h02017 5' end	Homo saplens A kinase (PRKA) anchor protein 1 (AKAP1), mRNA	Homo sapiens A kinase (PRKA) anchor protein 1 (AKAP1), mRNA	Homo sapiens zona pellucida glycoprotein 2 (sperm receptor) (ZP2) mRNA	Homo sapiens chromosome 21 segment HS21C084	Homo sapiens protein tyrosine phosphatase, receptor type, T (PTPRT), mRNA	Human prohormone converting enzyme (NEC2) gene, exon 2	Homo sapiens hypothetical protein PR01741 (PR01741), mRNA	Homo sapiens nuclear receptor co-repressor 1 (NCOR1), mRNA	Human mRNA for dbl proto-oncogene	Human mRNA for dbl proto-oncogene	H. sapiens CKII-alpha gene	H. sapiens CKII-alpha gene	Homo sapiens gamma-glutamyttransferase-like activity 1 (GGTLA1), mRNA	zi98d05,s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:730377 3'	Homo sapiens interferon-induced protein p78 (MX1) gene, complete cds	EST180633 Jurkat T-cells V Homo sapiens cDNA 5' end	RCO-NT0036-100700-032-e07 NT0036 Homo sapiens cDNA	กิดวิทิง4.x1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:2861654 5'
Top Hit Database Source	FZ	NT	TN	TN	FZ	EST_HUMAN	Ŋ		ΤN	NT	LΝ	EST_HUMAN	EST_HUMAN	NT	NT	NT	LN	ΝT	NT	IN	TN	ΙN	Ν	ΙZ	LZ	Z	EST_HUMAN	LN	EST HUMAN	EST HUMAN	EST_HUMAN
Top Hit Acession Na	4505B18 NT	4506758 NT	4506758 NT	11034810 NT	4.0E-59 AF057720.1	3.0E-59 AW965524.1	7662247 NT	4505860 NT	4505860 NT	3.0E-59 AB029035.1	3.0E-59 AB029035.1	3.0E-59 T18865.1	3.0E-59 T18865.1	4502014 NT	4502014 NT	4508044 NT	3.0E-59 AL163284.2	7427522 NT	3.0E-59 M95961.1	8924074 NT	5454137 NT	3.0E-59 X12556.1	3.0E-59 X12556.1	3.0E-59 X70251.1	3.0E-59 X70251.1	11417866 NT	2.0E-59 AA470073.1	2.0E-59 AF135187.1	2.0E-59 AA309774.1	2.0E-59 BF365554.1	2.0E-59 AW410698.1
Most Similar (Top) Hit BLAST E Value	4.0E-59	4.05-59	4.0E-59	4.0E-59	4.0E-59	3.0E-59	3.0E-59	3.0E-59	3.0E-59	3.0E-59	3.0E-59	3.0E-59	3.0E-59	3.0E-59	3.0E-59	3.0E-59	3.0E-59	3.0E-59	3.0E-59	3.0E-59	3.0E-59	3.0E-59	3.0E-59	3.0E-59	3.0E-59	3.0E-59	2.0E-59	2.0E-59	2.0E-59	2.0E-59	2.0E-59
Expression Signal	0.61	1.14	1.14	0.95	3.89	6.74	3.88	10.81	10.81	8.54	8.54	0.67	0.67	4.27	4.27	1.19	2.75	2.12	1.22	2.4	1.85	1.11	1.11	1.04	1.04	11.11	0.59	0.59	4.84	1.34	2.19
ORF SEQ ID NO:	27490		31033	32130			26481	78872		28459	28490			29383	29384	98008	30929	14018		32877		[	34719		36881			33494			37780
Exan SEQ ID NO:	14423	1	18042	18848	25996	13248	13455			15333	15333			16374	16374			L		19520		ı	<u></u>	L	23285	25428	20259	20081	22877		24144
Probe SEQ ID NO:	1266	4912	4912	5654	12498	õ	234	1748	1748	2198	2198	3104	3104	3199	3199	3930	4808	4965	5162	6350	7516	8116	8116	10250	10250	12635	6946	7216	9837	10745	11069

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
100	04444	97784	2 10	20	F-59 AW 410698 1	EST HUMAN	fh07h04.x1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:2961654 5'
200	74144				Γ		wa36c12.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2300182 3' similar to TR:Q86642
12373	25266	32118	4.28	2.0		EST_HUMAN	Q86542 RTVL-H PROTEIN, contains LTR7.bt LTR7 repetitive element;
12963	26019			2.0		Ę	Home capiens alpha-tubulin mixink, complete cus
167	13392		5.65	1.0	-	EST_HUMAN	8011/6/5/F1 NIH MIGC. II Florida Sapiens Come more more more properties of semilar to SP-S21348
1569	14722	27803	40.	1.0	E-59 T92522.1	EST_HUMAN	ye25c09.r1 Strategene lung (#84/210) homo saplens curvo curre invoca o current S21348 HYPOTHETICAL PROTEIN 4 -:
2683	<u> </u>				1.0E-59 AA748468.1	EST_HUMAN	oa56h11.s1 NCI_CGAP_GCB1 Homo saplens cUNA done IMACE: 309028.3 similar to 17.3 15001 Q13637 MER37 TRANSPOSABLE ELEMENT, COMPLETE CONSENSUS SEQUENCE :
7735	20796	34285	1.14		AJ130894.1	Z	Homo sepiens mKNA for transcription tectual NA Plane WAA DE 3282802 R
7895	20947	34454	1.3		0E-59 BE256814.1	EST HUMAN	601111951F1 NIH_MGC_16 Home sapients converging him MAGE 325262 5
7895	Ĺ			1.	BE2568	EST_HUMAN	601111951F1 NIH MGC 16 Homo sapiens culvA cigne invivor. 3302092.3
9585	1	36296		1.		LN.	Homo sapiens zinc tinger protein 2/0 (Zivi 2/0), tiliniva
9804	1			1		Ĭ	Homo sapiens 3-hydroxylsdoutyry-coertsyme A hydrodase (HIBCH) mRNA
9804	1	36422	0.58		11428849 NT	Į,	Homo sapiens 3-hydroxylsodulyry-cuentygine A hydrodeso (moorly, missis
11094	20796	_	10.98		1.0E-59 AJ130894.1	Į.	Home sapiens mkink for transcription racion
783	L		1.45		AW9778	EST HUMAN	ES (389849 MACE resequences, MACO fullio sequences control (SANPDIN) MRNA
1499	Ĺ					LN.	Homo sapiens small nuclear ribonucieopirusii Da polybepuce (1982) (1982) (1982) (1982) (1982) (1982)
2241	_					INT	Homo saplens differentiation-related gene 1 (moket-specific induction protein) (RTP) mRNA
2241	L	4 28503	3 4.76	8	5174656 NT	LN 15	Homo sapiens differentiation defaute general (incher-specific included process)
6103	19283	3 32616	1.16	80	0E-60 AB029004.1	F.	Homo sapiens mKNA for KIAA 1001 protein, partial cus
6833	19792	33181	0.89	_	8.0E-60 S83182.1	N	hyaluronan-binding protein≂hepatocyte growth factor activator homolog [human, plasma, mRNA, 2408 nt]
7874	L.	L			11420841 NT	TN	Homo sapiens phosphate cylidylytransterase 1, choline, beta isolomi (FC 1 1 to), iliniya
8152	L		5	3 8.0E-60	X17033.1	INT	Human mRNA for integrin alpha-2 subunit
9139	L				11428949 NT	INT	Homo saplens S-antigen; retina and pineai gland (arrestin) (SAC), minux
9871	L	L	2 0.78		11417118 NT	3 NT	Homo sapiens KIAA0433 protein (KIAA0433), mKNA
9671	1_	3 36203			11417118 NT	3 NT	Homo sapiens KIAA0433 protein (KIAA0433), mKNA
10799	1_			L	8.0E-60 5453997 NT	7NT	Homo sapiens RAN binding protein 7 (RANBF7), mRNA
11071	L	L		L	0 AL163204.2	IN	Homo saplens chromosome 21 segment in 22 rough
11071	丄	L		L	0 AL163204.2	N	Homo sapiens chromosome 21 segment H321 C004
773	L		11.11		.0E-60 AF055066.1	Į.	Homo sepiens MHC class 1 region
774	L	27004	25.11	4	AF05506	۲	Homo saplens MHC class 1 region
838	1			7 7.0E-60	0 4504634 NT	4 NT	Homo sapiens interfeukin 10 receptor, pera (IL 10Kb), riinvin

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Top Hit Descriptor	Homo sapiens cullin 4A (CUL4A) mRNA, complete cds	Homo sapiens mRNA for KIAA0581 protein, partial cds	Homo sapiens omithine decarboxylase 1 (ODC1) mRNA	Homo sapiens ALR-like protein mRNA, partial cds	yr12704.r1 Soares fetal liver splean 1NFLS Homo sapiens cDNA clone IMAGE:205087 5' similar to contains	LTR5 repetitive element ;	yr12f04.r1 Soares fetal liver spleen 1NFLS Homo saplens cDNA clone IMAGE:205087 5' similar to contains.	CLISCO TENENTS WITH VICTOR OF LIBERT AND A JOHN (MACE 2000DD) 2.	501638751R1 NIH MGC 69 HOM6 Saplens CLINA GOTE IMAGE: 3000008 3	yq78h09.r1 Scares fetal liver spleen 1NFLS Homo sepiens cDNA clone IMAGE:201863 5 similar to contains. OFR repetitive element ;	wf52c07.x1 Soares_NRT_GBC_S1 Homo sapiens cDNA clone IMAGE:2359212.3'	wf52c07.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:23592123'	UI-HF-BN0-akt-g-07-0-UI.r1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3078348 5	UI-HF-BN0-akt-g-07-0-UI.r1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3078348 5	EST11498 Uterus Homo sapiens cDNA 5' end similar to similar to retrovirus-related pol	Treff05.x1 NCI_CGAP_Kid11 Homo sepiens cDNA clone IMAGE:3134913 3' similar to SW:RHOP_MOUSE Q61085 GTP-RHO BINDING PROTEIN 1;	Homo sapiens chromosome 21 segment HS21C078	601336446F1 NIH_MGC_44 Homo saplens cDNA done IMAGE:3690395 5	601336446F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3690395 5'	Homo saptens prohibitin (PHB) mRNA	Homo sapiens Xq pseudoautosomal region; segment 1/2	QV4-NN1149-250900-423-f01 NN1149 Homo sapiens cDNA	RC3-LT0023-200100-012-a01 LT0023 Homo sapiens cDNA	ol60h11.y5 NCI_CGAP_Kid3 Homo sapiens cDNA clone IMAGE:1534053 5' similar to SW:JDP_MOUSE	P52624 URIDINE PHOSPHORYLASE;	Homo sapiens proline dehydrogenase (proline axidase) (PRODH) mRNA	Homo sapiens proline dehydrogenase (proline oxidase) (PRODH) mRNA	ox58d09.x1 Soares_NhHMPu_S1 Homo septens cDNA clone IMAGE:1660337 3' similar to SW:FORM_MOUSE Q05860 FORMIN ;	Homo sapiens proline dehydrogenase (proline oxidase) (PRODH) mRNA	ab07h04.r1 Stratogene lung (#837210) Homo sapiens cDNA clone IMAGE:840151 5' similar to contains LTR10.t1 LTR10 repetitive element ;
Top Hit Database Source	N.	ΤN	TN	N		EST_HUMAN	TACE OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY	EST TOWNS	EST_HUMAN	EST HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	L	EST_HUMAN	EST HUMAN	FZ	TN	EST_HUMAN	EST_HUMAN		EST_HUMAN	NT	TN	EST HUMAN	F	EST_HUMAN
Top Hit Acession No.	7.0E-60 AF077188.1	7.0E-60 AB011153.1	4505488 NT	7.0E-80 AF264750.1		7.0E-60 H58041.1		.UE-60   13604   . 1	6.0E-60 BE964974.2	6.0E-60 H52456.1	5.0E-60 AI807917.1	5.0E-60 AI807917.1	4.0E-60 AW 503208.1	4.0E-60 AW 503208.1	4.0E-60 AA299037.1	4.0E-60 BF196068.1	4.0E-60 AL163278.2	3.0E-60 BE562611.1	3.0E-60 BE562611.1	6031190 NT	3.0E-60 AJ271735.1	3.0E-60 BF365143.1	3.0E-60 AW836196.1		3.0E-60 AI792814.1	5174644 NT	5174644 NT	3.0E-60 Al040235.1	5174644 NT	3.0E-60 AA485286.1
Most Similar (Top) Hit BLAST E Value	7.0E-60/	7.0E-60	7.0E-60	7.0E-80/		7.0E-60	L	7.00-00	6.0E-60	6.0E-60	5.0E-60	5.0E-60	4.0E-60	4.0E-60	4.0E-60	4.0E-60	4.0E-60	3.0E-60	3.05-60	3.0E-60	3.0E-60	3.0E-60	3.05-60		3.0E-60	3.0E-60	3.05-60	3.0E-60	3.0E-60	3.0E-60
Expression Signal	1.82	96.0	2.4	16.0		4.21		2/:	1.16	8.04	1.06	1.06	1.83	1.83	1.45	0.78	0.65	4.98	4.98	2.81	2.75	0.69	2.21		1.07			0.6	3.84	1.55
ORF SEQ ID NO:		29068		30818		36235			28509		26348	26349	28574	28575		34055			28162		30699	31709	32251				35216		35560	
Exan SEQ ID NO:	1	15959	L	17833	1	22062		н	15381	21712	13321	13321		1	16213	20582		15050	15050	15061	17716	18693	18949		18520	21678	21678	21862	1	
Probe SEQ ID NO:	2197	2845	4295	4698		2096	9,01	9	2248	8632	88	88	2308	2308	3037	7508	9326	1907	1907	1918	4579	5494	5757		7093	8597	8597	8783	8940	13053

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	Top Hit Descriptor	Homo sapiens solute carrier (SLC25A18) mRNA, complete cds; nuclear gene for mitochondrial product	H.sapiens 41kDa protein kinase related to rat ERK2	Human bcr protein mRNA, 5' end	Homo sapiens v-raf murine sarcoma viral oncogene homolog B1 (BRAF) mRNA	Homo sapiens chromosome 21 unknown mRNA	motf12 v5 NCI CGAP Cc9 Homo saplens cDNA clone IMAGE:1076495 5' similar to contains THR.t1 THR	repetitive element ;	Homo sapiens pro-alpha 2(1) collagen (COL1A2) gene, complete cos	Homo sapiens DNA polymerase zeta catalytic subunit (REV.5) minning, comprete cus	Hamo sapiens corticotropin releasing hormone receptor 2 (CKHK2) mKNA	Homo sapiens corticotropin releasing hormone receptor 2 (Charks) mayor	EST181949 Jurkat T-cells V Homo saplens cDNA 5 end similar to similar to proutynically, alpha	EST181949 Jurkat T-cells V Homo saplens cDNA 5 end similar to similar to proutyniusin, aprila	UFH-BW1-amu-c-02-0-UI.s1 NCI_CGAP_Sub/ Home sapens convenient invacing invacing invacing invacing invacing invacing invacing invacing invacing invacing invacing invacing invacing invacing invacing invacing invacing invacing invacing invacing invacing invacing invacing invacing invacing invacing invacing invacing invacing invacing invacing invacing invacing invacing invacing invacing invacing invacing invacing invacing invacing invacing invacing invacing invacing invacing invacing invacing invacing invacing invacing invacing invacing invacing invacing invacing invacing invacing invacing invacing invacing invacing invacing invacing invacing invacing invacing invacing invacing invacing invacing invacing invacing invacing invacing invacing invacing invacing invacing invacing invacing invacing invacing invacing invacing invacing invacing invacing invacing invacing invacing invacing invacing invacing invacing invacing invacing invacing invacing invacing invacing invacing invacing invacing invacing invacing invacing invacing invacing invacing invacing invacing invacing invacing invacing invacing invacing invacing invacing invacing invacing invacing invacing invacing invacing invacing invacing invacing invacing invacing invacing invacing invacing invacing invacing invacing invacing invacing invacing invacing invacing invacing invacing invacing invacing invacing invacing invacing invacing invacing invacing invacing invacing invacing invacing invacing invacing invacing invacing invacing invacing invacing invacing invacing invacing invacing invacing invacing invacing invacing invacing invacing invacing invacing invacing invacing invacing invacing invacing invacing invacing invacing invacing invacing invacing invacing invacing invacing invacing invacing invacing invacing invacing invacing invacing invacing invacing invacing invacing invacing invacing invacing invacing invacing invacing invacing invacing invacing invacing invacing invacing invacing invacing invacing invacing invacing invacing invacing invacing invacing inva	HS15BEST human adult testis Homo sapiens cDNA clone CAM ES 110	Human pre-B cell stimulating factor homologue (SDF1b) mkNA, complete cus	Homo sapiens sema domain, transmembrane domain (TM), and cytopiasmic domain, (semaphorin) od (SEMAGA), mRNA	Homo sapiens sema domain, transmembrane domain (TM), and cytoplasmic domain, (semaphorin) by	(SEMACA), MINA	Homo sapiens ribosome procen so writese, euch, pulyequae 3 (14 cossy), missis	Homo sepiens non-nistone critornosome protein z (o. cerevisiac) minor (cr. ii. e. r. ii. ii. e. ii. ii. e. ii. ii. e. ii. e. ii. e. ii. e. ii. e. ii. e. ii. e. ii. e. ii. e. ii. e. ii. e. ii. e. ii. e. ii. e. ii. e. ii. e. ii. e. ii. e. ii. e. ii. e. ii. e. ii. e. ii. e. ii. e. ii. e. ii. e. ii. e. ii. e. ii. e. ii. e. ii. e. ii. e. ii. e. ii. e. ii. e. ii. e. ii. e. ii. e. ii. e. ii. e. ii. e. ii. e. ii. e. ii. e. ii. e. ii. e. ii. e. ii. e. ii. e. ii. e. ii. e. ii. e. ii. e. ii. e. ii. e. ii. e. ii. e. ii. e. ii. e. ii. e. ii. e. ii. e. ii. e. ii. e. ii. e. ii. e. ii. e. ii. e. ii. e. ii. e. ii. e. ii. e. 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riyond rulesus box	AU119344 HEMBA1 Home sapiens count civile nembal court
	Top Hit Database Source	LN	LN LN	L	LZ	LN.		EST_HUMAN	NT	NT	NT	NT	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	LNT	ΤN		Į.	N	Ŋ	Þ	N	EST_HUMAN	EST_HUMAN	LΝ	EST_HUMAN		EST_HUMAN	EST_HUMAN	LN-	EST HUMAN
	Top Hit Acession No.	5.1			1757867	OE 60 A F921010 1		2.0E-60 AI791952.1	2.0E-60 AF004877.1	2.0E-60 AF157476.1	4503044 NT	4503044 NT	2.0E-60 AA311159.1	2.0E-60 AA311159.1	2.0E-60 BF512808.1	2.0E-60 X85597.1	2.0E-60 L36033.1	11991659 NT		11991659 NT	11434729 NT	11418192 NT	2.0E-60 AF068757.1	2.0E-60 AB011399.1	1.0E-60 BE178586.1	1.0E-60 AU143389.1	1.0E-60 AL163285.2	1.0E-60 BE064410.1		1.0E-60 AA244041.1	1.0E-60 AV754081.1	1.0E-60 AJ252313.1	9.0E-61 AU119344.1
	Most Similar (Top) Hit BLASTE	20E-60	2.0F-60 Z11694.1	2 DE-80 M24803 1	205-60	7 05 50 0	4.0E-00	2.0E-60	2.0E-60/	2.0E-60	2.0E-60	2.0E-60	2.0E-60	2.0E-80	2.05-60	2.0E-60	2.0E-60	2.0E-60			2.0E-60			2.0E-60			L						
	Expression Signal	1.7	9 00	66	2.2	22.0	0.73	0.85	1.26	1.08		2.15	8.18	8.18	6.0	1.33	3.12			1.83	1.7	2.36	1.47	1.5	1.02		257	1.39		2.84	1.35	1.49	8.4
	ORF SEO ID NO:	26273	276BB	10000	2007	2000	30190	32964	١	١	L			L		34799	١			36814					26752			Ì.			35601		3 27343
	Econ SEQ ID NO:	13269	ace,	200	000	700	1/182	19598	19781	1	Ł.		1_	L	1_	L	1	<b>L</b>	1_	23220	L		25985	<u> </u>	13728	L_	1	1_	L	22034	J	26079	L
	Probe SEQ ID NO:	8	,	2 5	200	2000	4025	6430	8621	6855	6869	6869	7259	7259	7810	8194	800	2000	2	10183	11759	12672	12829	12848	535	4011	5070	8134		8955	8982	12606	1123

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Top Hit Descriptar	Homo sapiens PHD finger protain 2 (PHF2) mRNA	Homo sapiens PHD finger protein 2 (PHF2) mRNA	wt05b10,x1 NCI_CGAP_Cc3 Homo saplens cDNA clone IMAGE:2506555 3'	wt05b10.x1 NCI_CGAP_Cc3 Homo sapiens cDNA clone IMAGE:2506555 3'	Human endogenous retrovirus pHE.1 (ERV9)	nn59g06.s1 NCI_CGAP_Lar1 Homo sapiens cDNA clone IMAGE:1088218 3'	Homo sapiens PXR2b protein (PXR2b), mRNA	Homo sapiens PXR2b protein (PXR2b), mRNA	601300938F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3635480 5	601300938F1 NIH_MGC_21 Homo saplens cDNA clone IMAGE:3635480 5	Homo sapiens PRO2014 mRNA, complete cds	601109238F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3350145 5	m68h09.s1 NCI_CGAP_Lar1 Homo sapiens cDNA clone IMAGE:1088897 3'	AU130689 NT2RP3 Home sapiens cDNA done NT2RP3001263 5	Ig-beta/B29=CD79b (alternatively spliced) [human, B cells, mRNA Partial, 375 nt]	Human autosomal dominant polycystic kidney disease protein 1 (PKD1) gene	Homo sapians general transcription factor 2-I (GTF2I) mRNA, complete cds	601300938F1 NIH_MGC_21 Home sapiens cDNA clone IMAGE:3635480 5'	Human breakpoint cluster region (BCR) gene, complete cds	Homo saplens hypothetical protain FLJ11316 (FLJ11316), mRNA	Homo sapiens hypothetical protein FLJ11316 (FLJ11316), mRNA	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA	Homo saplens protein phosphatase 1, regulatory subunit 10 (PPP1R10) mRNA	Homo sapiens chromosome 21 segment HS21C079	Homo sapiens amyloid beta (A4) precursor protein (protease nexin-ll, Alzheimer disease) (APP), mRNA	Homo saplens 959 kb contig between AML1 and CBR1 on chromosome 21q22; segment 1/3	Homo sapiens T-cell lymphama invasion and metastasis 1 (TIAM1) mRNA	AU140307 PLACE2 Homo sepiens cDNA done PLACE2000302 5'	Homo sapiens DKFZP568B023 protein (DKFZP566B023), mRNA	AV731140 HTF Homo sapiens cDNA clone HTFARB01 5'	AF150190 Human mRNA from cd34+ stem cells Homo sapiens cDNA clone CBDAGB04	Homo saplens hypothetical protein FLJ11026 (FLJ11026), mRNA	QV3-HT0513-060400-147-d01 HT0513 Homo sapiens cDNA
Top Hit Database Source	۲	F	EST_HUMAN	EST_HUMAN	TN	EST_HUMAN	TN	NT	EST_HUMAN	EST HUMAN	NT	EST_HUMAN	EST_HUMAN	EST_HUMAN	N⊤	ΓN	N⊤	EST HUMAN	TN	NT	TN	NT	INT	NT	- E	Į.	NT	EST_HUMAN	, N⊤	EST_HUMAN	EST_HUMAN	NT	EST_HUMAN
Top Hit Acession No.	4885546 NT	4885546 NT	8.0E-61 AW006478.1	1.8.1		3.1	7706670 NT	7706670 NT	6.0E-61 BE409310.1		6.0E-61 AF119860.1	6.0E-61 BE257400.1	6.0E-61 AA596033.1	6.0E-61 AU130689.1	6.0E-61 S79249.1	6.0E-61 U24498.1	6.0E-61 AF035737.1	6.0E-61 BE409310.1	100001	8922890 NT	8922990 NT	4507500 NT	4506008 NT	.0E-61 AL163279.2	4502166 NT	5.0E-61 AJ229041.1	4507500 NT	4.0E-61 AU140307.1	7861637 NT	4.0E-61 AV731140.1	3.0E-61 AF150190.1	8922829 NT	.0E-61 BE168410.1
Most Similar (Top) Hit BLAST E Value	9.0E-61	9.0E-61	8.0E-61	8.0E-61	8.0E-61 X57147.1	8.0E-61	7.0E-61	7.0E-61	6.0E-61	6.0E-61	6.0E-61	6.0E-61	6.0E-61	6.0E-61	6.0E-61	6.0E-61	6.0E-61	6.0E-61	6.0E-61 U07000.1	5.0E-81	5.0E-61	5.0E-61	5.0E-81	5.0E-81	5.0E-61	5.0E-61	5.0E-61	4.0E-61	4.0E-61	4.0E-61	3.0E-61	2.0E-61	2.0E-61
Expression Signal	0.63	0.53	1,41	1.41	2.63	1.03	0.79	67.0	3.06	6.49	12.72	1.04	2.91	8.16	2.96	1.49	1.85	1.68	1.42	2.54	2.64	2.0	2.84	2.19	1.82	222	0.75	1.94	0.71	9.47	2.0	1.8	5.33
ORF SEQ ID NO:	35526	35527	28965	28966		34679	26389	26390	26524	27068	27579	L		L	32677	34045						28612	27953		29462				32435				
Exon SEQ ID NO:	21987		Ì_	L	16192	<u> </u>	1	1			14507	ı	ı	16553	1	l	1	14012		13448	13448	13579	14864	16277	16442			1	19122	25252	i i	l	14398
Probe SEQ ID NO:	8908	8908	2735	2735	3016	8079	130	130	276	834	1352	1659	1679	3381	6155	7497	7795	12564	13157	226	228	370	1713	. 3101	3268	4090	5118	1798	5936	12349	8616	511	1239

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| Top Hit Descriptor                             | QV3-HT0513-060400-147-d01 HT0513 Hamo sapiens cDNA                                                                                                                          | yd53d11.s1 Soares fetal iver spleen 1NFLS Homo sepiens cDNA clone IMAUE 748433 3 simular to<br>gb.1.25444 60S RIBOSOMAL PROTEIN L35A (HUMAN);                                                                                  | yyo3f11.r1 Soares melanocyte 2NbHM Homo saplens cDNA clone IMAGE:2/0169 o                                                                                                                                                                                                                               | Homo sapiens ATPase, H+ transporting, Iysosomal (vacuolar proton pump) non-catalytic accessory process<br>1A (110/116kD) (ATP6N1A), mRNA                                                                                                                                                                                                              | AV694317 GKC Homo sapiens cDNA clone GKCELG06 5                                                                                                                                                                                                                                                                                                                                                                        | Home sapiens mRNA for KIAA0536 protein, partial cds                                                                                                                                                                                                                                                                                                                                                                                                                                                  | U-FRT-BNU-ard 4-12-0-01,1 1 Will mod                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | Inomio sapiens poymates (1997) (Caramater Proping 1 A4 (RPI 44) mRNA                                                                                                                                                                                                                                                                                                                                                             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|                                                | Exon         ORF SEQ         Expression         (Top) Hit Acession           SEQ ID         ID NO:         Signal         BLAST E         No.           Velue         Velue | Exon         ORF SEQ         Expression         (Top) Hit Acession           SEQ ID         ID NO:         Signal         BLASTE         No.           NO:         Value         Value         5.33         2.0E-61 BE168410.1 | Exon         ORF SEQ         Expression Signal         (Top) Hit Acession Signal         (Top) Hit Acession No.           NO:         ID NO:         Signal         BLASTE No.         No.           14398         27461         5.33         2.0E-61 BE168410.1           136         2.0E-61 NS3039.1 | Exon SEC ID         ORF SEQ Signal         Expression (Top) Hit Top Hit Acession Signal         Top Hit Acession No.           NO:         Signal         BLASTE No.           1439B         2746f         5.33         2.0E-61 BE168410.1           14861         27938         1.36         2.0E-61 N53039.1           152         2.0E-61 N33997.1 | Exon SEQ ID ID NO:         Expression Signal         (Top) Hit Top Hit Acession Velue         Top Hit Acession Velue           NO:         14398         27461         5.33         2.0E-61         BE168410.1           14861         27938         1.36         2.0E-61         N53039.1           15824         1.72         2.0E-61         N33997.1           14361         1.72         2.0E-61         N33997.1 | Exon SEQ ID ID NO:         Expression Signal         (Top) Hit Top Hit Acession Signal         (Top) Hit Top Hit Acession No:           NO:         Signal Signal         BLASTE No:         No:           14398         27461         5.33         2.0E-61         BE168410.1           15824         1.36         2.0E-61         Nisso397.1           19718         33094         0.88         2.0E-61         Nisso397.1           2226-61         AV694317.1         2.0E-61         AV694317.1 | Exon<br>SEQ ID<br>NO:         ORF SEQ<br>Signal<br>Signal         Expression<br>(Top) Hit<br>Velue         (Top) Hit<br>Velue         Top Hit Acession<br>Velue           14388         27461         5.33         2.0E-61         BE168410.1           14851         27938         1.36         2.0E-61         N53039.1           16724         1.72         2.0E-61         N35397.1           18718         33094         0.88         2.0E-61         N4894317.1           22729         35839         1.67         2.0E-61         AV694317.1           22700         0.98         2.0E-61         AB011108.1 | Exon SEQ ID ID NO:         Expression Signal         (Top) Hit Acession Value         Top Hit Acession Value           14388         27461         5.33         2.0E-61         BE168410.1           14851         27938         1.36         2.0E-61         N53039.1           16718         33094         0.88         2.0E-61         N35397.1           22706         35839         1.67         2.0E-61         AV694317.1           22706         35763         1.34         2.0E-61         AM5002561 | Exon<br>NO:         ORF SEQ<br>ID NO:         Expression<br>Signal         (Top) Hit<br>PLAST E         Top Hit Acession<br>Velue           14398         27461         5.33         2.0E-61         BE168410.1           14861         27938         1.36         2.0E-61         N53039.1           16724         1.72         2.0E-61         N53039.1           16718         33094         0.88         2.0E-61         N35097.1           22296         35839         1.67         2.0E-61         AV694317.1           22700         0.98         2.0E-61         AW600256.1           23164         36763         1.34         2.0E-61         AW600256.1           23491         37101         2.84         2.0E-61         AW600256.1                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | Exon ORF SEQ ID ID NO:         Expression Signal Signal         (Top) Hit Acession Value         Top Hit Acession Value           14398         27461         5.33         2.0E-61         BE168410.1           14861         27938         1.36         2.0E-61         N53039.1           16724         1.72         2.0E-61         N33997.1           16718         33094         0.88         2.0E-61         AV694317.1           22700         0.98         2.0E-61         AV694317.1           23164         36763         1.34         2.0E-61         AV694317.1           23491         37101         2.84         2.0E-61         AW600256.1           24195         37101         2.84         2.0E-61         AW600256.1 | Exon ORF SEQ         Expression Signal Plan         (Top) Hit Acession Value         Top Hit Acession Value           14398         27461         5.33         2.0E-61         BE168410.1           1622         27538         1.36         2.0E-61         N53039.1           16718         33094         0.88         2.0E-61         N53039.1           22295         35639         1.67         2.0E-61         ANG80263.1           23164         36763         1.34         2.0E-61         ANG80266.1           23491         37101         2.94         2.0E-61         AW500266.1           24196         37101         2.94         2.0E-61         AW995326.1           24196         31850         1.45         2.0E-61         AW995328.1                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         | Exon ORF SEQ         Expression Signal         (Top) Hit Acession Value         Top Hit Acession Value           NO:         Signal         LASTE No.         No.           14861         27938         1.36         2.0E-61         BE168410.1           16824         1.72         2.0E-61         NS3039.1           16718         33094         0.88         2.0E-61         NS3037.1           22700         0.98         2.0E-61         AV684317.1           23164         36763         1.67         2.0E-61         AV684317.1           23491         36763         1.34         2.0E-61         AW600268.1           24195         31950         1.45         2.0E-61         AW600268.1           24195         31950         1.45         2.0E-61         AW995328.1           24196         1.37         1.0E-61         AU163203.2 | Exon ORF SEQ         Expression (Top) Hit Acession SEQ ID ID NO: Signal 1486T         (Top) Hit Acession Value (Top) Hit Acession Value (Top) Hit Acession Value (Top) Hit Acession Value (Top) Hit Acession Signal (Top) Hit Acession Value (Top) Hit Acession Value (Top) Hit 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      14851         27938         1.36         2.0E-61         N53039.1           19718         33094         0.88         2.0E-61         N39397.1           22706         35839         1.67         2.0E-61         AV694317.1           23164         36763         1.67         2.0E-61         AV694317.1           23164         36763         1.67         2.0E-61         AV694317.1           23164         36763         1.34         2.0E-61         AV694317.1           23164         36763         1.34         2.0E-61         AV694317.1           23164         37101         2.94         2.0E-61         AV694317.1           24195         1.34         2.0E-61         AV694317.1           24196         1.34         2.0E-61         AV694317.1           25164         31950         1.34         2.0E-61         AV694317.1           24196         1.35         2.0E-61         AV694328.1           1364         1.36         1.0E-61         AV695 | Exon SEQ ID         ORF SEQ Signal         Kost Similar (Top) Hit Acession Signal         (Top) Hit Acession Value           NO:         Signal         (Top) Hit Acession Value         No.           14861         27461         5.33         2.0E-61         BE168410.1           14861         27938         1.36         2.0E-61         N53039.1           1674         2.0E-61         N35039.1         11426168           22296         35839         1.67         2.0E-61         AN694317.1           23164         36763         1.67         2.0E-61         AN694317.1           23164         36763         1.67         2.0E-61         AN600286.1           23491         37101         2.84         2.0E-61         AN600286.1           24196         36763         1.34         2.0E-61         AN905328.1           24196         1.37         1.0E-61         AN905328.1           13644         2.0E-61         AN905328.1           1364         2.0E-61         AN905328.1           14568         1.0E-61         AL163203.2           14568         1.07         1.0E-61         AL163203.2           14568         1.0E-61         1.0E-61         AL163203.2 <td>Exon SEQ ID ID NO:         Signal Signal Signal Signal Signal Signal No:         (Top) Hit Top Hit Acession Value Value           14358         27461         5.33         2.0E-61         BE168410.1           14851         27938         1.36         2.0E-61         N53039.1           15229         33094         0.88         2.0E-61         N35397.1           22700         1.67         2.0E-61         AV694317.1           23164         36763         1.67         2.0E-61         AV694317.1           23491         37101         2.84         2.0E-61         AV694317.1           24195         1.34         2.0E-61         AV694317.1           24196         1.34         2.0E-61         AV694317.1           24196         1.34         2.0E-61         AV694317.1           24196         1.34         2.0E-61         AV694317.1           24196         1.34         2.0E-61         AV694317.1           24196         1.34         2.0E-61         AV694317.1           24196         1.45         2.0E-61         AV694317.1           24196         1.46         2.0E-61         AV695328.1           14584         2.0E-61         AV695328.1           14584</td> <td>Exon ORF SEQ         Expression (Top) Hit Top Hit Acession SEC ID ID NO: Signal BLASTE No.         Most Signal Value Value Value Value         Top Hit Acession Value Value           14861         27461         5.33         2.0E-61 BE168410.1         E           122295         35839         1.36         2.0E-61 N53039.1         I           22700         0.88         2.0E-61 N38397.1         I           22701         0.98         2.0E-61 N38397.1         I           22702         35639         1.67         2.0E-61 N38397.1         I           22703         0.98         2.0E-61 N38397.1         I         I           22704         36783         1.67         2.0E-61 N38397.1         I           22494         36783         1.34         2.0E-61 N38397.1         I           24195         0.98         2.0E-61 N38397.1         I           24195         1.34         2.0E-61 AV6094317.1         I           24195         1.34         2.0E-61 AV6094317.1         I           24195         1.34         2.0E-61 AV6094317.1         I           24195         1.35         1.0E-61 AV609538.1         I           14584         1.0E-61 AV6095328.1         I           14584         <t< td=""><td>Expn<br/>NO:         ORF SEQ<br/>Signal         Expression<br/>(Top) Hit<br/>Value         Most Similar<br/>Value           14861         27461         5.33         2.0E-61         BE168410.1         E           14862         27461         5.33         2.0E-61         NIS3039.1         E           15824         1.72         2.0E-61         NIS3039.1         E           22295         35839         1.67         2.0E-61         AN59039.1         E           22700         0.88         2.0E-61         NIS3039.1         E           22700         0.98         2.0E-61         AN59039.1         E           23164         36763         1.67         2.0E-61         AN59039.1         E           24195         2.0E-61         AN59039.1         E         A         2.0E-61           22700         0.98         2.0E-61         AN5904317.1         I           24195         1.67         2.0E-61         AN5904317.1         I           24391         37101         2.84         2.0E-61         AN5904363.1           13644         1.37         1.0E-61         AN590536.1         I           14858         2.7026         1.45         2.0E-61         AN9905328.1</td><td>Exon ORF SEQ         Expression Signal         (Top) Hit Top Hit Acession No: SEQ ID ID NO: Signal         Most Similar Acression Value           14861         27461         5.33         2.0E-61 BE168410.1           15824         1.36         2.0E-61 N53039.1           15825         1.36         2.0E-61 N33039.1           15826         35839         1.67         2.0E-61 N33037.1           22700         0.88         2.0E-61 N33037.1           22700         1.67         2.0E-61 AV694317.1           23164         36763         1.67         2.0E-61 AV604317.1           24195         1.67         2.0E-61 AV602317.1           24195         1.67         2.0E-61 AV602317.1           24195         1.57         2.0E-61 AV602317.1           25744         31950         1.34         2.0E-61 AV60236.1           13673         27028         1.37         1.0E-61 AV809336.1           14958         1.07         1.0E-61 AV8093326.1           14658         1.02         1.0E-61 AV8093326.1           14658         1.0E-61 AV809333.1           15403         2853         1.0E-61 AV827281.1           15640         2863         1.0E-61 BE1838633.1           16630         29650</td><td>Exon ORF SEQ         Expression Signal         (Top) Hit Top Hit Acession Value           NO:         Signal         (Top) Hit Top Hit Acession Value           14861         27461         5.33         2.0E-61 BE168410.1           15824         1.36         2.0E-61 BE168410.1           15824         1.72         2.0E-61 N53039.1           19718         33094         0.88         2.0E-61 N38397.1           22700         0.98         2.0E-61 AV694317.1           23164         36763         1.67         2.0E-61 AV694317.1           24195         1.67         2.0E-61 AV694317.1           24795         1.67         2.0E-61 AV60280.1           24195         1.67         2.0E-61 AV602317.1           25164         31950         1.34         2.0E-61 AV602317.1           25744         31950         1.34         2.0E-61 AV60232.2           13673         27026         1.45         2.0E-61 AV605236.1           14958         1.05         1.0E-61 AV60533.1           15049         27026         1.26         1.0E-61 AV60533.1           15049         28531         1.0E-61 BE184363.1           15049         28650         0.98         1.0E-61 BE184536.1           <t< td=""><td>Exon<br/>NO:         ORF SEQ<br/>Signal         Expression<br/>(Top) Hit<br/>Vellue         (Top) Hit<br/>Vellue         Top Hit Acession           1435B         27461         5.33         2.0E-61         BE168410.1           14851         2793B         1.36         2.0E-61         N53039.1           15824         1.72         2.0E-61         N53039.1           15824         1.72         2.0E-61         N38397.1           22700         0.38         2.0E-61         AV694317.1           23164         36763         1.67         2.0E-61         AV60231.7           23491         37101         2.94         2.0E-61         AV60231.7           24795         1.67         2.0E-61         AV60231.7           24796         1.67         2.0E-61         AV60231.7           25164         31950         1.34         2.0E-61         AV60236.1           13649         2.0E-61         AV60236.1         11419729           25744         31950         1.26         1.0E-61         AV60236.1           14958         1.0E-61         1.0E-61        
AV60233.1           15049         28531         1.0E-61         AV60233.1           15049         28630         1.0E-61</td><td>Evon ORF SEQ         Expression Signal         (Top) Hit Top Hit Acession Value           NO:         Signal         (Top) Hit Top Hit Acession Value           14358         27461         5.33         2.0E-61         BE168410.1           14851         27938         1.36         2.0E-61         N53039.1           15824         1.72         2.0E-61         N38397.1           22706         33094         0.88         2.0E-61         AV694317.1           22707         0.98         2.0E-61         AV694317.1           23164         36763         1.67         2.0E-61         AV60238.1           23491         37101         2.94         2.0E-61         AV602317.1           23491         37101         2.94         2.0E-61         AV60238.1           13643         27026         1.37         1.0E-61         AV60238.1           14584         27026         1.26         1.0E-61         AV6323.2           14584         27026         1.26         1.0E-61         AV6323.1           15049         28150         1.0E-61         AV6323.1           15049         28160         0.98         1.0E-61         BE374455.1           1567         30487</td><td>Evon ORF SEQ         Expression Signal         (Top) Hit Top Hit Acession Vellue           NO:         Signal         (Top) Hit Top Hit Acession Vellue           14358         27461         5.33         2.0E-61         BE168410.1           14851         27938         1.36         2.0E-61         N53039.1           1674         2.0E-61         N53039.1         1.426166           22296         35839         1.67         2.0E-61         AV694317.1           23164         36763         1.67         2.0E-61         AV60298.1           23164         36763         1.67         2.0E-61         AV602917.1           23164         36763         1.34         2.0E-61         AV602917.1           23164         37101         2.84         2.0E-61         AV60288.1           24195         1.37         1.0E-61         AV60282.2           14584         27026         1.26         1.0E-61         AV60283.1           14584         27026         1.26         1.0E-61         AV60283.1           15049         28150         1.0E-61         AV3         AV6383.1           15649         28150         1.0E-61         BE174455.1           16810         1.0E-61</td><td>Evon ORF SEQ         Expression Signal         (Top) Hit Top Hit Acession Vellue           NO:         Signal         (Top) Hit Top Hit Acession Vellue           14861         27461         5.33         2.0E-61         BE168410.1           14861         27938         1.36         2.0E-61         N53039.1           16824         1.72         2.0E-61         N53039.1           16824         1.72         2.0E-61         N53039.1           16824         1.72         2.0E-61         N53039.1           16824         1.67         2.0E-61         N53039.1           22706         36763         1.67         2.0E-61         AV694317.1           23164         36763         1.67         2.0E-61         AV604317.1           23164         36763         1.34         2.0E-61         AV604317.1           23491         37101         2.84         2.0E-61         AV60280.1           23491         37101         2.84         2.0E-61         AV600280.1           23491         37101         2.84         2.0E-61         AV600280.1           14958         1.0E-61         AV600280.1         1.4192073           14968         1.0E-61         AV600280.2         <t< td=""><td>Evon NO:         ORF SEQ Signal         Expression Signal         (Top) Hit Top Hit Acession Value           NO:         10 NO:         Signal         (Top) Hit Top Hit Acession Value           14861         27461         5.33         2.0E-61         BE168410.1           14861         27938         1.36         2.0E-61         N53039.1           16229         35829         1.67         2.0E-61         N53039.1           22700         0.98         2.0E-61         AV694317.1           23491         37101         2.84         2.0E-61         AV600256.1           23492         37101         2.84         2.0E-61         AV600256.1           23491         37101         2.84         2.0E-61         AV600256.1           23491         37101         2.84         2.0E-61         AV600256.1           23491         37101         2.84         2.0E-61         AV600256.1           23491         37101         2.84         2.0E-61         AV600256.1           23491         37101         2.84         2.0E-61         AV600256.1           14584         27026         1.35         1.0E-61         AV63026.1           14549         27026         1.0E-61</td><td>Exon ORF SEQ         Expression Signal         (Top) Hit Top Hit Acession No: SEQ ID         Most Similar IT Top Hit Acession No: SEQ ID           NO: NO: NO: NO: NO: Signal         2.0E-61 BE168410.1         No. No: No: No: No: No: No: No: No: No: No:</td><td>Exon ORF SEQ         Expression Signal         (Top) Hit Top Hit Acession No: No: No: No: No: No: No: No: No: No:</td><td>Expn<br/>NO:         ORF SEQ<br/>Signal         Expression<br/>(Top) Hit<br/>Vellue         (Top) Hit<br/>Vellue         Top Hit Acession<br/>Vellue           14861         27461         5.33         2.0E-61         BE168410.1           14861         27638         1.36         2.0E-61         N53039.1           15824         1.72         2.0E-61         N53039.1           15824         1.72         2.0E-61         N83039.1           22700         0.38         2.0E-61         AV694317.1           22700         0.38         2.0E-61         AV602317.1           24195         36763         1.67         2.0E-61         AV602317.1           24795         36763         1.67         2.0E-61         AV602317.1           24795         1.67         2.0E-61         AV602317.1           25744         31950         1.34         2.0E-61         AV60231.1           15649         27026         1.37         1.0E-61         AV60232.2           14958         1.0E-61         AV60233.1         1.0E-61         AV60233.1           15649         27026         1.0E-61         AV60233.1           15640         28531         1.0E-61         AV60233.1           16680         26650&lt;</td><td>Ewn ORF SEQ         Expression Signal         (Top) Hit Top Hit Acession Value           NO:         Signal         (Top) Hit Top Hit Acession Value           14851         27461         5.33         2.0E-61 BE168410.1           14851         27938         1.36         2.0E-61 N53039.1           15824         1.72         2.0E-61 N38397.1           15824         33094         0.88         2.0E-61 AV694317.1           22700         0.98         2.0E-61 AV694317.1           23164         35701         2.0E-61 AV694317.1           23491         37101         2.94         2.0E-61 AV694317.1           24795         1.67         2.0E-61 AV694317.1           24796         1.67         2.0E-61 AV694317.1           24796         1.67         2.0E-61 AV694317.1           24796         1.67         2.0E-61 AV694317.1           25744         31950         1.34         2.0E-61 AV694317.1           14584         27026         1.26         1.0E-61 AV69431.1           15049         27026         1.26         1.0E-61 AV6943.1           15049         28150         1.0E-61 AV6943.1           15049         28160         0.98         1.0E-61 AV6943.1           1</td><td>Ewon ORF SEQ         Expression Signal         (Top) Hit Top Hit Acession Value           NO:         Signal         (Top) Hit Top Hit Acession Value           14358         27461         5.33         2.0E-61 N53039.1           15226         35829         1.36         2.0E-61 N39397.1           19718         33094         0.88         2.0E-61 AV694317.1           22296         35839         1.67         2.0E-61 AV60238.1           23164         37101         2.94         2.0E-61 AV60238.1           24196         0.98         2.0E-61 AV602317.1           24196         1.67         2.0E-61 AV60238.1           13649         2.0E-61 AV60231.1           14884         27026         1.26         1.0E-61 AV60233.1           14884         27026         1.26         1.0E-61 AV60233.1           15049         28160         4.43         1.0E-61 AV60233.1           15049         28160         1.0E-61 AV60233.1           15049         28160         1.0E-61 AV60233.1           15049         28160         1.0E-61 AV60233.1           15049         28160         1.0E-61 AV60233.1           15049         28160         1.0E-61 AV60233.1           15640         2</td><td>Evan ORF SEQ         Expression Signal         (Top) Hit Top Hit Acession Vellue           NO:         10 NO:         Signal         (Top) Hit Top Hit Acession Vellue           14398         27461         5.33         2.0E-61         NG3039.1           15824         1.36         2.0E-61         NG3039.1           15824         1.72         2.0E-61         NG3039.1           22706         33094         0.88         2.0E-61         AV694317.1           22707         36783         1.67         2.0E-61         AV602317.1           23164         37101         2.94         2.0E-61         AV602317.1           23491         37101         2.94         2.0E-61         AV602317.1           23494         36783         1.67         2.0E-61         AV602317.1           23491         37101         2.94         2.0E-61         AV60231.2           14584         27026         1.26         1.0E-61         AV60238.1           14584         27026         1.26         1.0E-61         AV60233.1           15049         28150         1.0E         1.0E-61         AV62303.2           15049         28150         1.0E-61         AV6231.1           16504</td></t<></td></t<></td></t<></td> | Exon SEQ ID ID NO:         Signal Signal Signal Signal Signal Signal No:         (Top) Hit Top Hit Acession Value Value           14358         27461         5.33     
   2.0E-61         BE168410.1           14851         27938         1.36         2.0E-61         N53039.1           15229         33094         0.88         2.0E-61         N35397.1           22700         1.67         2.0E-61         AV694317.1           23164         36763         1.67         2.0E-61         AV694317.1           23491         37101         2.84         2.0E-61         AV694317.1           24195         1.34         2.0E-61         AV694317.1           24196         1.34         2.0E-61         AV694317.1           24196         1.34         2.0E-61         AV694317.1           24196         1.34         2.0E-61         AV694317.1           24196         1.34         2.0E-61         AV694317.1           24196         1.34         2.0E-61         AV694317.1           24196         1.45         2.0E-61         AV694317.1           24196         1.46         2.0E-61         AV695328.1           14584         2.0E-61         AV695328.1           14584 | Exon ORF SEQ         Expression (Top) Hit Top Hit Acession SEC ID ID NO: Signal BLASTE No.         Most Signal Value Value Value Value         Top Hit Acession Value Value           14861         27461         5.33         2.0E-61 BE168410.1         E           122295         35839         1.36         2.0E-61 N53039.1         I           22700         0.88         2.0E-61 N38397.1         I           22701         0.98         2.0E-61 N38397.1         I           22702         35639         1.67         2.0E-61 N38397.1         I           22703         0.98         2.0E-61 N38397.1         I         I           22704         36783         1.67         2.0E-61 N38397.1         I           22494         36783         1.34         2.0E-61 N38397.1         I           24195         0.98         2.0E-61 N38397.1         I           24195         1.34         2.0E-61 AV6094317.1         I           24195         1.34         2.0E-61 AV6094317.1         I           24195         1.34         2.0E-61 AV6094317.1         I           24195         1.35         1.0E-61 AV609538.1         I           14584         1.0E-61 AV6095328.1         I           14584 <t< td=""><td>Expn<br/>NO:         ORF SEQ<br/>Signal         Expression<br/>(Top) Hit<br/>Value         Most Similar<br/>Value           14861         27461         5.33         2.0E-61         BE168410.1         E           14862         27461         5.33         2.0E-61         NIS3039.1         E           15824         1.72         2.0E-61         NIS3039.1         E           22295         35839         1.67         2.0E-61         AN59039.1         E           22700         0.88         2.0E-61         NIS3039.1         E           22700         0.98         2.0E-61         AN59039.1         E           23164         36763         1.67         2.0E-61         AN59039.1         E           24195         2.0E-61         AN59039.1         E         A         2.0E-61           22700         0.98         2.0E-61         AN5904317.1         I           24195         1.67         2.0E-61         AN5904317.1         I           24391         37101         2.84         2.0E-61         AN5904363.1           13644         1.37         1.0E-61         AN590536.1         I           14858         2.7026         1.45         2.0E-61         AN9905328.1</td><td>Exon ORF SEQ         Expression Signal         (Top) Hit Top Hit Acession No: SEQ ID ID NO: Signal         Most Similar Acression Value           14861         27461         5.33         2.0E-61 BE168410.1           15824         1.36         2.0E-61 N53039.1           15825         1.36         2.0E-61 N33039.1           15826         35839         1.67         2.0E-61 N33037.1           22700         0.88         2.0E-61 N33037.1           22700         1.67         2.0E-61 AV694317.1           23164         36763         1.67         2.0E-61 AV604317.1           24195         1.67         2.0E-61 AV602317.1           24195         1.67         2.0E-61 AV602317.1           24195         1.57         2.0E-61 AV602317.1           25744         31950         1.34         2.0E-61 AV60236.1           13673         27028         1.37         1.0E-61 AV809336.1           14958         1.07         1.0E-61 AV8093326.1           14658         1.02         1.0E-61 AV8093326.1           14658         1.0E-61 AV809333.1           15403         2853         1.0E-61 AV827281.1           15640         2863         1.0E-61 BE1838633.1           16630         29650</td><td>Exon ORF SEQ         Expression Signal         (Top) Hit Top Hit Acession Value           NO:         Signal         (Top) Hit Top Hit Acession Value           14861         27461         5.33         2.0E-61 BE168410.1           15824         1.36         2.0E-61 BE168410.1           15824         1.72         2.0E-61 N53039.1           19718         33094         0.88         2.0E-61 N38397.1           22700         0.98         2.0E-61 AV694317.1           23164         36763         1.67         2.0E-61 AV694317.1           24195         1.67         2.0E-61 AV694317.1           24795         1.67         2.0E-61 AV60280.1           24195         1.67         2.0E-61 AV602317.1           25164         31950         1.34         2.0E-61 AV602317.1           25744         31950         1.34         2.0E-61 AV60232.2           13673         27026         1.45         2.0E-61 AV605236.1           14958         1.05         1.0E-61 AV60533.1           15049         27026         1.26         1.0E-61 AV60533.1           15049         28531         1.0E-61 BE184363.1           15049         28650         0.98         1.0E-61 BE184536.1           <t< td=""><td>Exon<br/>NO:         ORF SEQ<br/>Signal         Expression<br/>(Top) Hit<br/>Vellue         (Top) Hit<br/>Vellue         Top Hit Acession           1435B         27461         5.33         2.0E-61         BE168410.1           14851         2793B         1.36         2.0E-61         N53039.1           15824         1.72         2.0E-61         N53039.1           15824         1.72         2.0E-61         N38397.1           22700         0.38         2.0E-61         AV694317.1           23164         36763         1.67         2.0E-61         AV60231.7           23491         37101         2.94         2.0E-61         AV60231.7           24795         1.67         2.0E-61         AV60231.7           24796         1.67         2.0E-61         AV60231.7           25164         31950         1.34         2.0E-61         AV60236.1           13649         2.0E-61         AV60236.1         11419729           25744         31950         1.26         1.0E-61         AV60236.1           14958         1.0E-61         1.0E-61         AV60233.1           15049         28531         1.0E-61         AV60233.1           15049         28630         1.0E-61</td><td>Evon ORF SEQ         Expression Signal         (Top) Hit Top Hit Acession Value           NO:         Signal         (Top) Hit Top Hit Acession Value           14358         27461         5.33         2.0E-61         BE168410.1           14851         27938         1.36         2.0E-61         N53039.1           15824         1.72         2.0E-61         N38397.1           22706         33094         0.88         2.0E-61         AV694317.1           22707         0.98         2.0E-61         AV694317.1           23164         36763         1.67         2.0E-61         AV60238.1           23491         37101         2.94         2.0E-61         AV602317.1           23491         37101         2.94         2.0E-61         AV60238.1           13643         27026         1.37         1.0E-61         AV60238.1           14584         27026         1.26         1.0E-61         AV6323.2           14584         27026         1.26         1.0E-61         AV6323.1           15049         28150         1.0E-61         AV6323.1           15049         28160         0.98         1.0E-61         BE374455.1           1567         30487</td><td>Evon ORF SEQ         Expression Signal         (Top) Hit Top Hit Acession Vellue           NO:         Signal         (Top) Hit Top Hit Acession Vellue           14358         27461         5.33         2.0E-61         BE168410.1           14851         27938         1.36         2.0E-61         N53039.1           1674         2.0E-61         N53039.1         1.426166           22296         35839         1.67         2.0E-61         AV694317.1           23164         36763         1.67         2.0E-61         AV60298.1           23164         36763         1.67         2.0E-61         AV602917.1           23164         36763         1.34         2.0E-61         AV602917.1           23164         37101         2.84         2.0E-61         AV60288.1           24195         1.37         1.0E-61         AV60282.2           14584         27026         1.26         1.0E-61         AV60283.1           14584         27026         1.26         1.0E-61         AV60283.1           15049         28150         1.0E-61         AV3         AV6383.1           15649         28150         1.0E-61         BE174455.1           16810         1.0E-61</td><td>Evon ORF SEQ         Expression Signal         (Top) Hit Top Hit Acession Vellue           NO:         Signal         (Top) Hit Top Hit Acession Vellue           14861         27461         5.33         2.0E-61         BE168410.1           14861         27938         1.36         2.0E-61         N53039.1           16824         1.72         2.0E-61         N53039.1           16824         1.72         2.0E-61         N53039.1           16824         1.72         2.0E-61         N53039.1           16824         1.67         2.0E-61         N53039.1           22706         36763         1.67         2.0E-61         AV694317.1           23164         36763         1.67         2.0E-61         AV604317.1           23164         36763         1.34         2.0E-61         AV604317.1           23491         37101         2.84         2.0E-61        
AV60280.1           23491         37101         2.84         2.0E-61         AV600280.1           23491         37101         2.84         2.0E-61         AV600280.1           14958         1.0E-61         AV600280.1         1.4192073           14968         1.0E-61         AV600280.2         <t< td=""><td>Evon NO:         ORF SEQ Signal         Expression Signal         (Top) Hit Top Hit Acession Value           NO:         10 NO:         Signal         (Top) Hit Top Hit Acession Value           14861         27461         5.33         2.0E-61         BE168410.1           14861         27938         1.36         2.0E-61         N53039.1           16229         35829         1.67         2.0E-61         N53039.1           22700         0.98         2.0E-61         AV694317.1           23491         37101         2.84         2.0E-61         AV600256.1           23492         37101         2.84         2.0E-61         AV600256.1           23491         37101         2.84         2.0E-61         AV600256.1           23491         37101         2.84         2.0E-61         AV600256.1           23491         37101         2.84         2.0E-61         AV600256.1           23491         37101         2.84         2.0E-61         AV600256.1           23491         37101         2.84         2.0E-61         AV600256.1           14584         27026         1.35         1.0E-61         AV63026.1           14549         27026         1.0E-61</td><td>Exon ORF SEQ         Expression Signal         (Top) Hit Top Hit Acession No: SEQ ID         Most Similar IT Top Hit Acession No: SEQ ID           NO: NO: NO: NO: NO: Signal         2.0E-61 BE168410.1         No. No: No: No: No: No: No: No: No: No: No:</td><td>Exon ORF SEQ         Expression Signal         (Top) Hit Top Hit Acession No: No: No: No: No: No: No: No: No: No:</td><td>Expn<br/>NO:         ORF SEQ<br/>Signal         Expression<br/>(Top) Hit<br/>Vellue         (Top) Hit<br/>Vellue         Top Hit Acession<br/>Vellue           14861         27461         5.33         2.0E-61         BE168410.1           14861         27638         1.36         2.0E-61         N53039.1           15824         1.72         2.0E-61         N53039.1           15824         1.72         2.0E-61         N83039.1           22700         0.38         2.0E-61         AV694317.1           22700         0.38         2.0E-61         AV602317.1           24195         36763         1.67         2.0E-61         AV602317.1           24795         36763         1.67         2.0E-61         AV602317.1           24795         1.67         2.0E-61         AV602317.1           25744         31950         1.34         2.0E-61         AV60231.1           15649         27026         1.37         1.0E-61         AV60232.2           14958         1.0E-61         AV60233.1         1.0E-61         AV60233.1           15649         27026         1.0E-61         AV60233.1           15640         28531         1.0E-61         AV60233.1           16680         26650&lt;</td><td>Ewn ORF SEQ         Expression Signal         (Top) Hit Top Hit Acession Value           NO:         Signal         (Top) Hit Top Hit Acession Value           14851         27461         5.33         2.0E-61 BE168410.1           14851         27938         1.36         2.0E-61 N53039.1           15824         1.72         2.0E-61 N38397.1           15824         33094         0.88         2.0E-61 AV694317.1           22700         0.98         2.0E-61 AV694317.1           23164         35701         2.0E-61 AV694317.1           23491         37101         2.94         2.0E-61 AV694317.1           24795         1.67         2.0E-61 AV694317.1           24796         1.67         2.0E-61 AV694317.1           24796         1.67         2.0E-61 AV694317.1           24796         1.67         2.0E-61 AV694317.1           25744         31950         1.34         2.0E-61 AV694317.1           14584         27026         1.26         1.0E-61 AV69431.1           15049         27026         1.26         1.0E-61 AV6943.1           15049         28150         1.0E-61 AV6943.1           15049         28160         0.98         1.0E-61 AV6943.1           1</td><td>Ewon ORF SEQ         Expression Signal         (Top) Hit Top Hit Acession Value           NO:         Signal         (Top) Hit Top Hit Acession Value           14358         27461         5.33         2.0E-61 N53039.1           15226         35829         1.36         2.0E-61 N39397.1           19718         33094         0.88         2.0E-61 AV694317.1           22296         35839         1.67         2.0E-61 AV60238.1           23164         37101         2.94         2.0E-61 AV60238.1           24196         0.98         2.0E-61 AV602317.1           24196         1.67         2.0E-61 AV60238.1           13649         2.0E-61 AV60231.1           14884         27026         1.26         1.0E-61 AV60233.1           14884         27026         1.26         1.0E-61 AV60233.1           15049         28160         4.43         1.0E-61 AV60233.1           15049         28160         1.0E-61 AV60233.1           15049         28160         1.0E-61 AV60233.1           15049         28160         1.0E-61 AV60233.1           15049         28160         1.0E-61 AV60233.1           15049         28160         1.0E-61 AV60233.1           15640         2</td><td>Evan ORF SEQ         Expression Signal         (Top) Hit Top Hit Acession Vellue           NO:         10 NO:         Signal         (Top) Hit Top Hit Acession Vellue           14398         27461         5.33         2.0E-61         NG3039.1           15824         1.36         2.0E-61         NG3039.1           15824         1.72         2.0E-61         NG3039.1           22706         33094         0.88         2.0E-61         AV694317.1           22707         36783         1.67         2.0E-61         AV602317.1           23164         37101         2.94         2.0E-61         AV602317.1           23491         37101         2.94         2.0E-61         AV602317.1           23494         36783         1.67         2.0E-61         AV602317.1           23491         37101         2.94         2.0E-61         AV60231.2           14584         27026         1.26         1.0E-61         AV60238.1           14584         27026         1.26         1.0E-61         AV60233.1           15049         28150         1.0E         1.0E-61         AV62303.2           15049         28150         1.0E-61         AV6231.1           16504</td></t<></td></t<></td></t<> | Expn<br>NO:         ORF SEQ<br>Signal         Expression<br>(Top) Hit<br>Value         Most Similar<br>Value           14861         27461         5.33         2.0E-61         BE168410.1         E           14862         27461         5.33         2.0E-61         NIS3039.1         E           15824         1.72         2.0E-61         NIS3039.1         E           22295         35839         1.67         2.0E-61         AN59039.1         E           22700         0.88         2.0E-61         NIS3039.1         E           22700         0.98         2.0E-61         AN59039.1         E           23164         36763         1.67         2.0E-61         AN59039.1         E           24195         2.0E-61         AN59039.1         E         A         2.0E-61           22700         0.98         2.0E-61         AN5904317.1         I           24195         1.67         2.0E-61         AN5904317.1         I           24391         37101         2.84         2.0E-61         AN5904363.1           13644         1.37         1.0E-61         AN590536.1         I           14858         2.7026         1.45         2.0E-61         AN9905328.1 | Exon ORF SEQ         Expression Signal         (Top) Hit Top Hit Acession No: SEQ ID ID NO: Signal         Most Similar Acression Value           14861         27461         5.33         2.0E-61 BE168410.1           15824         1.36         2.0E-61 N53039.1           15825         1.36         2.0E-61 N33039.1           15826         35839         1.67         2.0E-61 N33037.1           22700         0.88         2.0E-61 N33037.1           22700         1.67         2.0E-61 AV694317.1           23164         36763         1.67         2.0E-61 AV604317.1           24195         1.67         2.0E-61 AV602317.1           24195         1.67         2.0E-61 AV602317.1           24195         1.57         2.0E-61 AV602317.1           25744         31950         1.34         2.0E-61 AV60236.1           13673         27028         1.37         1.0E-61 AV809336.1           14958         1.07         1.0E-61 AV8093326.1           14658         1.02         1.0E-61 AV8093326.1           14658         1.0E-61 AV809333.1           15403         2853         1.0E-61 AV827281.1           15640         2863         1.0E-61 BE1838633.1           16630         29650 | Exon ORF SEQ         Expression Signal         (Top) Hit Top Hit Acession Value           NO:         Signal         (Top) Hit Top Hit Acession Value           14861         27461         5.33         2.0E-61 BE168410.1           15824         1.36         2.0E-61 BE168410.1           15824         1.72         2.0E-61 N53039.1           19718         33094         0.88         2.0E-61 N38397.1           22700         0.98         2.0E-61 AV694317.1           23164         36763         1.67         2.0E-61 AV694317.1           24195         1.67         2.0E-61 AV694317.1           24795         1.67         2.0E-61 AV60280.1           24195         1.67         2.0E-61 AV602317.1           25164         31950         1.34         2.0E-61 AV602317.1           25744         31950         1.34         2.0E-61 AV60232.2           13673         27026         1.45         2.0E-61 AV605236.1           14958         1.05         1.0E-61 AV60533.1           15049         27026         1.26         1.0E-61 AV60533.1           15049         28531         1.0E-61 BE184363.1           15049         28650         0.98         1.0E-61
BE184536.1 <t< td=""><td>Exon<br/>NO:         ORF SEQ<br/>Signal         Expression<br/>(Top) Hit<br/>Vellue         (Top) Hit<br/>Vellue         Top Hit Acession           1435B         27461         5.33         2.0E-61         BE168410.1           14851         2793B         1.36         2.0E-61         N53039.1           15824         1.72         2.0E-61         N53039.1           15824         1.72         2.0E-61         N38397.1           22700         0.38         2.0E-61         AV694317.1           23164         36763         1.67         2.0E-61         AV60231.7           23491         37101         2.94         2.0E-61         AV60231.7           24795         1.67         2.0E-61         AV60231.7           24796         1.67         2.0E-61         AV60231.7           25164         31950         1.34         2.0E-61         AV60236.1           13649         2.0E-61         AV60236.1         11419729           25744         31950         1.26         1.0E-61         AV60236.1           14958         1.0E-61         1.0E-61         AV60233.1           15049         28531         1.0E-61         AV60233.1           15049         28630         1.0E-61</td><td>Evon ORF SEQ         Expression Signal         (Top) Hit Top Hit Acession Value           NO:         Signal         (Top) Hit Top Hit Acession Value           14358         27461         5.33         2.0E-61         BE168410.1           14851         27938         1.36         2.0E-61         N53039.1           15824         1.72         2.0E-61         N38397.1           22706         33094         0.88         2.0E-61         AV694317.1           22707         0.98         2.0E-61         AV694317.1           23164         36763         1.67         2.0E-61         AV60238.1           23491         37101         2.94         2.0E-61         AV602317.1           23491         37101         2.94         2.0E-61         AV60238.1           13643         27026         1.37         1.0E-61         AV60238.1           14584         27026         1.26         1.0E-61         AV6323.2           14584         27026         1.26         1.0E-61         AV6323.1           15049         28150         1.0E-61         AV6323.1           15049         28160         0.98         1.0E-61         BE374455.1           1567         30487</td><td>Evon ORF SEQ         Expression Signal         (Top) Hit Top Hit Acession Vellue           NO:         Signal         (Top) Hit Top Hit Acession Vellue           14358         27461         5.33         2.0E-61         BE168410.1           14851         27938         1.36         2.0E-61         N53039.1           1674         2.0E-61         N53039.1         1.426166           22296         35839         1.67         2.0E-61         AV694317.1           23164         36763         1.67         2.0E-61         AV60298.1           23164         36763         1.67         2.0E-61         AV602917.1           23164         36763         1.34         2.0E-61         AV602917.1           23164         37101         2.84         2.0E-61         AV60288.1           24195         1.37         1.0E-61         AV60282.2           14584         27026         1.26         1.0E-61         AV60283.1           14584         27026         1.26         1.0E-61         AV60283.1           15049         28150         1.0E-61         AV3         AV6383.1           15649         28150         1.0E-61         BE174455.1           16810         1.0E-61</td><td>Evon ORF SEQ         Expression Signal         (Top) Hit Top Hit Acession Vellue           NO:         Signal         (Top) Hit Top Hit Acession Vellue           14861         27461         5.33         2.0E-61         BE168410.1           14861         27938         1.36         2.0E-61         N53039.1           16824         1.72         2.0E-61         N53039.1           16824         1.72         2.0E-61         N53039.1           16824         1.72         2.0E-61         N53039.1           16824         1.67         2.0E-61         N53039.1           22706         36763         1.67         2.0E-61         AV694317.1           23164         36763         1.67         2.0E-61         AV604317.1           23164         36763         1.34         2.0E-61         AV604317.1           23491         37101         2.84         2.0E-61         AV60280.1           23491         37101         2.84         2.0E-61         AV600280.1           23491         37101         2.84         2.0E-61         AV600280.1           14958         1.0E-61         AV600280.1         1.4192073           14968         1.0E-61         AV600280.2         <t< td=""><td>Evon NO:         ORF SEQ Signal         Expression Signal         (Top) Hit Top Hit Acession Value           NO:         10 NO:         Signal         (Top) Hit Top Hit Acession Value           14861         27461         5.33         2.0E-61         BE168410.1           14861         27938         1.36         2.0E-61         N53039.1           16229         35829         1.67         2.0E-61         N53039.1           22700         0.98         2.0E-61         AV694317.1           23491         37101         2.84         2.0E-61         AV600256.1           23492         37101         2.84         2.0E-61         AV600256.1           23491         37101         2.84         2.0E-61         AV600256.1           23491         37101         2.84         2.0E-61         AV600256.1           23491         37101         2.84         2.0E-61         AV600256.1           23491         37101         2.84         2.0E-61         AV600256.1           23491         37101         2.84         2.0E-61         AV600256.1           14584         27026         1.35         1.0E-61         AV63026.1           14549         27026         1.0E-61</td><td>Exon ORF SEQ         Expression Signal         (Top) Hit Top Hit Acession No: SEQ ID         Most Similar IT Top Hit Acession No: SEQ ID           NO: NO: NO: NO: NO: Signal         2.0E-61 BE168410.1         No. No: No: No: No: No: No: No: No: No: No:</td><td>Exon ORF SEQ         Expression Signal         (Top) Hit Top Hit Acession No: No: No: No: No: No: No: No: No: No:</td><td>Expn<br/>NO:         ORF SEQ<br/>Signal         Expression<br/>(Top) Hit<br/>Vellue         (Top) Hit<br/>Vellue         Top Hit Acession<br/>Vellue           14861         27461         5.33         2.0E-61         BE168410.1           14861         27638         1.36         2.0E-61         N53039.1           15824         1.72         2.0E-61         N53039.1           15824         1.72         2.0E-61         N83039.1           22700         0.38         2.0E-61         AV694317.1           22700         0.38         2.0E-61         AV602317.1           24195         36763         1.67         2.0E-61         AV602317.1           24795         36763         1.67         2.0E-61         AV602317.1           24795         1.67         2.0E-61         AV602317.1           25744         31950         1.34         2.0E-61         AV60231.1           15649         27026         1.37         1.0E-61         AV60232.2           14958         1.0E-61         AV60233.1         1.0E-61         AV60233.1           15649         27026         1.0E-61         AV60233.1           15640         28531         1.0E-61         AV60233.1           16680         26650&lt;</td><td>Ewn ORF SEQ         Expression Signal         (Top) Hit Top Hit Acession Value           NO:         Signal         (Top) Hit Top Hit Acession Value           14851         27461         5.33         2.0E-61 BE168410.1           14851         27938         1.36         2.0E-61 N53039.1           15824         1.72         2.0E-61 N38397.1           15824         33094         0.88         2.0E-61 AV694317.1           22700         0.98         2.0E-61 AV694317.1           23164         35701         2.0E-61 AV694317.1           23491         37101         2.94         2.0E-61 AV694317.1           24795         1.67         2.0E-61 AV694317.1           24796         1.67         2.0E-61 AV694317.1           24796         1.67         2.0E-61 AV694317.1           24796         1.67         2.0E-61 AV694317.1           25744         31950         1.34         2.0E-61 AV694317.1           14584         27026         1.26         1.0E-61 AV69431.1           15049         27026         1.26         1.0E-61 AV6943.1           15049         28150         1.0E-61 AV6943.1           15049         28160         0.98         1.0E-61 AV6943.1           1</td><td>Ewon ORF SEQ         Expression Signal         (Top) Hit Top Hit Acession Value           NO:         Signal         (Top) Hit Top Hit Acession Value           14358         27461         5.33         2.0E-61 N53039.1           15226         35829         1.36         2.0E-61 N39397.1           19718         33094         0.88         2.0E-61 AV694317.1           22296         35839         1.67         2.0E-61 AV60238.1           23164         37101         2.94         2.0E-61 AV60238.1           24196         0.98         2.0E-61 AV602317.1           24196         1.67         2.0E-61 AV60238.1           13649         2.0E-61 AV60231.1           14884         27026         1.26         1.0E-61 AV60233.1           14884         27026         1.26         1.0E-61 AV60233.1           15049         28160         4.43         1.0E-61 AV60233.1           15049         28160         1.0E-61 AV60233.1           15049         28160         1.0E-61 AV60233.1           15049         28160         1.0E-61 AV60233.1           15049         28160         1.0E-61 AV60233.1           15049         28160         1.0E-61 AV60233.1           15640         2</td><td>Evan ORF SEQ         Expression Signal         (Top) Hit Top Hit Acession Vellue           NO:         10 NO:         Signal         (Top) Hit Top Hit Acession Vellue           14398         27461         5.33         2.0E-61         NG3039.1           15824         1.36        
2.0E-61         NG3039.1           15824         1.72         2.0E-61         NG3039.1           22706         33094         0.88         2.0E-61         AV694317.1           22707         36783         1.67         2.0E-61         AV602317.1           23164         37101         2.94         2.0E-61         AV602317.1           23491         37101         2.94         2.0E-61         AV602317.1           23494         36783         1.67         2.0E-61         AV602317.1           23491         37101         2.94         2.0E-61         AV60231.2           14584         27026         1.26         1.0E-61         AV60238.1           14584         27026         1.26         1.0E-61         AV60233.1           15049         28150         1.0E         1.0E-61         AV62303.2           15049         28150         1.0E-61         AV6231.1           16504</td></t<></td></t<> | Exon<br>NO:         ORF SEQ<br>Signal         Expression<br>(Top) Hit<br>Vellue         (Top) Hit<br>Vellue         Top Hit Acession           1435B         27461         5.33         2.0E-61         BE168410.1           14851         2793B         1.36         2.0E-61         N53039.1           15824         1.72         2.0E-61         N53039.1           15824         1.72         2.0E-61         N38397.1           22700         0.38         2.0E-61         AV694317.1           23164         36763         1.67         2.0E-61         AV60231.7           23491         37101         2.94         2.0E-61         AV60231.7           24795         1.67         2.0E-61         AV60231.7           24796         1.67         2.0E-61         AV60231.7           25164         31950         1.34         2.0E-61         AV60236.1           13649         2.0E-61         AV60236.1         11419729           25744         31950         1.26         1.0E-61         AV60236.1           14958         1.0E-61         1.0E-61         AV60233.1           15049         28531         1.0E-61         AV60233.1           15049         28630         1.0E-61 | Evon ORF SEQ         Expression Signal         (Top) Hit Top Hit Acession Value           NO:         Signal         (Top) Hit Top Hit Acession Value           14358         27461         5.33         2.0E-61         BE168410.1           14851         27938         1.36         2.0E-61         N53039.1           15824         1.72         2.0E-61         N38397.1           22706         33094         0.88         2.0E-61         AV694317.1           22707         0.98         2.0E-61         AV694317.1           23164         36763         1.67         2.0E-61         AV60238.1           23491         37101         2.94         2.0E-61         AV602317.1           23491         37101         2.94         2.0E-61         AV60238.1           13643         27026         1.37         1.0E-61         AV60238.1           14584         27026         1.26         1.0E-61         AV6323.2           14584         27026         1.26         1.0E-61         AV6323.1           15049         28150         1.0E-61         AV6323.1           15049         28160         0.98         1.0E-61         BE374455.1           1567         30487 | Evon ORF SEQ         Expression Signal         (Top) Hit Top Hit Acession Vellue           NO:         Signal         (Top) Hit Top Hit Acession Vellue           14358         27461         5.33         2.0E-61         BE168410.1           14851         27938         1.36         2.0E-61         N53039.1           1674         2.0E-61         N53039.1         1.426166           22296         35839         1.67         2.0E-61         AV694317.1           23164         36763         1.67         2.0E-61         AV60298.1           23164         36763         1.67         2.0E-61         AV602917.1           23164         36763         1.34         2.0E-61         AV602917.1           23164         37101         2.84         2.0E-61         AV60288.1           24195         1.37         1.0E-61         AV60282.2           14584         27026         1.26         1.0E-61         AV60283.1           14584         27026         1.26         1.0E-61         AV60283.1           15049         28150         1.0E-61         AV3         AV6383.1           15649         28150         1.0E-61         BE174455.1           16810         1.0E-61 | Evon ORF SEQ         Expression Signal         (Top) Hit Top Hit Acession Vellue           NO:         Signal         (Top) Hit Top Hit Acession Vellue           14861         27461         5.33         2.0E-61         BE168410.1           14861         27938         1.36         2.0E-61         N53039.1           16824         1.72         2.0E-61         N53039.1           16824         1.72         2.0E-61         N53039.1           16824         1.72         2.0E-61         N53039.1           16824         1.67         2.0E-61         N53039.1           22706         36763         1.67         2.0E-61         AV694317.1           23164         36763         1.67         2.0E-61         AV604317.1           23164         36763         1.34         2.0E-61         AV604317.1           23491         37101         2.84         2.0E-61         AV60280.1           23491         37101         2.84         2.0E-61         AV600280.1           23491         37101         2.84         2.0E-61         AV600280.1           14958         1.0E-61         AV600280.1         1.4192073           14968         1.0E-61         AV600280.2 <t< td=""><td>Evon NO:         ORF SEQ Signal         Expression Signal         (Top) Hit Top Hit Acession Value           NO:         10 NO:         Signal         (Top) Hit Top Hit Acession Value           14861         27461         5.33         2.0E-61         BE168410.1           14861         27938         1.36         2.0E-61         N53039.1           16229         35829         1.67         2.0E-61         N53039.1           22700         0.98         2.0E-61         AV694317.1           23491         37101         2.84         2.0E-61         AV600256.1           23492         37101         2.84         2.0E-61         AV600256.1           23491         37101         2.84         2.0E-61         AV600256.1           23491         37101         2.84         2.0E-61         AV600256.1           23491         37101         2.84         2.0E-61         AV600256.1           23491         37101         2.84         2.0E-61         AV600256.1           23491         37101         2.84         2.0E-61         AV600256.1           14584         27026         1.35         1.0E-61         AV63026.1           14549         27026         1.0E-61</td><td>Exon ORF SEQ         Expression Signal         (Top) Hit Top Hit Acession No: SEQ ID         Most Similar IT Top Hit Acession No: SEQ ID           NO: NO: NO: NO: NO: Signal         2.0E-61 BE168410.1         No. No: No: No: No: No: No: No: No: No: No:</td><td>Exon ORF SEQ         Expression Signal         (Top) Hit Top Hit Acession No: No: No: No: No: No: No: No: No: No:</td><td>Expn<br/>NO:         ORF SEQ<br/>Signal         Expression<br/>(Top) Hit<br/>Vellue         (Top) Hit<br/>Vellue         Top Hit Acession<br/>Vellue           14861         27461         5.33         2.0E-61         BE168410.1           14861         27638         1.36         2.0E-61         N53039.1           15824         1.72         2.0E-61         N53039.1           15824         1.72         2.0E-61         N83039.1           22700         0.38         2.0E-61         AV694317.1           22700         0.38         2.0E-61         AV602317.1           24195         36763         1.67         2.0E-61         AV602317.1           24795         36763         1.67         2.0E-61         AV602317.1           24795         1.67         2.0E-61         AV602317.1           25744         31950         1.34         2.0E-61         AV60231.1           15649         27026         1.37         1.0E-61         AV60232.2           14958         1.0E-61         AV60233.1         1.0E-61         AV60233.1           15649         27026         1.0E-61         AV60233.1           15640         28531         1.0E-61         AV60233.1           16680         26650&lt;</td><td>Ewn ORF SEQ         Expression Signal         (Top) Hit Top Hit Acession Value           NO:         Signal         (Top) Hit Top Hit Acession Value           14851         27461         5.33         2.0E-61 BE168410.1           14851         27938         1.36         2.0E-61 N53039.1           15824         1.72         2.0E-61 N38397.1           15824         33094         0.88         2.0E-61 AV694317.1           22700         0.98         2.0E-61 AV694317.1           23164         35701         2.0E-61 AV694317.1           23491         37101         2.94         2.0E-61 AV694317.1           24795         1.67         2.0E-61 AV694317.1           24796         1.67         2.0E-61 AV694317.1           24796         1.67         2.0E-61 AV694317.1           24796         1.67         2.0E-61 AV694317.1           25744         31950         1.34         2.0E-61 AV694317.1           14584         27026         1.26         1.0E-61 AV69431.1           15049         27026         1.26         1.0E-61 AV6943.1           15049         28150         1.0E-61 AV6943.1           15049         28160         0.98         1.0E-61 AV6943.1           1</td><td>Ewon ORF SEQ         Expression Signal         (Top) Hit Top Hit Acession Value           NO:         Signal         (Top) Hit Top Hit Acession Value           14358         27461         5.33         2.0E-61 N53039.1           15226         35829         1.36         2.0E-61 N39397.1           19718         33094         0.88         2.0E-61 AV694317.1           22296         35839         1.67         2.0E-61 AV60238.1           23164         37101         2.94         2.0E-61 AV60238.1           24196         0.98         2.0E-61 AV602317.1           24196         1.67         2.0E-61 AV60238.1           13649    
    2.0E-61 AV60231.1           14884         27026         1.26         1.0E-61 AV60233.1           14884         27026         1.26         1.0E-61 AV60233.1           15049         28160         4.43         1.0E-61 AV60233.1           15049         28160         1.0E-61 AV60233.1           15049         28160         1.0E-61 AV60233.1           15049         28160         1.0E-61 AV60233.1           15049         28160         1.0E-61 AV60233.1           15049         28160         1.0E-61 AV60233.1           15640         2</td><td>Evan ORF SEQ         Expression Signal         (Top) Hit Top Hit Acession Vellue           NO:         10 NO:         Signal         (Top) Hit Top Hit Acession Vellue           14398         27461         5.33         2.0E-61         NG3039.1           15824         1.36         2.0E-61         NG3039.1           15824         1.72         2.0E-61         NG3039.1           22706         33094         0.88         2.0E-61         AV694317.1           22707         36783         1.67         2.0E-61         AV602317.1           23164         37101         2.94         2.0E-61         AV602317.1           23491         37101         2.94         2.0E-61         AV602317.1           23494         36783         1.67         2.0E-61         AV602317.1           23491         37101         2.94         2.0E-61         AV60231.2           14584         27026         1.26         1.0E-61         AV60238.1           14584         27026         1.26         1.0E-61         AV60233.1           15049         28150         1.0E         1.0E-61         AV62303.2           15049         28150         1.0E-61         AV6231.1           16504</td></t<> | Evon NO:         ORF SEQ Signal         Expression Signal         (Top) Hit Top Hit Acession Value           NO:         10 NO:         Signal         (Top) Hit Top Hit Acession Value           14861         27461         5.33         2.0E-61         BE168410.1           14861         27938         1.36         2.0E-61         N53039.1           16229         35829         1.67         2.0E-61         N53039.1           22700         0.98         2.0E-61         AV694317.1           23491         37101         2.84         2.0E-61         AV600256.1           23492         37101         2.84         2.0E-61         AV600256.1           23491         37101         2.84         2.0E-61         AV600256.1           23491         37101         2.84         2.0E-61         AV600256.1           23491         37101         2.84         2.0E-61         AV600256.1           23491         37101         2.84         2.0E-61         AV600256.1           23491         37101         2.84         2.0E-61         AV600256.1           14584         27026         1.35         1.0E-61         AV63026.1           14549         27026         1.0E-61 | Exon ORF SEQ         Expression Signal         (Top) Hit Top Hit Acession No: SEQ ID         Most Similar IT Top Hit Acession No: SEQ ID           NO: NO: NO: NO: NO: Signal         2.0E-61 BE168410.1         No. No: No: No: No: No: No: No: No: No: No:                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | Exon ORF SEQ         Expression Signal         (Top) Hit Top Hit Acession No: No: No: No: No: No: No: No: No: No: | Expn<br>NO:         ORF SEQ<br>Signal         Expression<br>(Top) Hit<br>Vellue         (Top) Hit<br>Vellue         Top Hit Acession<br>Vellue           14861         27461         5.33         2.0E-61         BE168410.1           14861         27638         1.36         2.0E-61         N53039.1           15824         1.72         2.0E-61         N53039.1           15824         1.72         2.0E-61         N83039.1           22700         0.38         2.0E-61         AV694317.1           22700         0.38         2.0E-61         AV602317.1           24195         36763         1.67         2.0E-61         AV602317.1           24795         36763         1.67         2.0E-61         AV602317.1           24795         1.67         2.0E-61         AV602317.1           25744         31950         1.34         2.0E-61         AV60231.1           15649         27026         1.37         1.0E-61         AV60232.2           14958         1.0E-61         AV60233.1         1.0E-61         AV60233.1           15649         27026         1.0E-61         AV60233.1           15640         28531         1.0E-61         AV60233.1           16680         26650< | Ewn ORF SEQ         Expression Signal         (Top) Hit Top Hit Acession Value           NO:         Signal         (Top) Hit Top Hit Acession Value           14851         27461         5.33         2.0E-61 BE168410.1           14851         27938         1.36         2.0E-61 N53039.1           15824         1.72         2.0E-61 N38397.1           15824         33094         0.88         2.0E-61 AV694317.1           22700         0.98         2.0E-61 AV694317.1           23164         35701         2.0E-61 AV694317.1           23491         37101         2.94         2.0E-61 AV694317.1           24795         1.67         2.0E-61 AV694317.1           24796         1.67         2.0E-61 AV694317.1           24796         1.67         2.0E-61 AV694317.1           24796         1.67         2.0E-61 AV694317.1           25744         31950         1.34         2.0E-61 AV694317.1           14584         27026         1.26         1.0E-61 AV69431.1           15049         27026         1.26         1.0E-61 AV6943.1           15049         28150         1.0E-61 AV6943.1           15049         28160         0.98         1.0E-61 AV6943.1           1 | Ewon ORF SEQ         Expression Signal         (Top) Hit Top Hit Acession Value           NO:         Signal         (Top) Hit Top Hit Acession Value           14358         27461         5.33         2.0E-61 N53039.1           15226         35829         1.36         2.0E-61 N39397.1           19718         33094         0.88         2.0E-61 AV694317.1           22296         35839         1.67         2.0E-61 AV60238.1           23164         37101         2.94         2.0E-61 AV60238.1           24196         0.98         2.0E-61 AV602317.1           24196         1.67         2.0E-61 AV60238.1           13649         2.0E-61 AV60231.1           14884         27026         1.26         1.0E-61 AV60233.1           14884         27026         1.26         1.0E-61 AV60233.1           15049         28160         4.43         1.0E-61 AV60233.1           15049         28160         1.0E-61 AV60233.1           15049         28160         1.0E-61 AV60233.1           15049         28160         1.0E-61 AV60233.1           15049         28160         1.0E-61 AV60233.1           15049         28160         1.0E-61 AV60233.1           15640         2 | Evan ORF SEQ         Expression Signal         (Top) Hit Top Hit Acession Vellue           NO:         10 NO:         Signal         (Top) Hit Top Hit Acession Vellue           14398         27461         5.33         2.0E-61         NG3039.1           15824         1.36         2.0E-61         NG3039.1           15824         1.72         2.0E-61         NG3039.1           22706         33094         0.88         2.0E-61         AV694317.1           22707         36783         1.67         2.0E-61         AV602317.1           23164         37101         2.94         2.0E-61         AV602317.1           23491         37101         2.94         2.0E-61         AV602317.1           23494         36783         1.67         2.0E-61         AV602317.1           23491         37101         2.94         2.0E-61         AV60231.2           14584         27026         1.26         1.0E-61         AV60238.1           14584         27026         1.26         1.0E-61         AV60233.1           15049         28150         1.0E         1.0E-61         AV62303.2           15049         28150         1.0E-61         AV6231.1           16504 |

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Top Hit Descriptor	Homo sapiens hypothetical protein FLJ20128 (FLJ20128), mRNA	Homo sapiens growth hormone releasing hormone (GHRH), mRNA	Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D3) genes, complete cds	MR0-BN0070-040400-010-h01 BN0070 Homo sapiens cDNA	Homo sapiens cadherin 18 (CDH18), mRNA	Нопо saplens KIAA0971 protein (KIAA0971), mRNA	Homo saplens actinin, alpha 4 (ACTN4), mRNA	Homo sapiens P/OKcl.19 mRNA for ubiquilln-conjyugating enzyme E2, complete cds	Homo sapiens mRNA for CSR2, complete cds	Homo saplens gene for AF-6, complete cds	Homo saplens low density lipoprotein-related protein 2 (LRP2), mRNA	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA	Homo sapiens GTP binding protein 1 (GTPBP1), mRNA	RC4-BT0310-110300-015-f10 BT0310 Homo sapiens cDNA	co66h11.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1354725 3' similar to SW:POL_MLVRK	TOURS FOLLOWING	AV714334 DCB Homo sapiens cDNA clone DCBAMA08 5	NUCLEOLAR TRANSCRIPTION FACTOR 1 (UPSTREAM BINDING FACTOR 1) (UBF-1) (AUTOANTIGEN NOR-90)	Homo saplens hypothetical protein (FLJ20261), mRNA	og56e04.x1 Scares_testis_NHT Homo capiens cDNA done IMAGE:1839150 3' similar to TR:O15103 015103 HYPOTHETICAL 27.3 KD PROTEIN.;	Human zinc finger protein ZNF131 mRNA, partial cds	Homo sapiens CGI-56 protein (CGI-56), mRNA	wi04d02x1 NCI_CGAP_CLL1 Homo sapiens cDNA clone IMAGE:2389251 3'	wi04d02.x1 NCI_CGAP_CLL1 Homo saplens cDNA clone IMAGE:2389251 3'	UI-HF-BPop-aif-d-09-0-UI.11 NIH_MGC_51 Homo sapiens cDNA clone IMAGE:3072833 5'	Homo sapiens CGI-18 protein (LOC51008), mRNA	MR3-ST0203-130100-025-a09 ST0203 Homo sepiens cDNA	wx51e07.x1 NCI_CGAP_Lu28 Homo saplens cDNA clone IMAGE:2547204.3' similar to SW:GG95_HUMAN_C00370 CDI_CIN_O5_contains_alament to SW:GG95_HUMAN_C00370 CDI_CIN_O5_contains_alament.	Homo sepiens Xa bseudosuma region: segment 1/2	Homo sapiens Xq pseudoautocomal ragion; segment 1/2
Top Hit Database Source	M	F	5	EST HUMAN	M	F	IN	FZ	Ę	NT	Σ	Į.	N	EST_HUMAN	146441111111111111111111111111111111111	NAMOR - CO	EST_HUMAN	SWISSPROT	NT	EST HUMAN	NT.	۲	EST_HUMAN	EST_HUMAN	EST HUMAN	۲	EST_HUMAN	1444 III 1400	L L	Ę
Top Hit Acession No.	R923130 NT	11034840 NT	1.0E-61 AF224669.1	1.0E-61 AW999726.1	11416280 NT	11428892 NT	11425578 NT	1.0E-61 AB044550.1	1.0E-61 AB007830.1	1.0E-61 AB011399.1	11430460 NT	11430460 NT	11418127 NT	9.0E-62 BE064386.1	7 000 000 0	8.UE-02 AMOSU42U.1	7.0E-62 AV714334.1	217480	11427985 NT	7.0E-62 AI208681.1	J09410.1	11418255 NT	6.0E-62 AI762801.1	6.0E-62 AI762801.1	6.0E-62 AW 501124.1	11431139 NT	6.0E-62 AW814393.1	TO A	5.0E-62 A.1271735.1	5.0E-62 AJ271735.1
Most Similar (Top) Hit BLAST E Value	1.0E-61	1.0E-61	1.0E-61	1.0E-61	1.0E-61	1.0E-61	1.0E-61	1.0E-61	1.0E-61	1.0E-61	1.0E-61	1.0E-61	1.0E-61	9.0E-62	00 20 0	8.UE-02/	7.0E-82	7.0E-62 P17480	7.0E-62	7.0E-82	6.0E-62 U09410.1	8.0E-62	6.0E-62	6.0E-62	6.0E-82	6.0E-62	6.0E-62	100	5.0E-82	5.0E-62
Expression Signal	1.39	2.69	3.84	2.78	0.58	4.8	5.61	1.72	1.44	21.57	4	4	10.94	1.06	90	0.00	1.12	48.0	76.0	4.05	1.55	5.37	3.47	3.47	0.68	1.52	3.67	4	5 18	5.16
ORF SEQ ID NO:	33884	_	35123	L	36193			37880	L		31677						27351	29775			L			34352		35063		79900		28730
Exen SEQ ID NO:	20421	ı	21589	ı	22622	23270		24247	24388		26031		25676	23600	l	-1	14296	16759	•	24712	L			[	•	21533	22619	70307	1	1
Probe SEQ ID NO:	7341	8326	8508	9482	9557	10235	10871	11178	11325	12242	12286	12286	13028	10565	7670	2/04	1131	3595	6038	11632	3063	3471	7803	. 7803	8277	8452	9554	50,	2478	2478

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	Top Hit Descriptor	Homo saplens ryanodine receptor 3 (RYR3) mRNA	zw78e09.s1 Soares_testis_NHT Homo sepiens cDNA clone IMAGE:782344 3' similar to SW INRDC_RA I	P47245 NARDILYSIN;	Homo saplens ryanodina receptor 5 (N 10.5) intoving	mo7go9.x1 NIH_MGC_17 Homo sapienc curva cione image: 2301010 3	Homo sapiens muscle specific gane (MS), mKNA	Homo sapiens muscle specific gene (M9), mRNA	au71403.yf Schnedder fetal brain 00004 Homo sapiens cDNA cone INAGE:2781/01 3 simusi in gb.in3.7 104- ATP SYNTHASE COUPLING FACTOR 6, MITOCHONDRIAL PRECURSOR (HUMAN);	au71403.yf Schneider fetal brain 00004 Homo sapiens cJNA clone INACE:2761701 3 silliata to go.ins. 1 oc. ATP SyNTHASE COUPLING FACTOR 6, MITOCHONDRIAL PRECURSOR (HUMAN);	274.400 of Schmolder fetal brain 00004 Homo sapiens cDNA clone IMAGE:2781701 5' similar to gb:\M37104	ATP SYNTHASE COUPLING FACTOR 6, MITOCHONDRIAL PRECURSOR (HUMAN);  ATP SYNTHASE COUPLING FACTOR 6, MITOCHONDRIAL PRECURSOR (HUMAN);	au71d03.yl Schneider fetal brain u0004 Fibrito septeris Colva Civile Information (HUMAN); ATP SYNTHASE COUPLING FACTOR 6, MITOCHONDRIAL PRECURSOR (HUMAN);	Wf12b08.x1 Soares_NFL_T_GBC_S1 Home sapiens cDNA cione invade	gb:X57138_mat HISTONE H28.2 (HUMAN);	wrizbokxi soeres into Toulo september of the Arabida September of the Arabida September of the Arabida September of the Arabida September of the Arabida September of the Arabida September of the Arabida September of the Arabida September of the Arabida September of the Arabida September of the Arabida September of the Arabida September of the Arabida September of the Arabida September of the Arabida September of the Arabida September of the Arabida September of the Arabida September of the Arabida September of the Arabida September of the Arabida September of the Arabida September of the Arabida September of the Arabida September of the Arabida September of the Arabida September of the Arabida September of the Arabida September of the Arabida September of the Arabida September of the Arabida September of the Arabida September of the Arabida September of the Arabida September of the Arabida September of the Arabida September of the Arabida September of the Arabida September of the Arabida September of the Arabida September of the Arabida September of the Arabida September of the Arabida September of the Arabida September of the Arabida September of the Arabida September of the Arabida September of the Arabida September of the Arabida September of the Arabida September of the Arabida September of the Arabida September of the Arabida September of the Arabida September of the Arabida September of the Arabida September of the Arabida September of the Arabida September of the Arabida September of the Arabida September of the Arabida September of the Arabida September of the Arabida September of the Arabida September of the Arabida September of the Arabida September of the Arabida September of the Arabida September of the Arabida September of the Arabida September of the Arabida September of the Arabida September of the Arabida September of the Arabida September of the Arabida September of the Arabida September of the Arabida September of the Arabida September of the Arabida September of the Arabida September of the A	Homo sapiens keratin 18 (KK 118) mKNA  Homo sapiens keratin 18 (KK 118) mKNA	Homo sapiens solute carrier tarning 13 (socialing dependent cacarony)	Homo sapiens ubiquitin specific protease 9, X chromosome (Drosophila fat facets related) (USP9X), mRNA	Homo septens phosphoribosyl pyrophosphate synthetase 2 (PNF 52), tilinyly Homo septens phosphoribosyl pyrophosphate syntheta 30(A) (FIF 3R2), mRNA	Homo sapiens eukaryotic translation initiation ractor zb, subunit z (beta, sanz) (Eli 2011), ill. 1900.	Homo saplens eukaryoto translation intradiori rackir zo, subulin z (bodus) poly	Homo sapiens 26S proteasome-associated pad 1 nomolog (PORT), minute	Homo sapiens mRNA for KIAA1263 protein, partial cas	H.sapiens flow-sorted chromosome 6 Hindill Tragment, Scopk 1905	H.sapiens flow-sorted chromosome o ningili itaginetti, occur i occur i occur i occur i occur i occur i occur i occur i occur i occur i occur i occur i occur i occur i occur i occur i occur i occur i occur i occur i occur i occur i occur i occur i occur i occur i occur i occur i occur i occur i occur i occur i occur i occur i occur i occur i occur i occur i occur i occur i occur i occur i occur i occur i occur i occur i occur i occur i occur i occur i occur i occur i occur i occur i occur i occur i occur i occur i occur i occur i occur i occur i occur i occur i occur i occur i occur i occur i occur i occur i occur i occur i occur i occur i occur i occur i occur i occur i occur i occur i occur i occur i occur i occur i occur i occur i occur i occur i occur i occur i occur i occur i occur i occur i occur i occur i occur i occur i occur i occur i occur i occur i occur i occur i occur i occur i occur i occur i occur i occur i occur i occur i occur i occur i occur i occur i occur i occur i occur i occur i occur i occur i occur i occur i occur i occur i occur i occur i occur i occur i occur i occur i occur i occur i occur i occur i occur i occur i occur i occur i occur i occur i occur i occur i occur i occur i occur i occur i occur i occur i occur i occur i occur i occur i occur i occur i occur i occur i occur i occur i occur i occur i occur i occur i occur i occur i occur i occur i occur i occur i occur i occur i occur i occur i occur i occur i occur i occur i occur i occur i occur i occur i occur i occur i occur i occur i occur i occur i occur i occur i occur i occur i occur i occur i occur i occur i occur i occur i occur i occur i occur i occur i occur i occur i occur i occur i occur i occur i occur i occur i occur i occur i occur i occur i occur i occur i occur i occur i occur i occur i occur i occur i occur i occur i occur i occur i occur i occur i occur i occur i occur i occur i occur i occur i occur i occur i occur i occur i occur i occur i occur i occur i occur i occur i occur i occur i occur i occur i occur i	thyroid-samulating norther parties (HRIHFB2122) mRNA	Homo septens putative increal protein ( )	
	Top Hit Database Source			T_HUMAN		EST_HUMAN f			T_HUMAN		Т	EST_HUMAN	EST_HUMAN		EST HUMAN	T_HUMAN			۲	LN	NT	NT	NT	NT	NT	LN.	LZ.	LN I	N
	Top Hit Acession No.	4506758 NT		5.0E-62 AA431093.1	4506758 NT	5.0E-62 AW410687.1	5574	11425574 NT	0E-62 AW161479.1		UE-02 AW 101179	.0E-62 AW161479.1	.0E-62 AW 161479.1		4.0E-62 AI827900.1	4.0E-62 AI827800.1	4557887 NT	4506978 NT	11420654 NT	11421041 NT	7657057 NT	7657057 NT	11429973 NT	4.0E-62 AB033089.1	4.0E-62 Z78766.1	4.0E-62 Z78766.1	4.0E-62 S70584.1		11418192INI
	Most Similar (Top) Hit BLAST E	5 0F-62	1	5.0E-62 A	5.0E-62	5.0E-62	5.0E-62	5.0E-62	4.0E-62	Lo	4.0E-02/	4.0E-62	4.0E-62		4.0E-62	4.0E-62	4.0E-62	4.0E-62	4.0E-62			4.0E-62	L		L				4.0E-62
-	Expression Signal	255	30.3	1.75	0.74	12.91					2.1/	1,32	1.32		1.9	1.9	60'6	17.1	2.81								63.7		1.65
	ORF SEQ ID NO:		20057	30568			1	38275			27103	27102			28778	28779		32553				34362	L	L	37973				6
	SEQ ID	1	100/3	17587	L	22782	L				14040	14040	L		15654		ì	l .	<u> </u>	1	1	20867		1	┸	3 24332		_'	Ш
	Probe SEQ ID NO:	300	3206	4447	8778	0747	11 10	3	34011	3	88	864	798	3	2529	2529	3486	8046	8428	7322		7813	8364	8	11263	1128	11500	12269	12497

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Top Hit Descriptor	Homo sapiens cadherin EGF LAG seven-pass G-type receptor 1 (CELSR1), mRNA	Homo saplens calcineurin binding protein 1 (KJAA0330), mRNA	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA	Homo saplens neurofibromin 2 (bilateral acoustic neuroma) (NF2) mRNA	Homo sapiens mRNA for KIAA1476 protein, partial cds	Homo saplens mRNA for K/AA1476 protein, partial cds	Human cyclophilin-related processed pseudogene	was3804.x1 NCI_CGAP_Kid11 Homo saplens cDNA clone IMAGE:2299903 3' similar to contains THR.t2 THR repetitive element :	Homo sapiens chromosome 21 segment HS21C084	RC0-BN0284-300500-031-e05 BN0284 Homo sapiens oCNA	RC0-BN0284-300500-031-e05 BN0284 Homo saplens cDNA	Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3	(UBE2D3) genes, complete cds	QV4-BT0257-081199-017-e03 BT0257 Homo sapiens cDNA	Homo sapiens intersectin 2(SH3D1B) mRNA, complete cds	Homo saplens ADP/ATP carrier protein (ANT-2) gene, complete cds	ef70e11.r1 Soares_NhHMPu_S1 Homo saplens cDNA clone IMAGE:1047404 5' similar to WP:K01H12.1 CE03453 :	DKFZp566F104_r1 566 (synonym: hfkd2) Homo sapiens cDNA clone DKFZp566F104 5	Homo sapiens hypothetical protein FLJ20212 (FLJ20212), mRNA	Homo sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal	protein L18a (RPL18a), Ca2+/Calmodulin-dependent protein kinase I (CAMKI), creatine transporter (CRTR),	CDM protein (CDM), adrenoleukodystrophy protein >	eb05c02.sr] Stratagene fetal retina 937202 Homo sapiens cDNA clone IMAGE:839906 3'	zg89f10.s1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:409771 3'	zg89f10.s1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:409771 3'	zs93e07.r1 NCI_CGAP_GC81 Homo saplens cDNA clone IMAGE:705060 5'	Homo sapiens KIAA0763 gene product (KIAA0763), mRNA	Homo sepiens KIAA0763 gene product (KIAA0763), mRNA	H. sapiens lysosomel acid phosphatase gene (EC 3.1.3.2) Exon 9	H.sapiens lysosomal acid phosphatase gene (EC 3.1.3.2) Exon 9	aa33d08.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:815055 3'
Top Hit Detabase Source	NT	TN	님	N-	NT	۲	۲	NT	EST HUMAN	NT	EST HUMAN	EST HUMAN		ΝŢ	EST HUMAN	ĽΝ	F	EST HUMAN	EST_HUMAN	8923201 NT			ħ	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	뉟	۲Z	۲	NT	EST_HUMAN
Top Hit Acesslon No.	11418322 NT	11417862 NT	11417862 NT	11430460 NT	4557794 NT	3.0E-62 AB040909.1	3.0E-62 AB040909.1	K52858.1	3 0F-62 A 632733 1	2.0E-62 AL163284.2	2.0E-62 BF329911.1	2.0E-62 BF329911.1		2.0E-62 AF224669.1	2.0E-62 BF330676.1	1.0E-62 AF248540.1	78810.1	1.0F-62 AA625207.1	1.0E-62 AL039044.1	8923201			J52111.2	1.0E-62 AA490060.1	1.0E-62 AA722878.1	1.0E-62 AA722878.1	1.0E-62 AA280050.1	7662289 NT	7662289 NT	X15533.1	1.0E-62 X15533.1	1.0E-62 AA465170.1
Most Similar (Top) Hit BLAST E Value	4.0E-62	4.0E-62	4.0E-62	4.0E-62	3.0E-62	3.0E-62	3.0E-62	3.0E-62 X52858.1	3.05-62	2.0E-62	2.0E-62	2.0E-62		2.0E-62	2.0E-62	1.0E-62	1.0E-62 L78810.1	1.0E-62	1.0E-62	1.0E-62			1.0E-62 U52111.2	1.0E-62	1.0E-62	1.0E-62	1.0E-62	1.05-62	1.0E-62	1.0E-62 X15533.1	1.0E-62	1.0E-62
Expression Signal	1.66	6.86	6.86	2.16	0.69	1.13	1.13	4.19	3.74	2.71	5.59	5.59		3.71	8.83	1.14	18.41	164	1.22	<u>2</u>			2.02	1.07	2.69	2.69	0.54	1.65	1.65	1.92	1.92	3.03
ORF SEQ ID NO:	31955	31952			26338		29302	29956	35361	27482	35595	35596				27294	27809			30767			32960	33820	33834	33835	35577	35885		35928		36263
Exon SEQ ID NO:	25657		Į	1	13312	16287	16287	16950	21816	Ł	L	<u> </u>	ı	23411	24973	14235	14728	14988	1	17784					20377	L.	22036	22335	22335	22378	22378	22695
Probe SEQ ID NO:	12946	13004	13004	13059	76	3111	3111	3789	8737	1259	8974	8974		10376	11988	1069	1575	1842	2981	4648			6418	7284	7295	7295	8957	9258	9258	9302	9302	9757

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Most Similar (Top Hit Acession Database Top Hit Descriptor Source Source	1.0E-62 Z78698.1 NT	1.0E-62 11418322 NT	1.0E-62 11430460 NT	9.0E-63 AW816405.1   EST_HUMAN   QV4-ST0234-181199-037-405 ST0234 Homo sapiens cDNA	9.0E-63 C18159.1 EST_HUMAN   C18159 Human placenta cDNA (TFujiwara) Homo saplens cDNA done GEN-558C10 5"	9.0E-63 AB002348.2 NT Homo saplens mRNA for KIAA0350 protein, partial cds		9.0E-63 11418185 NT	9.0E-63 Y15056.1 NT	9.0E-63 11426985 NT		9.0E-63 11421160 NT	9.0E-63 BF2034	8.0E-63 4557734 NT Homo sapiens monoamine oxidase A (MAOA), nuclear gene encoding mitochondrial protein, mRNA	8.0E-63 5031810 NT	8.0E-63 AF198349.1 NT	8.0E-63 AF198349.1 NT	8.0E-63 AL163268.2 NT	7.0E-63 AI872137.1 EST HUMAN	REGS102.11 NCI_CGAP_Pr1 Homo sapiens cDNA clone IMAGE:745947 similar to gb:Y00361 60S in FIRE THI MAN RIBOSOMAL PROTEIN (HUMAN):	5.0E-63 11526464 NT	4.0E-63 AL163278.2 NT	4.0E-63 AB014607.1 NT	4.0E-63 AB014607.1 NT	4.0E-63 AW 750372.1 EST_HUMAN	4.0E-63 AW750372.1   EST_HUMAN	4.0E-63 AW134709.1 EST_HUMAN	4.0E-63 AW134709.1 EST_HUMAN	3.0E-63 AB018260.1 NT	3.0E-63 J00310.1 NT	3.0E-63 6005963 NT	3.0E-63 11545810 NT Homo saplens hepatocellular carcinoma antigen gene 520 (LOC63928), mRNA
 Cop Hit Acession No.		11418322 NT	11430460 NT					11418185 NT		11426985 NT	4885544 NT	11421160 NT		4557734 NT	5031810 NT						26464										LN 5969009	11545810 NT
Similar p) Hit ST E	1.0E-62	1.0E-62	1.0E-62	9.0E-63 /	9.0E-63 (	9.0E-63	9.0E-63	9.0E-63	9.0E-63	9.0E-63	9.0E-63	9.0E-63	9.0E-63	8.0E-63	8.0E-63	8.0E-63	8.0E-63	8.0E-63	7.0E-63	8.0E-83.	5.0E-63	4.0E-63	4.0E-63				4.0E-63	4.0E-63			3.0E-63	3.0E-63
	ळ	122	9	12.	2.17	8.77	8.77	4.69	44.	3.78	1.77	1.18	65	3.05	2.58	4.26	8	4.36	3,38	70 50	0.62	0.88	1.06	1.06	2.6	2.6	202	202	15.19	1.49	11.84	33.93
Expression Signal	2.26	4.63	3.15	2.27	2.	80	8	4	-	8	-	<del>-</del>		3	2	4													1		Ì	e.
ORF SEQ Expression ID NO: Signal	38419 2.2			26587 2.2		30297	30298	38824	31822	33875	34571	35139	38003	28877	28703	29727	29728	30505			35698	29584	30066	30067	33116			38122	28235	29061	27493	33151
								18484 38824	31822	20413 33875	21059 34571	21602 35139	38003		28703	29727	L		14125		22154 35698	29584	17069 30066	17069 30067	19737		24458		28235	15954 29061	14425 27493	19763 33151

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庆평>	Hit Top Hit Acession	11 co	
22947         36533         0.83           22947         36534         0.83           13419         28449         1.69           13420         26457         1.05           13704         1.16         1.16           1470         27087         3.07           1476         27834         1.54           14966         28049         2.02	. e	Database	Top Hit Descriptor
22947 36534 0.83 13410 28440 1.69 13425 26457 1.05 13704 1.19 14027 27087 3.07 14750 27884 1.54 14956 28049 2.02	3.0E-63 BE876158.1	EST HUMAN	601485656F1 NIH MGC 69 Homo sapiens cDNA clone IMAGE 3888253 5
13410         28440         1,69           13420         26457         1,05           13704         1,19         1,19           14702         27087         3,07           14760         27884         1,54           14966         28049         2,02           14800         28049         2,02	3.0E-63 BE876158.1	EST HUMAN	601485656F1 NIH MGC 69 Homo sapiens cDNA cone IMAGE:3889253 5/
13704 26457 1.05 13704 1.19 14727 27087 3.07 14760 27884 1.54 14956 28049 2.02	2.0E-63 U07804.1	LN	Human DNA topoisomerase I mRNA, partial cds
13704 1.19 14027 27087 3.07 14750 27834 1.54 14750 27835 1.54 14955 28049 2.02	2.0E-63 4885226 NT	9 NT	Iomo sapiens eyes absent (Drosophila) homolog 2 (EYA2), mRNA
14027 27087 3.07 14760 27834 1.54 14760 27835 1.54 14966 28049 2.02	2.0E-63 4557624 NT	TN P	Homo saplens glutamate-cysteine ligase (gamma-glutamytoysteine synthetase), catalytic (72.8kD) (GLCLC) mRNA
14760 27834 1,54 14760 27835 1,54 14966 28049 2.02	2.0E-63 7657042 NT	2NT	Homo sapiens Down syndrome candidate region 1 (DSCR1), mRNA
14750 27835 1.54 14955 28049 2.02	2.0E-63 AB030388.1	N	Homo sapiens RHCE mRNA for Rh blood CE group anticen notwertifide complete add
14956 28049 2.02	2.0E-63 AB030388.1	N <sub>T</sub>	Homo sapiens RHCE mRNA for Rh blood CF group antique profuse and complete cds
15202 20407	2.0E-63 BE410739.1	EST HUMAN	601301627F1 NIH MGC 21 Homo sapiens cDNA clone IMAGE:3838103 5'
co 1	2.0E-63 Al863961.1	EST_HUMAN	wj54b02.x1 NCI_CGAP_Lu19 Homo sapiens cDNA clone IMAGE.2406603 3' sImilar to gb:M57609 GL 3 PROTEIN (HUMAN);
16399 29411 1.94	2.0E-63 4502166 NT	S NT	Homo sepiens emvicid beta (A4) precursor protein (professe nevin II Atheimor disease) (ADD)
16529 29544 2,4	2.0E-63 AF109718.1	Ŋ	Homo satiens chromosome 3 subfelements review
30179 3.19	2.0E-63 L39891.1	ΕŃ	Homo sapiens polycystic kidney disease-associated profess (PKD1) none complete cole
4988 18117 31096 1.28 2.0E	2.0E-63 AF111167.2	Į.	Homo sepiens iun dimerization norbein nene narfial reference communication and university
5376 25802 31447 0.95 2.0F	2.0F-63	L N	Homo sepiens similar to ectonucleotide pyrophosphatase/phosphodiesterase 3 (H. sapiens) (LOC63214), PRIVITATION OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPE
19190 32509 2.41	BF3735	EST HIMAN	OV4-FT0470-040700-298-005 FT0470 Home straiges and A
19190 32510 2.41	2.0E-63 BF373541.1	EST HUMAN	QV1-FT0170-040700-285-005 FT0170 Homo saniens cDNA
19487 32842 1.07	2.0E-63 11421940 NT	LN 0	Homo saplens protein kinase, cAMP-dependent, regulatory, type II, beta (PRKAR2R), mRNA
19487 32843 1.07	2.0E-63 11421940 NT	0 NT	Homo sapiens protein kinase, cAMP-dependent, regulatory, type II, beta (PRKAR2B), mRNA
8841 19994 33403 1.43 2.0E	2.0E-63 U66059.1	L.	Human germiline T-cell receptor beta chain Doparnine-beta-hydroxylase-like, TRY1, TRY2, TRY3, TCRBV2781P, TCRBV2781P, TCRBV2781P, TCRBV2781P, TCRBV278341T, TCRBV381A1T, TCRBV1383, TCRBV887P, TCRBV78342T, TCRBV138241T, TCRBV982A2PT, TCRBV782A1N4T, TCRBV1389/1382
20039 33448 0.72	20E-63 AB032369.1	Ę	Homo saplens MIST mRNA, partial cds
20039 33449 0.72	2.0E-63 AB032369.1	Ę	Homo sapiens MIST mRNA, partial cds
33502 1.72	2.0E-63 9910365 NT	5 NT	Homo sapiens Carbonic anhydrase-related protein 10 (LOC56934), mRNA
20086 33503 1.72	2.0E-63 9910365 NT	5 NT	Homo sapiens Carbonic anhydrase-related protein 10 (LOC56934), mRNA
21007 34517 0.96	2.0E-63 AB046844.1		Homo sapiens mRNA for KIAA1624 protein, partial cds
21810 35346 4.29	2.0E-63 AL163210.2	N	Homo saplens chromosome 21 segment HS21C010

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Topos Evidence III Placenta	Top Hii Descriptor	The state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the s	WY 138U3.X1 NCI_CGAP_Bm23 Homo saplens cDNA clone IMAGE:2529438 3'	wy 3803.X1 NCI_CGAP_Bm23 Homo saplens cDNA clone IMAGE:2529436 3*	Inomo sapiens MCP-1 gene and enhancer region	Homo serience contain the contained of the contained of the contained of the contained of the contained of the contained of the contained of the contained of the contained of the contained of the contained of the contained of the contained of the contained of the contained of the contained of the contained of the contained of the contained of the contained of the contained of the contained of the contained of the contained of the contained of the contained of the contained of the contained of the contained of the contained of the contained of the contained of the contained of the contained of the contained of the contained of the contained of the contained of the contained of the contained of the contained of the contained of the contained of the contained of the contained of the contained of the contained of the contained of the contained of the contained of the contained of the contained of the contained of the contained of the contained of the contained of the contained of the contained of the contained of the contained of the contained of the contained of the contained of the contained of the contained of the contained of the contained of the contained of the contained of the contained of the contained of the contained of the contained of the contained of the contained of the contained of the contained of the contained of the contained of the contained of the contained of the contained of the contained of the contained of the contained of the contained of the contained of the contained of the contained of the contained of the contained of the contained of the contained of the contained of the contained of the contained of the contained of the contained of the contained of the contained of the contained of the contained of the contained of the contained of the contained of the contained of the contained of the contained of the contained of the contained of the contained of the contained of the contained of the contained of the contained of the contained of the contained of the contained of the contained of t	reams depend protein fundse C beta-II type (PRKCB1) mRNA, complete cds	Homo sapiens atrophin-1 interacting protein 1; activin receptor interacting protein 1 (KIAAA7NE)DNIA	Homo sapiens calcitonin receptor (CALCR), mRNA	Homo sapiens calcitonin receptor (CALCR), mRNA	Homo saplens mesenchyme homeo box 1 (MEOX1), mRNA	Homo sapiens mesendryme homeo box 1 (MEOX1), mRNA	Homo sepiens acetyl-CoA synthetase (LOC55902), mRNA	Homo sapiens progressive ankylosis-like protein (ANK) mRNA, complete ods	trkC Ihuman, brain, mRNA, 2715 nt]	Homo sapiens stromal antigen 3 (STAG3), mRNA	Homo sapiens stromal antigen 3 (STAG3), mRNA	wv13e03.x1 NCL_CGAP_Bm23 Homo sapiens cDNA clone IMAGE::5526436 3	wv/3e03.x1 NCI_CGAP_Bm23 Homo sapiens cDNA clone IMAGE:2529436 3'	Fromo sapiens interleukin 10 receptor, beta (IL 10RB), mRNA	Homo saplens chromosome 21 unknown mRNA	norio sapens ciromosome 21 unknown mRNA	Tidnio sapiens mittina for KiAA0903 protein, partial cds	Homo sapiens phosphogiucomutase-related protein (PGMRP) gene, complete cds	Human (3) mht protein homelee — — — — — — — — — — — — — — — — — —	Amor explaints (IAAAAAA) III.NAA, Cultiplette cas	Homo septems NAAGO 18 gene product (KIAA0618), mRNA	Homo scalence and the product (KIAA0618), mRNA	From Septems putative transcription factor CR53 (CR53) mRNA, partial cds	RCs ST0107 12000 015 - 20 0 20 0 20 0 20 0 0 0 0 0 0 0 0 0 0	PC3 ST0197 120200-013-803 S10197 Homo capiens cDNA	7.03-51 U.S 1.20.200-015-803 S.10197 Homo sepiens cDNA	G01589568E1 NIH 14CC 7 House aplens cDNA clone GEN-569E02 51	AV711714 DCA Homo segiens CDNA clone INA GE:3943577 5	C IONINGO DINO CITA CIDIO
100	Top Hit Database Source	EST DIMANI	EST CITY	ES I TOMAIN	- F	Z Z		LN.	LN.	Į.	NT	Ł	Z	Z	2	Z		7	HOMAN										T HI MAAN	Т	7	_	EST HUMAN		
	Top Hit Acession No.	6.0E-64 AW028445 1	8.0E-64 AW026445 4	6.0E-64 V18933 1	6.0E-64 V18933 4	6.0E-64 M13975.1		6912461 NT	11422189 NT	11422189 NT	TN 67862611	11525879 NT	N 05.024-1		10,000	1142019/ N	3 0F-64 AMODEANE	T	6.0E-64 AWV020445.1	50E-64 AF231919 1			ŀ		Γ	7662205 NT	7682205 NT	5.0E-64 AF017433 1	T		T	1	1		
	Most Similar (Top) Hit BLAST E Value	6.0E-64	8.0E-64	6.DE-64	6.0F-64	6.0E-64	100	8.0E-04	90.00	8.0E-04	0.0E-04	6.0E-04	R OF RA	6.0F-64	8 20 8	6 0F-64	6 OF SA	805 647	S OF SA	5.0E-64.A	5.0E-64 A	5.0E-64 A	5.0E-64 L40933 1	5.0E-64 L40933.1	5.0E-64 U89358.1	5.0E-64	5.0E-64	5.0E-64 A	4.0E-64 B	4.0E-64 A	4.0E-64 A	3.0E-64 C	3.0E-64 BE794381.1	3.0E-64 A	
	Expression Signal	3.91	3.91	2.95	2.95	5.32	09	27.0	27.0	254	2 54	730	175	2.16	4 68	4 68	1 73	173	2.98	4.18	4.18	1.02	1.15	1.15	1.54	. 4.43	4.43	7.25	0.71	2.34	234	8.77	0.82	1.83	
	ORF SEQ ID NO:	29372			L		32280	32452	32453	33925	33926	36164	36326	36546	37724	37725	29372	29373	32081	27078	27079	27598	27685	27686	27994	27746	27747	30231	34563	37763	37764	28532	29518	29704	
	Exon SEQ ID NO:			ı		Ц	18959	L	19137	1	20462	1	1	1	ı	24087			25280	14021	14021	14524	14608	14606	14898	14663	14683	17224	21050	24128	24128	15404	16500	16694	
	Probe SEQ ID NO:	3192	3192	5739	5739	5758	5767	5951	5951	7384	7384	9528	9026	9919	11008	11008	11269	11269	12400	843	843	1369	1453	1453	1749	/887	2887	4068	8000	11051	11051	2271	3327	3529	
																								_			_	_	_	-			_	_	

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Single Exon Probes Expressed in Placenta	. Top Hit Descriptor	AV711714 DCA Homo sapiens cDNA clone DCAAMCO1 5'	H. saplens isoform 1 gene for L-type calcium channel, exon 28	UI-HF-BP0p-akr-0-06-0-UI-r/ NIH MGC 51 Homo sapiens cDNA clone IMAGE:3073161 5	RC6-FN0019-290600-011-G11 FN0019 Homo sapiens cDNA	Homo saplens golgi matrix protein GM130 (GOLGA2) mRNA, complete cds	Homo sapiens golgi matrix protein GM130 (GOLGA2) mRNA, complete cds	bb72h12.y1 NIH_MGC_12 Homo sepiens cDNA clone IMAGE:3047975 5' similær to gb:L08069 DNAJ PROTEIN HOMOLOG 2 (HUMAN);	bb/2h12.y1 NIH MGC_12 Homo sapiens cDNA clone IMAGE:3047975 5' similar to gb:L08069 DNAJ PROTEIN HOMOLOG 2 (HUMAN):	Homo sapiens chromosome 21 segment HS21C046	Homo saplens chromosome 21 segment HS21C046	EST389493 MAGE resequences, MAGO Homo sapiens cDNA	EST389493 MAGE resequences, MAGO Homo saplens cDNA	Homo sapiens chromosome 21 segment HS21C046	Homo sapiens chromosome 21 segment HS21C046	Homo saplens chromosome 21 segment HS21 C027	af09d08.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:10311513'	Homo sapiens elF4E-like cap-binding protein (4EHP) mRNA	wo87b01.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2482281 3' similar to contains element L1 repetitive element:	Homo saplens chromosome 21 segment HS21C046	Homo sapiens chromosome 21 segment HS21C046	EST370215 MAGE resequences, MAGE Homo sapiens cDNA	EST370215 MAGE resequences, MAGE Homo sapiens cDNA	AU124387 NT2RM2 Homo sapiens cDNA clone NT2RM2002113 5	Homo sapiens anglopoietin 4 (ANG4) mRNA, partial cds	602123474F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4280395 5'	oz29b03.x1 Scares_total_fetus_Nb2HF8_9w Homo saplens cDNA clone IMAGE:1876717.3'	H. sapiens dopamine receptor D6 pseudogene 1, partial eds	Homo sapiens ataxin 2-binding protein 1 (A2BP1), mRNA	Homo saplens lymphocyte cytosolic protein 1 (L-plastin) (LCP1), mRNA	Homo saplens lymphocyte cytosolic protein 1 (L-plastin) (LCP1), mRNA	AU132570 NT2RP4 Homo sepiens cDNA clone NT2RP4000109 5'
e Exon Prope	Top Hit Database Source	EST HUMAN	Ę	EST HUMAN	EST HUMAN	Ę	Þ	EST_HUMAN	EST HUMAN	F	FN	EST HUMAN	EST HUMAN	LN LN	NT	- TN	EST_HUMAN	TN	EST HUMAN	F	TN	EST_HUMAN	EST_HUMAN	EST_HUMAN	ΤN	EST_HUMAN	EST_HUMAN	LN	TN	۲N	F	EST_HUMAN
Buis	Top Hit Acession No.	3.0E-64 AV711714.1	3.0E-64 Z26273.1	3.0E-64 AW 500861.1	3.0E-64 BF370000.1	3.0E-64 AF248953.1	3.0E-64 AF248953.1	3.0E-64 BE206521.1	3.0E-64 BE206521.1	3.0E-64 AL163246.2	3.0E-64 AL163246.2	3.0E-64 AW977384.1	3.0E-64 AW977384.1	3.0E-64 AL163246.2	3.0E-64 AL163246.2	.0E-64 AL163227.2	.0E-64 AA609940.1	4757701 NT	2.0E-64 AI927030.1	2.0E-84 AL163245.2	2.0E-64 AL163246.2	2.0E-64 AW958145.1	2.0E-64 AW958145.1	2.0E-64 AU124387.1	2.0E-64 AF113708.1	2.0E-64 BF668537.1	2.0E-64 AI078387.1	2.0E-64 M77185.1	11431054 NT	11434008 NT	11434008 NT	2.0E-64 AU132570.1
	Most Similar (Top) Hit BLAST E Value	3.0E-64	3.0E-64	3.0E-64	3.0E-64	3.0E-64	3.0E-64	3.0E-64	3.0E-64	3.0E-64	3.0E-64	3.0E-64	3.0E-64	3.0E-64	3.0E-64	3.0E-64	2.0E-64	2.0E-64	2.0E-64	2.0E-84 /	2.0E-64	2.0E-64	2.0E-64	2.0E-64	2.0E-64	2.0E-64	2.0E-64	2.0E-64	2.0E-64	2.05-64	2.0E-64	2.0E-64
	Expression Signal	1.83	1.31	. 0.68	3.2	1.86	1.85	1.48	1.48	1.12	1.12	0.66	99.0	1.54	1.54	2.16	1.1	3.2	1.28	2.4	2.4	0.98	0.98	2.28	1.23	5.04	1.3	2.96	0.67	1.08	1.08	1.09
	ORF SEQ ID NO:		32731				35282	35303	35304				36350	38248			27334	27655		28840			30046		32900		33272	33402	34562	35480	35481	38071
	Exan SEQ ID NO:	ı		ı	1		21741	21772	21772	22682	22682	22779	22779	24571	24571	24975	14277	14582	15717	15721	15721	17046	17046	19308	19541	19774	19881	19993	21040	21947	21947	22505
	Probe SEQ ID NO:	3529	6206	6471	6622	8661	8861	8692	8692	9627	9627	9714	9714	11514	11514	11990	1112	1428	2592	2597	2597	3887	3887	6129	6372	6614	6724	6840	2000	8868	8888	9431

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Probe SEQ ID NO:	Exen SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
10184		36815			2.0E-64 T06397.1	EST HUMAN	EST04286 Fetal brain, Stratagene (cat#696206) Horm saniens cONA class HEB is a
10184	l		9.0	١,	2.0E-64 T06397.1	EST HUMAN	EST04286 Fetal brain. Stratagene (cet#836206) Hormo saniens cDNA clane Lippose
11000		37714	2.21	2.0E-64	2.0E-64 BF528114.1	EST HUMAN	602042882F1 NCI CGAP Briefy Homo saniens CNA Abras MAGE: 4480FE8 E1
11306		38012	4.28	2.0E-64	2.0E-64 AI922911.1	EST HUMAN	wn81b08.xf NCI CGAP Utf Homo septens cDNA clare IMAGE: 2452244 2
11306		38013	4.28	2.0E-64	2.0E-64 AI922911.1	EST HUMAN	wn81b06.xf NCI CGAP Utf Home septeme CDNA clare IMAGE: 2452241.3
11509		38244	1.46	2.0E-64	2.0E-64 AW864773.1	EST HUMAN	PMZ-SN0018-220300-002-e12 SN0018 Homo saniens cDNA
12804			3.59	2.0E-64		EST HUMAN	CHR220101 Chromosome 22 exon Homo sapiens cDNA clone C22 132 F
268	13487	26517	1.39	1.0E-64	1.0E-64 AF231919.1	NT	Homo saplens chromosome 21 unknown mRNA
1820	14969	28061	24.22	1.0E-64	1.0E-64 AI929419.1	FST HIMAN	au60c01.x1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2619136 3' similar to
3076	16252	29274	9.0	1.0E-64	4507334 NT	LN	Homo sabiens synabtorian in 1 (SYN.11) mRNA
							Homo saplens transcription factor IGHM enhancer 3. JM11 profain. IM4 profain. IM5 profain. TEX professional control of the professional control of the professional control of the professional control of the professional control of the professional control of the professional control of the professional control of the professional control of the professional control of the professional control of the professional control of the professional control of the professional control of the professional control of the professional control of the professional control of the professional control of the professional control of the professional control of the professional control of the professional control of the professional control of the professional control of the professional control of the professional control of the professional control of the professional control of the professional control of the professional control of the professional control of the professional control of the professional control of the professional control of the professional control of the professional control of the professional control of the professional control of the professional control of the professional control of the professional control of the professional control of the professional control of the professional control of the professional control of the professional control of the professional control of the professional control of the professional control of the professional control of the professional control of the professional control of the professional control of the professional control of the professional control of the professional control of the professional control of the professional control of the professional control of the professional control of the professional control of the professional control of the professional control of the professional control of the professional control of the professional control of the professional control of the professional control of the professional control of the professional contro
3601	16765	29781	5.47	10.4	4 OF 84 AE408770 4	<u> </u>	JM10 protein, A4 differentiation-dependent protein, triple LIM domain protein 6, and synaptophysin genes,
3675		29848	41.1	1.01.64	Ī	E Z	Colliptere cas, and L-type calcium channel a> Homo emigne TRIATS = BNA
3675		29849	1.14	1.0E-64		LN	Homo saniana TRIADA mental cala
4008		30173	0.98	1.0E-64	2829	LZ	Homo sapiens hypothetical profein El 111008 (El 111003)DNA
10269		36901	1.17	1.0E-64	1.0E-64 AA042975.1	EST HUMAN	2K53108.s1 Soares, pregnant uterus, NNHPIT Home canians CINA class MACE ages 27 2
12291			4.56	1.0E-64	1.0E-64 AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
2350	_	28613	1.87	9.0E-65		NT	H. sapiens DNA for endogenous retroviral like element
2350	_	28614	1.87	9.0E-65	9.0E-65 X89211.1	NT	H.saplens DNA for endogenous retroviral like element
11826	24815		19.08	9.0E-65	9.0E-65 BF330676.1	EST_HUMAN	QV4-BT0257-081199-017-e03 BT0257 Homo sapiens cDNA
11799	24789	38486	7.24	8.0E-65	8.0E-65 Al929244.1	EST HUMAN	au58h07.x1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2519005 3' similar to SW.RL21 HUMAN P46778 60S RIBOSOMAI DEOTTEIN 121
10358		37004	2.16	7.0E-65	7.0E-65 BE081653.1		QV2-BT0635-240400-162-c02 BT0635 Homo saniens cDNA
12095		38782	2.88	7.0E-65	7.0E-65 Z21378.1	Г	HSAAAEAWO TEST1, Human adult Testis tissue Homo saciens of DNA clone cem feetfade (h.)
<u>1</u>	14247	27304	0.81	6.0E-65	7.	EST_HUMAN	AV721898 HTB Homo sapiens cDNA clone HTBBZC06 5
1974	15117		20.04	6.0E-65	5.0E-65 AA550929.1	EST HUMAN	nj86410.s1 NCL_CGAP_Pr11 Homo sapiens cDNA clone IMAGE:999379 similar to gb:K03002 60S RBOSOMAI PROTEIN 132 (HI IMAN):
6688	19857	33247	0.8	6.0E-65		EST HUMAN	nh37b07.s1 NCI_CGAP_Pr5 Homo sapiens cDNA clone IMAGE:954517
8945	22024	35564	2.45	6.0E-65	3.0E-65 AW0832521		xx07b09.x1 NCI_CGAP_Co21 Homo sapiens cDNA clone IMAGE:2683545 3' similar to TR:Q63306 Q63306
9213	22291	35833	4.63	6.0E-65	Ī	Т	2010 IN LEAST ENGED REFEITING DINA CONTAINS ( ORF'S, contains L1.b2 L1 repetitive element; 2010 IN SECURITY ( OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFI
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			clone IMAGE: 773747 3'	17504253	1750425 3	382677 6	E:41856// 5					type I, complete cds	13) mKNA	713) mRNA	mKNA	al cds	ane DKFZp761G108 5	ens cDNA clone IMAGE-1891900 3		ens cDNA done IMAGE:1891800 3'	K1), mKNA		31/1102 3	1111023			IVA, complete cds			NA, perusi cos	A, parual cas			NA.
	Top Hit Descriptor	ZWS3hff of Coorse foth fothis NEGHES A	of 1865 ST OCALES TOTAL TOTAL STATE OF THE SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SEC	MARCH NO. 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	Top Hit Database Source	EST HIMAN	EST HIMAN	EST HIMAN	EST HIMAN	EST HUMAN	LV	LZ	LZ	LX	NT	Z	Ę	Ę	LN	T HIMAN	Т	EST HUMAN	FST HIMAN			T HIMAN		Г							Ł			
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	Most Similar (Top) Hit BLAST E Value	6.0E-85	6.0E-65	6.0E-65	8.0E-65	6.0E-65	6.0E-65	5.0E-65	5.0E-65	5.0E-65	5.0E-65	6.0E-65	5.0E-65	5.0E-65	5.0E-65	4.0E-65		4.0E-85	4.0E-65/	4.0E-65	4.0E-65	4.0E-65	4.0E-65	4.0E-65	4.0E-65	4.0E-65	4.0E-65 M19879.1	4.0E-65	4.0E-65 U40372.1	4.0E-65	4.0E-65 U	4.0E-65		4.0E-65
İ	Expression Signal	4.63	0.62	0.62	3.68	4.18	1.86	1.89	1.92	1.92	1.07	1.79	1.79	1.38	1.36	6.		1.23	1.23	1.44	24.91	1.02	1.02	4.96	4.96	99.0	5.04	2.3	0.65	0.65	29.0	0.83	0.83	0.88
	ORF SEQ ID NO:	35834	35902	35903	37817	38001	38475	26859			28487	29519	29520	33583	37324	26452		26991	26992	27326	27751	28670	28671	32807	32808	33760	33801	33910	34273	34274	34555	34624	34625	35975
	Exan SEQ ID NO:			22351		24360							16501		23718	13421		13945	13945	14268	14668	16543	15543	19457	19457	20317	20349	20447	20785	20785	21043	21108	21108	22422
	Probe SEQ ID NO:	9213	9275	9275	11113	11294	11788	648	1384	1384	2223	3328	3328	7008	10684	198	-	76	764	1103	1515	2413	2413	6284	6284	7233	7286	7368	7721	7721	7993	8025	8025	9346

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		T	T	Т	$\top$	Ţ	Т	Т	Т	Т	Т	1	Т	Т	Т	Т	T	۳,	T	T ====	ή	_	7	7	T	-	ή.	Т'''
	Top Hit Descriptor	Homo sapiens WEE1 gene for protein kinase and partiel NS F143 anea for an anathrasement franchischer for brother	Homo sapiens PRO1474 mRNA, complete cds	Homo saplens fragile X mental retardation, autosomal homolog 1 (FXR1), mRNA	DKFZp761G108 r1 761 (synonym; hamy2) Homo sepiens cDNA clone DKFZp761G108 5	Homo saplens pre-B-cell colony-enhancing factor (PREF) mRNA	H. sapiens HZF9 mRNA for zho finger protein	Homo sapiens Immunoglobin superfamily, member 3 (IGSF3) mRNA, and translated products	ov2303.st Scares_tests_NHT Homo sapiens cDNA clone IMAGE:1638173 3' similar to contains element MSR1 renefflius element	Homo sapiens laminin, beta 1 (LAMB1), mRNA	ov23f03.st Sceres_tosts_NHT Homo sapiens cDNA clone IMAGE:1638173.3' similar to contains element MSR1 repetitive element;	Homo sapiens rab6 GTPase activating protein (GAP and centrosome associated) (CADCENIA) in DNA	801479686F1 NIH MGC 68 Homo sablens cDNA clone IMAGE:3882405 5	zw65a06.r1 Scares testis NHT Homo saplens cDNA chine IMAGE-781042 5	602155062F1 NIH MGC 83 Homo sapiens cDNA clone IMAGE 4295966 5	601190883F1 NIH MGC 7 Homo septens cDNA clone IMAGE:3534741 5	602134359F1 NIH MGC 81 Homo sapiens cDNA clone IMAGE:4289295 5'	Homo sapiens mRNA for FLJ00056 protein, partial cds	Homo sapiens mRNA for FLJ00056 protein, partial ods	Homo sepiens SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily d, member 3 (SMARCD3), mRNA	EST178755 Colon carcinoma (HCC) cell line Homo sapiens cDNA 5' end similar to similar to endogenous	601854033F1 NIH MGC 57 Home seniers cOMA clare IMA CE:40727569 F1	601763488F1 NIH MGC 20 Homo sapiens cDNA clone IMAGF-4026501 51	Homo sapiens putative Rab5 GDP/GTP exchange factor homologue (RABEX5), mRNA	Homo sapiens DNA, DLEC1 to ORCTE4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cite)	Homo seplens mRNA for KIAA1513 protein partial cds	hz24e09.x1 NCI CGAP GC6 Homo sapiens cDNA clone IMAGE:3208888 3	Homo sapiens glypican 4 (GPC4) mRNA
	Top Hit Database Source	ΤN	LN LN	LN LN	EST HUMAN	LZ	TN	¥	EST HIMAN	Į.	EST_HUMAN	Z	EST HUMAN	EST HUMAN	EST HUMAN	EST HUMAN	EST HUMAN	LΝ	LN	Ę	HST HIMAN	EST HIMAN	EST HUMAN	Ę	F N	LN	EST HUMAN	LV.
`[ 	Top Hit Acession No.	4.0E-65 AJ277546.2	4.0E-65 AF119846.1	4826735 NT	4.0E-65 AL120419.1	1978		4504626 NT	3.0E-65 Algoo692.1	04950	3.0E-65 Al000692.1	6912385 NT	3.0E-65 BE787366.1	3.0E-65 AA430006.1		2.0E-65 BE263373.1	2.0E-65 BF576922.1		2.0E-65(AK024463.1	11419247 NT	2.0E-65 AA307904.1	T		37495	1 0E-65 AB026898 1		1.0E-65 BE466881.1	4504082 NT
	Most Similar (Top) Hit BLAST E Value	4.0E-65	4.0E-65	4.0E-65	4.0E-65	3.0E-65	3.0E-65 X78932.1	3.0E-65	3.0E-65	3.0E-65	3.0E-65	3.0E-65	3.0E-65	3.0E-65	2.0E-65	2.0E-65	2.0E-65	2.0E-85	2.0E-65	2.0E-65	2.0E-65	2.0E-65	1,0E-85	1.0E-65	1 05-65	1.0E-65/	1.0E-65	1.0E-65
	Expression Signal	2.12	1.92	2.03	1.26	9.0	18.37	4.52	1.31	1.24	1.08	1.38	1.61	8.41	7.53	3.73	20.62	1.2	1.2	1.46	6.27	399	0.69	1.43	334	1.48	8.0	2,07
	ORF SEQ ID NO:				26452	26364		27822	28122	29538	29978	30891	36905	37523	29670		33818	35668	35869	37608				26770	28141	28360	29645	30259
	Exon SEQ ID NO:	23841			13421	13336	15990	14741	15014	16522	16975	17908	23309	23900	16657	19825	20365	22125	22125	23976	25184	26906	13328	13745	15033	15238	10625	17259
	Probe SEQ ID NO:	10808	11360	12628	13201	100	1260	1589	1868	3350	3815	4773	10274	11672	3490	9999	7282	9046	9048	10892	12241	12748	8	252	1880	2098	3458	4105

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Top Hit Descriptor Source	Homo sapiens chairean 4 (GPCA) mRNA	Ť	Т	Т	Т	Т	Т		T	Т	Т	Т	Т	Т	Г	Т	Γ	Г	Homo sapiens KIAA0656 gene product (KIAA0656) mRNA	_	7	7	Г	Human platelet factor 4 varation 1 (PF4var1) nane complete cdc	Homo saplens ribosomel protein L7a (RPL7A) mRNA			T	Homo saplens cadherin EGF   AG seven-base G-than Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Co	Novel human gene mapping to chomosome 22	Novel human gene mapping to chomoscome 22
Top Hit Acession Dis	4504082 NT	1.0E-65 AW029340,1   EST HUMAN	T	T	T		T	1.0E-65 AI243738.1   EST HUMAN	-		T		.0E-65 AU141295.1 EST HUMAN	Γ	Γ		.0E-65 AU129040.1 EST HUMAN	11431994 NT	7662227 NT		.0E-65 AU153793.1 EST HUMAN	.0E-65 AA069559.1 EST HUMAN	.0E-65 AB037832.1 NT	26167.1 NT	4508880 NT	.0E-85 BF698707.1 EST_HUMAN	621017.1 FST HIMAN	18041	11418322 NT	.160311.1 NT	160311.1 NT
Most Similar (Top) Hit BLAST E Value	1.0E-65	1.0E-65	1.0E-65 /	1.0E-65	1.0E-65	1.0E-65 E	1.0E-65 B	1.0E-65IA	1.0E-85/A	1.0E-65 A	1.0E-65 B	1.0E-65 B	1.0E-65 A	1.0E-65 A	1.0E-65 B	1.0E-65 A	1.0E-65 A	1.0E-65	1.0E-65	1.0E-65 AI191716.1	1.0E-65 AI	1.0E-65 A	1.0E-65 At	1.0E-65 M26167.1	1.0E-65	1.0E-85 BI	1.0E-65 AI621017.1	1.0E-65	1.0E-65	9.0E-66 AL160311.1	9.0E-68 AL160311.1
Expression Signal	2.07	2.53	2.53	1.57	1.57	0.86	0.86	0.58	1.5	1.5	99.0	0.68	2.04	2.04	1.01	1.33	1.33	2.79	0.55	5.5	1.32	0.65	1.23	1.91	6:39	1.9	2.58	2.38	3.77	6.0	6.0
ORF SEQ ID NO:			30452		31236			31837		35058	35088						35844		35937	36210	36730	37155	37453	37599	37734	38118	38217		32078	28334	26335
Exon SEQ (D NO:	17259					L	18602		21529	ı		21556	- 1	- 1	- 1	22300	- 1	- (	22385	22640	23127	ı	- [	- [	- 1	24456	24545	25217	25276	13310	13310
Probe SEQ ID NO:	4105	4323	4323	5143	5143	5400	2400	5594	8448	8448	8475	8475	8514	8514	9041	9222	9222	9231	8309	9678	10089	10609	10796	10885	11016	11395	11486	12292	12391	23	73

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Table 4
Single Exon Probes Expressed in Placenta

	Г	Т	Τ	Г	Г	Т		Т		$\overline{}$	T	Τ	Γ	Г	Γ	Γ	Τ	ľ	*****	T " "	۲	r	1	Inc. Ac.	T	T'	1	TT
Top Hit Descriptor	Homo sapiens 28S proteasome-associated pad1 homolog (POH1) mRNA	Homo sapiens 26S proteasome-associated pad1 homdog (POH1) mRNA	Human transposon-like element, partial	Human calcium-dependent phospholipid-binding protein (PLA2) mRNA, complete cds	Human calcium-dependent phospholipid-binding protein (PLA2) mRNA, complete cds	RC4-BT0311-141199-011-h06 BT0311 Homo sapiens cDNA	wn57h07.x1 NC!_CGAP_Lu19 Homo sapiens cDNA clone IMAGE:2449597 3' similar to WP:F15G9.4A CE18595 ;	wn57h07x1 NCI_CGAP_Lu19 Homo sapiens aDNA clane IMAGE:2449597 3' similar to WP:F15G9.4A	CE18595;	wn57h07.x1 NCL_CGAP_Lu19 Homo sapiens cDNA clone IMACE:2449597 3' similar to WP:F15G9.4A CE18595 ;	PM2-HT0604-030300-001-b06 HT0604 Homo sapiens cDNA	H. sapiens mRNA for ribosomal protein L31	RC4-BT0311-141189-011-h06 BT0311 Homo sapiens cDNA	Homo saplens thyroid hormone receptor binding protein (AIB3), mRNA	Mus musculus fragile X mental retardation syndrome 1 homolog (Fmr1), mRNA	RC1-NN0063-100500-022-a02 NN0063 Homo sapiens cDNA	H.sapiens DNA for endogenous retroviral like element	Homo sepiens germ-line DNA upstream of Jkappa locus	Human endogenous retrovirus, complete genome	Homo sapiens methylene tetrahydrofolate dehydrogenase (NAD+ dependent), methenyltetrahydrofolate cyclohydrolase (MTHFD2), mRNA	QV1-DT0069-110200-067-g10 DT0069 Hamo saplens cDNA	EST377546 MAGE resequences, MAGI Homo sapiens cDNA	Homo sapiens cAMP-regulated guanine nucleotide exchange factor I (cAMP-GEFI) mRNA, complete cds	Homo sapiens methylene tetrahydrofolate dehydrogenase (NAD+ dependent), methenyltetrahydrofolate cyclohydrolase (MTHFD2), mRNA	Homo sapiens hypothetical protein FLJ20116 (FLJ20116), mRNA	luman endogenous retrovirus pHE.1 (ERV9)	UI-H-BW 1-amr-a-10-0-UI.s1 NCI_CGAP_Sub7 Homo sapiens cDNA done IMAGE:3070747 3'	Homo sapiens mRNA for KIAA0998 protein, partial cds
Top Hit Database Source	5	5	LN TN	F	FN	EST_HUMAN	EST_HUMAN		EST_HUMAN	EST HUMAN	Т	F	Г	F	Ę	EST_HUMAN	뒫	LN	NT.	Ę	EST_HUMAN	EST_HUMAN	M	Ę	Ę	NT.	EST_HUMAN	Σ
Top Hit Acession No.	5031980 NT	5031980 NT				7.0E-66 BE064410.1			6.0E-66 AI924653.1	6.0E-66 AI924653.1	L		1.0	20557	6679816 NT	1.8		4.0E-66 AJ223364.1	9635487 NT	11428643 NT	Γ	4.0E-66 AW865473.1		11428643 INT	11421638 NT		4.0E-66 BF507493.1	4.0E-66 AB023215.1
Most Similar (Top) Hit BLAST E Value	9.0E-86	9.0E-66	9.0E-66 M87299.1	9.0E-86 M72393.1	9.0E-66	7.0E-66	6.0E-66		6.0E-86	6.0E-66	6.0E-66	6.0E-66 X69181.1	5.0E-66	5.0E-66	4.0E-86	4.0E-88	4.0E-66 X89211.1	4.0E-86	4.0E-66	4.0E-66	4.0E-86	4.0E-66	4.0E-66 U78168.1	4.0E-66	4.0E-66	4.0E-66 X57147.1	4.0E-66	4.0E-66
Expression Signal	1.53	1.53	5.93	0.89	99.0	1.6	1.16		1.16	1.16	0.46	3.22	2.45	8.4	1.8	76.0	5.3	3.15	5.02	3.57	78.0	4.91	7.88	0.83	6.14	0.7	1.49	1.63
ORF SEQ ID NO:	27615	27616		30171			30805		30606	30607		38152			27046		28618			32147		31506	33817	32147				38430
Exan SEQ ID NO:	14540	14540		i i	17164	24708	17625		17625	17625	21709	24488	14552	22551	13992	14924	15486	15668	18035			18514	20364	18862	21351	21409	23980	24739
Probe SEQ ID NO:	1385	1385	1513	4007	4007	11628	4485		4485	4485	8620	11427	1398	9484	813	1775	2355	2543	4905	5668	1989	6995	7281	7807	8269	8327	10896	11660

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1			_		_		-,	<u>.</u>	_	_	_			_													_	
	Top Hit Descriptor	Homo saplens solute carrier family 25 (mitochondrial carrier; adenine nucleotide translocator), member 5 (SLC25A5), nuclear gene encoding mitochondrial protein, mRNA	Homo sapiens solute carrier family 25 (mitochondriat carrier; adenine nucleotide translocator), member 5 (SLC26A5), nuclear gene encoding mitochondrial protein, mRNA	y27g12.r1 Soares_multiple_sclerosis_2NbHMSP Homo sapiens cDNA clone IMAGE:284326 5' similar to SW:H281_TIGCA P35063 HISTONE H28 1/H28_2. [2] PIR:B56812:	y277g12.r1 Soares, multiple, sclerosts, 2NbHMSP Homo sepiens cDNA clone IMAGE:284326 5' similar to SW:H2B1_TIGCA P35068 HISTONE H2B 1.h2B 2.12  PIR:B56612.	y27g12.r1 Scares_multiple_sclerosis_ZNbHMSP Homo sapiens cDNA clone IMAGE:284326 5' similar to SW:H281_TIGCA P35068 HISTONE H28.1/H28.2. [2] PIR:856812;	Homo septens TGF(beta)-Induced transcription factor 2 (TGIF2), mRNA	Homo sapiens KIAA0649 gene product (KIAA0649), mRNA	Homo sapiens mRNA for KIAA0892 protein, partial cds	Homo sapiens protein kinase C beta-II type (PRKCB1) mRNA, complete cds	Homo sapiens NIPSNAP, C. elegans, homdog 1 (NIPSNAP1), mRNA	Homo sapiens NiPSNAP, C. elegans, homolog 1 (NIPSNAP1), mRNA	H. sapiens germline Immunoglobulin heavy chain, variable region, (15-1)	Homo sapiens mRNA for FLJ00045 protein, partial cds	Homo sapiens KIAA0433 protein (KIAA0433), mRNA	Homo sapiens protocadherin beta 1 (PCDH-beta1), mRNA	Homo saplens molybdenum cofactor biosysthesis protein E (MCBPE) mRNA, complete cds	Homo saplens protein phosphatase 2, regulatory subunit B (B56), eloha isoform (PPP-2854) mRNA	Homo sapiens Misshapen/NIK-related kinase (MINK), mRNA	Homo saplens Misshapen/NIK-related kinase (MINK), mRNA	Homo saplens origin recognition complex, subunit 5 (yeast homolog)-like (ORCSL) mRNA, and translated	products	Homo sapiens origin recognition complex, subunit 5 (yeast homolog)-like (ORC5L) mRNA, and translated products	Homo sapieno chromosome 21 segment HS21C101	H.sapiens pseudogene for the low affinity IL-8 receptor	Homo sapiens hypothetical protein FLJ20309 (FLJ20309), mRNA	Novel human gene mapping to chomosome 1	Homo sepiens sodlum/calcium exchanger isoform NaCa3 (NCX1) mRNA, complete cols
	Top Hit Database Source	μN	Ę	EST HUMAN	EST HUMAN	EST HUMAN	NT.	NT	NT .	LN TN	TN	NT	μN	. LN	N	N-I	FZ	Ā	N	NT	!	Z		NT	불			뒫
	Top Hit Acession No.	4502098 NT	4502098 NT	3.0E-66 N55323.1	V55323.1	V55323.1	11141880 NT	7662223 NT	3.0E-66 AB020699.1	A13975.1	11417948 NT	11417946 NT		3.0E-66 AK024453.1	11417118 NT	7019480 NT	3.0E-66 AF155659.1	5453949 NT	7857334 NT	7657334 NT		4505524 N	4505524 NT	1.2		8923290 NT		2.0E-66 AF108389.1
	Most Similar (Top) Hit BLAST E Value	3.0E-66	3.0E-88	3.0E-66	3.0E-66 N55323.1	3.0E-66 N55323.1	3.0E-86	3.0E-66	3.0E-66	3.0E-66 M13975.1	3.0E-66	3.0E-66	3.0E-66 X92211.1	3.0E-66	3.0E-86	3.0E-66	3.0E-66	3.0E-66	2.0E-66	2.0E-66	100	2.UE-00	2.0E-66	2.0E-66/	2.0E-66 X65859.1	2.0E-66	2.0E-66 /	2.0E-66/
	Expression Signal	14.93	14.93	1.04	1.04	1.04	3.44	7.29	0.85	0.65	1.72	1.72	1.74	0.59	0.62	0.86	0.95	4.55	1.48	1.48		0.0	0.87	2.02	1.07	0.85	0.78	0.69
	ORF SEQ ID NO:	27692	27693	28290	28291	28292	78997			32180	32391	32392	34134	36361	36547	36911	37386			26305	1000	00707	26236	28126	29236	29788	30019	30317
	Exon SEQ ID NO:	14611	14611	15180	15180	15180	15887	16361	18778		19081		20657	22790	22960	23313	23774		13291	13291	1000	15235	13235	15017	16215	16773	17021	17326
	Probe SEQ ID NO:	1458	1458	2039	2039	5039	2772	3186	5583	5695	5833	5833	7585	9725	9920	10278	10741	11800	52	52	101	2	435	1873	3030	3609	3861	4178

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Top Hit Descriptor	Homo sapiens HLA-B gene for human leucocyte antiden R	Homo sapiens HLA-B gene for human leucocode antiden B	EST380930 MAGE resecuences. MAGJ Homo seniens CDNA	EST380930 MAGE reseguences, MAGJ Homo capiens cDNA	1959c02.r1 Source multiple sclerosis 2NbHMSP Homoseniens cDNA close MAAGE 2778 28 E	Homo sapiens G-2 and S-phase expressed 1 (GTSE1) mRNA	601508376F1 NIH MGC 71 Homo sapiens cDNA clone INAGE:3808931 5	AV717817 DCB Homo sapiens cDNA clone DCBADC07 5	AV717817 DCB Homo sapiens cDNA clone DCBADC07 6	AV717817 DCB Homo sapiens cDNA clone DCBADCO7 5'	AV717817 DCB Homo sapiens cDNA clone DCBADC07 5	602152996F1 NJH MGC 81 Homo sepiens cDNA clone IMAGE:4294151 F	L2-NT0101-280700-116-E04 NT0101 Homo sapiens cDNA	IL2-NT0101-280700-116-E04 NT0101 Homo sapiens cDNA	RC5-BN0193-010900-034-G06 BN0193 Homo sapiens cDNA	aa80e04.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:827262 3'	2657e12.r1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:3631185	AV748749 NPC Homo sapiens cDNA clone NPCBVA05 5	AV748749 NPC Homo sapiens cDNA clone NPCBVA05 5	Homo saplans iun dimerization archein nere nartial role: rote cena completo rote: and inscription archein archein rotes and inscription archein archein archein archein archein archein archein archein archein archein archein archein archein archein archein archein archein archein archein archein archein archein archein archein archein archein archein archein archein archein archein archein archein archein archein archein archein archein archein archein archein archein archein archein archein archein archein archein archein archein archein archein archein archein archein archein archein archein archein archein archein archein archein archein archein archein archein archein archein archein archein archein archein archein archein archein archein archein archein archein archein archein archein archein archein archein archein archein archein archein archein archein archein archein archein archein archein archein archein archein archein archein archein archein archein archein archein archein archein archein archein archein archein archein archein archein archein archein archein archein archein archein archein archein archein archein archein archein archein archein archein archein archein archein archein archein archein archein archein archein archein archein archein archein archein archein archein archein archein archein archein archein archein archein archein archein archein archein archein archein archein archein archein archein archein archein archein archein archein archein archein archein archein archein archein archein archein archein archein archein archein archein archein archein archein archein archein archein archein archein archein archein archein archein archein archein archein archein archein archein archein archein archein archein archein archein archein archein archein archein archein archein archein archein archein archein archein archein archein archein archein archein archein archein archein archein archein archein archein archein archein archein archein archein archein archein archein archein archei	Homo saplens Ran GTPase activating protein 1 (RANGAP1) mRNA	EST01750 Subtracted Hippocampus, Stratagene (cat. #836205) Homo sapiens oDNA clone HHCPN31 similar to L1 repetitive element	RU75402.x1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2782083 3' similar to gb:M37104 ATP SYNTHASE COUPLING FACTOR 6, MTOCHONDRIAL PRECLIRSOR (H.IMAN)	EST96812 Tests I Homo sapiens cDNA 5' end similar to cimilar to C. clegans hypothetical protein, cosmid	2456b05,r1 Soares fetal liver spleen 1NFLS S1 Homo saniens CDNA close NAA CE 2446040 E	Zh36b05.r1 Soares fetal liver spicen 1NFI S S1 Home saniens chind chara IMAGE-446046	Homo saplens inositol 1,3,4-triphosphate 5/6 kinase (ITPK1), mRNA	Homo sapiens Inositol 1,3,4-triphosphate 5/6 kinase (ITPK1), mRNA	au75d02.x1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2782083 3' similar to gb:M37104 ATP SYNTHASE COUPLING FACTOR 6, MITOCHONDRIAL PRECURSOR (HUMAN);
Top Hit Database Source	, E	₽.	EST HUMAN	HUMAN	EST HUMAN	9	EST HUMAN	EST HUMAN	Т	EST HUMAN	T	T	EST_HUMAN	EST_HUMAN	EST HUMAN	EST_HUMAN	EST HUMAN	EST_HUMAN /	П	ΤN		EST HUMAN	EST HUMAN	EST HUMAN	Г	Т			EST_HUMAN A
Top Hit Acession No.	2.0E-66 AJ133267.2	2.0E-66 AJ133267.2	2.0E-66 AW968854.1	2.0E-66 AW968854.1	2.0E-66 N45480.1	11418318 NT	1.0E-66 BE887173.1	1.0E-66 AV717B17.1	1.0E-66 AV717817.1	1.0E-66 AV717B17.1	1.0E-66 AV717817.1	1.0E-66 BF673088.1	1.0E-69 BE765232.1	1.0E-66 BE765232.1	1.0E-66 BF328623.1	1.0E-66 AA668B58.1	1.0E-66 AA018828.1	1.0E-66 AV748749.1	1.0E-66 AV748749.1	1.0E-66 AF111167.2	11418177 NT	8.0E-67 M78158.1	7.0E-67 AW162232.1	7.0E-67 AA383416.1	7.0E-67 W85947.1	7.0E-67 W85947.1	7657243 NT	7657243 NT	7.0E-67 AW162232.1
Most Similar (Top) Hit BLAST E Value	2.0E-66	2.0E-66	2.0E-66	2.0E-66	2.0E-66	2.0E-66	1.0E-66	1.0E-66	1.0E-66	1.0E-66	1.0E-66	1.0E-68	1.0E-89	1.0E-66	1.0E-66	1.0E-66	1.0E-66	1.0E-66	1.0E-66	1.0E-66	9.0E-67	8.0E-67	7.0E-67	7.0E-67	7.0E-67	7.0E-67	7.0E-67	7.0E-67	7.0E-67
Expression Signal	13.88	13.88	0.82	0.82	3.57	2.84	1.14	1.47	1.47	4.18	4.18	5.97	0.67	0.67	1.53	1.2	0.64	0.93	0.93	2.24	1.92	0.91	1.63	2.66	1.39	1.39	1.94	1.94	1.36
ORF SEQ ID NO:	30808	66808			35671			29153	29154			31712		32403	33548	35271	36260	37223	37224	37889			26665	27641	27817	27818	28350	28351	26665
Exon SEQ ID NO:	17913	17913		19123		26147		_		_					- 1	21732	- 1	23617	23617	24254	25278	18162	13628	14567	14737	14737	15229	15229	13628
Probe SEQ ID NO:	4778	4778	5937	5937	9048	12637	1717	2929	2969	4504	4504	5497	2900	2300	7078	8652	9626	10582	10582	11185	12398	5034	391	1413	1585	1585	2089	2089	2871

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	Top Hit Descriptor	Homo saplens zinc finger protein 304 (ZNF304), mRNA	Homo saplens adaptor-related protein complex 2 heta 1 subunit (AP2R1) mRNA	Homo sapiens adaptor-related protein complex 2, beta 1 subunit (AP2B1), mRNA	Homo sapiens ATP ese, H+ transporting, lysosomel (vecuolar proton pump) non-calalytic accessory protein 14 (110/1/6kp) (ATP6N4A) mena	Homo sapiens mitochondrial carrier family protein (LOCEG972) mRNA	Homo sapiens mitochondrial carrier family protein (LOC:55972) mRNA	Homo sapiens phosphodiesterase (Inucleotide pyrophosphatase 3 (PDNP3) mRNA	Homo sapiens latent transforming growth factor beta binding protein 2 (LTBP2) mRNA	Homo saplens retinal dehydre dehydrogenase 2 (RALD-12), mRNA	Homo saplens fucosyltransferase 8 (alpha (1.6) fucosyltransferaso) (FLTB) mRNA	Human cytochrome oxidase subunit VIa (COX6A1P) pseudogene, complete cits	Homo saptens low density (pooroten-related protein 2 (LRP2) mRNA	Homo saplens low density lipoprotein-related protein 2 (LRP2), mRNA	Homo sabiens gene for AF-6, complete cds	Homo saplens calcium channel, voltade-dependent, alpha 2/delta subunit 1 (CACNA2011, mRNA	H. sapiens mRNA for acetyl-CoA carboxylase	Homo sapiens mRNA for transmebrane receptor protein	Homo sapiens PMP69 gene, exons 3,4,5,6 & 7	Homo saplens retinoblastoma 1 (including osteosarcoma) (RB1) mRNA	Homo capions Synapsin III (SYN3) mRNA, and translated products	Homo saplens Synapsin III (SYN3) mRNA, and translated products	Homo saplens chromosome 21 segment HS21C001	Homo saplens chromosome 21 segment HS21C001	Homo saplens DKFZp434P211 protein (DKFZP434P211), mRNA	Homo sapiens DKFZp434P211 protein (DKFZP434P211), mRNA	H.sapiens mRNA for acetyl-CoA carboxylase	Homo saplens T cell receptor beta locus, TCRBV7S3A2 to TCRBV12S2 region	PM3-BN0176-100400-001-g04 BN0176 Homo sapiens cDNA	yn02d11.r1 Soares adult brain N2b4HB55Y Homo capient cDNA clone IMAGE:167253 51	o28e05.x5 NCL CGAP_Kld3 Homo saplens cDNA clone IMAGE:1483288 3' similar to SW:Z33A_HUMAN Co6730 ZINC FINČER PROTEIN 33A	RC0-HT0934-150900-026-c03 HT0934 Homo saplens cDNA
' I	Top Hit Database Source	LN LN	Į.	N L		Ľ.	FZ	Z	Į,	¥	ΙŻ	F	5	FZ	LN	Ę	F	TN	LZ LZ	ラ	5	L7	LN	L	누	17	LN	FZ	EST_HUMAN	EST_HUMAN	EST HUMAN	T
	Top Hit Acessian No.	10190695 NT	11425672 NT	11425572 NT	4885084INT	11419212 NT	11419212 NT	4826895 NT	4557732 NT	10835044 NT	11434579 NT		11430460 NT	11430450 NT	7.0E-67 AB011399.1	11421527 NT				4506434 NT	4507332 NT	4507332 NT		6.0E-67 AL163201.2	7657020 NT	7857020 NT		5.0E-67 AF009880.1	3.1		4.0E-67 AI733032.1 E	_
	Most Similar (Top) Hit BLAST E Value	7.05-67	7.0E-67	7.0E-67	7.0E-67	7.0E-67	7.0E-67	7.0E-67	7.0E-67	7.0E-67	7.0E-67	7.0E-67 U82486.1	7.0E-67	7.0E-67	7.0E-67	7.0E-67	6.0E-67 X68968.1	6.0E-67 Z17227.1	6.0E-67 Y14320.1	6.0E-67	6.0E-67	6.0E-67	6.0E-67	6.0E-67	6.0E-67	6.0E-67	6.0E-67 X68968.1	5.0E-67	5.0E-67	4.0E-67 R90819.1	4.0E-67	4.0E-67
	Expression Signal	0.98	1.67	1.67	1.12	0.99	0.99	0.52	0.7	99'0	2.42	2.02	4.05	4.05	1.92	1.74	1.09	2.4	1.07	1.39	1.32	1.32	0.82	0.92	2.22	2.22	2.74	2.26	2.17	1.13	0.8	1.48
	ORF SEQ ID NO:		L	32831	33425	34358	34359	34857	35134	35756		38680	38829	38830	32053		26788	27051	27524	29426	29698	29669	30375	30376	30947	30948	26788	29486		27588	34813	
	Exon SEQ ID NO:		19569	19569	20015	20864			1	22211	24620	24958	25131	25131	25441	25721	13765	13997	14458	16411	16689	16689	7388	17389	17960	17960	13765	16467	24299	14814	21293	21657
	Probe SEQ ID NO:	6205	6400	6400	6863	7809	5082	8258	8518	9132	11565	11973	12168	12168	12664	13106	573	818	1302	3237	3524	3524	4243	4243	4827	4827	13224	3283	11230	1369	8211	8576

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Top Hit Descriptor	Inv08a01.s.1 NCI_CGAP_SS1 Homo expiens cDNA clone IMAGE:1238472.3' similar to TR:O10385 O10385 PRO-POL-DUTPASE POLYPROTEIN:	EST37903 Embryo, 9 week Homo saplens cDNA 5' end	RC4-BT0311-141199-011-h06 BT0311 Homo saplens cDNA	MR3-SN0066-040500-008-f01 SN0066 Homo sapiens cDNA	Homo sapiens chromosome 21 segment HS21C079	hr81f05.x1 NCI_CGAP_Kid11 Home sapiens cDNA clone IMAGE:3134913 3' similar to SW:RHOP_MOUSE Q41085 GTP-RHO BINDING PROTEIN 1:	om18b07.s1 Sogres NFL T GBC S1 Homo sapiens aDNA done IMAGE:1541365.3'	Iw/16g09.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3183136 3' similar to WP:F23H11.9 CE08617 ;	QV4-ST0234-181199-037-105 ST0234 Homo sapiens cDNA	Homo saplens double stranded RNA activated protein kinase (PKR) gene, exons 29, 3, and 4.	ba72g05,71 NIH_MGC_20 Homo seplens cDNA clone IMAGE:2905976 5' similar to TR:094892 094892 KIAA0798 PROTEIN ;	ba72g05;y1 NIH_MGC_20 Homo saplens cDNA clone IMAGE:2805976 5' similar to TR:094892 094892 KIAA0788 PROTEIN	Homo sablens KRAB zinc finger profein ZEOR mRNA complete cds	Homo sapiens developmentally regulated GTP-binding protein 1 (DRG1) mRNA	zu91g01.s1 Soares, testis, NHT Homo saplens cDNA clone IMAGE:745392.31	Homo saplens chromosome 21 segment HS21C100	Novel human gane mapping to chomosome 13	601875351F1 NIH_MGC_55 Homo saplens cDNA clone IMAGE:4091893 5'	Homo sapiens mRNA for NADPH-cytochrome P-450 reductase, complete cds	Hamo sapiens mRNA for NADPH-cytochrane P-450 reductase, complete cds	DKFZp761A229_r1 761 (synonym: hamy2) Homo sapiens cDNA clone DKFZp761A229 5'	EST38850 Embryo, 9 week Hamo sapiens cDNA 5' and similar to similar to cerebellin	EST38860 Embryo, 9 week Homo sapiens cDNA 5' end similar to similar to cerebellin	RC4-BT0566-170100-011-c07 BT0568 Homo sapiens cDNA	RC4-BT0568-170100-011-c07 BT0566 Homo sapiens cDNA	AV731333 HTF Homo sepiens cDNA clone HTFARD03 5'	UI-H-BI2-ahn-e-10-0-UI,s1 NCI_CGAP_Sub4 Homo sapiens cDNA clone IMAGE:2727283 3	on86b07.s1 Soares_NFL_T_GBC_S1 Homo saplens cDNA clone IMAGE:1563541 3'	602140470F1 NIH MGC_46 Homo sapiens cDNA clone IMAGE.4301705 5'
Top Hit Database Source	EST HUMAN	EST HUMAN	EST HUMAN	EST HUMAN	노	EST HUMAN	EST HUMAN	EST HUMAN	EST HUMAN	LN	EST_HUMAN	EST HUMAN	L	FZ	EST HUMAN	LN	LN	EST_HUMAN	LN⊤	TN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN
Top Hit Acesslon No.	4.0E-67 AA714294.1	3.0E-67 AA333768.1	3.0E-67 BE064410.1	L	3.0E-67 AL163279.2	3.0E-67 BF196068.1	3.0E-67 AA927874.1	2.0E-67 BE348354.1	2.0E-67 AW816405.1	2.0E-67 AF167460.1	2.0E-67 BE303037.1	2.0E-67 BE303037.1	2.0E-67 AF309561.1	4758795 NT	2.0E-67 AA625755.1		2.0E-67 AL049784.1	2.0E-67 BF240758.1	2.0E-67 AB051763.1		2.0E-67 AL120542.1	20E-67 AA334609.1	2.0E-67 AA334609.1	2.0E-67 AW602635.1	2.0E-67 AW602635.1	2.0E-67 AV731333.1	2.0E-67 AW 293624.1		.0E-67 BF685788.1
Most Similar (Top) Hit BLAST E Value	4.0E-67	3.0E-67	3.0E-67	3.0E-67	3.0E-67	3.0E-67	3.0E-67	2.0E-67	2.0E-67	2.0E-67	2.0E-67	2.0E-67	2.0E-67	2.0E-67	2.0E-67	2.0E-67	2.0E-67	2.0E-67	2.0E-67	2.0E-67	2.0E-67	20E-67	2.0E-67	2.0E-67	2.0E-67	2.0E-67	2.0E-67	2.0E-67	2.0E-67
Expression Signal	1.76	2.03	2.05	2.96	1.38	1.37	15.42	65.0	5.29	2.48	1.23	1.23	1.18	1.37	3.76	3.13	0.83	4.95	1.74	1.74	0.64	1.09	1.09	1.31	1.31	0.55	66.0	0.53	1.75
ORF SEQ ID NO:		26862	29718			34980		26445	27109		28179	28180	28713	28749	29737	30263	32723	32772	32958	32959	33330	35374	35375	35812	35813	36332	36536	37501	37840
Exan SEQ ID NO:	24381	13835	li	l	17978	21456	24593	13416	14044	14294	15076	15076	15585	15629					- [	- 1	- 1	- 1	- 1	ı	- 1	22763	- 1	١	24213
Probe SEQ ID NO:	11318	2874	3542	4816	4845	8375	11537	193	898	1129	1933	1933	2458	2502	3557	4109	6197	6252	6425	6425	6779	8755	8755	9197	9187	9766	9910	10848	11141

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Table 4
Single Exon Probes Expressed in Placenta

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|                                               | Exon ORF SEQ Expression (Top) Hit Top Hit Acession ID NO: Signal BLAST E No. Source | Exon         ORF SEQ         Expression Signal         (Top) Hit Top Hit Acession NO:         Top Hit Acession Signal         Top Hit Acession Database Source           NO:         Signal Signal         BLAST E No.         Source Source           26230         2.66         2.0E-67         11486448 NT         Homo septens KIAA0985 profile If KIAAA0885 | Exon         ORF SEQ<br>ID NO:         Expression<br>Signal         (Top) Hit<br>BLAST E<br>Value         Top Hit Acession<br>No.         Top Hit Acession<br>No.         Top Hit Acession<br>Source           28230         2.656         2.0E-67         11436448 NT         Source           24562         38240         2.05         2.0E-67         BE285744.1         EST HUMAN | Exon         ORF SEQ         Expression Signal         (Top) Hit Acession NO:         Top Hit Acession Signal         Top Hit 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Exon<br>NO:         ORF SEQ<br>ID NO:         Expression<br>Signal         (Top) Hit<br>BLASTE<br>Value         Top Hit Acession<br>No.         Top Hit Acession<br>Polatbase         Top Hit Acession<br>Source           265230         2.65         2.06-67         11436448         NT           24562         38240         2.05         2.06-67         H1436448         NT           25929         37556         2.44         2.06-67         BE295714.1         EST_HUMAN           25988         31770         2.47         2.06-67         BF377169.1         EST_HUMAN           13908         26954         0.95         1.06-67         AA702794.1         EST_HUMAN           17956         30954         0.73         1.06-67         BE010038.1         EST_HUMAN           24337         1.47         1.06-67         BE010038.1         EST_HUMAN           17750         30133         6.75         8.06-68         AA209456.1         EST_HUMAN           17730         30134         6.75         8.06-68         AA209456.1         EST_HUMAN | Exon NO:         CRF SEQ ID ID NO:         Expression Signal         (Top) Hit Top Hit Acession No.         Top Hit Acession Source Noise         Top Hit Acession Noise         Top Hit Acession Noise         Top Hit Acession Noise         Top Hit Acession Noise         Top Hit Acession Noise         Top Hit Acession Noise         Top Hit Acession Noise         Top Hit Acession Noise         Top Hit Acession Noise         Top Hit Acession Noise         Top Hit Acession Noise         Top Hit Acession Noise         Top Hit Acession Noise         Top Hit Acession Noise         Top Hit Acession Noise         Top Hit Acession Noise         Top Hit Acession Noise         Top Hit Acession Noise         Top Hit Acession Noise         Top Hit Acession Noise         Top Hit Acession Noise         Top Hit Acession Noise         Top Hit Acession Noise         Top Hit Acession Noise         Top Hit Acession Noise         Top Hit Acession Noise         Top Hit Acession Noise         Top Hit Acession Noise         Top Hit Acession Noise         Top Hit Acession Noise         Top Hit Acession Noise         Top Hit Acession Noise         Top Hit Acession Noise         Top Hit Acession Noise         Account Noise         Account Noise         Account Noise         Account Noise         Account Noise         Account Noise         Account Noise         Account Noise         Account Noise         Account Noise         Account Noise         Account Noise         Account Noise         Account Noise         Account Noise         Account | Exon<br>NO:         ORF SEQ<br>Signal<br>ID NO:         Expression<br>Signal<br>ID NO:         (Top) Hit<br>BLASTE<br>Value         Top Hit Acession<br>No.         Top Hit Acession<br>Politabase<br>Source         Top Hit Acession<br>No.         Top Hit Acession<br>Source           26230         2.66         2.06-67         11436448         NT           24562         38240         2.05         2.06-67         BE295714.1         EST_HUMAN           25828         31770         2.47         2.06-67         BE377169.1         EST_HUMAN           25828         2.44         2.06-67         BE377169.1         EST_HUMAN           13908         26948         0.95         1.06-67         AA702794.1         EST_HUMAN           17956         30954         0.73         1.06-67         BE499247.1         EST_HUMAN           24337         1.47         1.06-67         BE100038.1         EST_HUMAN           16378         30133         6.75         8.06-68         BE870732.1         EST_HUMAN           17130         30134         6.75         8.06-68         BA209456.1         EST_HUMAN           21375         34895         0.56         7.06-68         BA209456.1         EST_HUMAN           213750         366         7.06-68         BA805096.1 <t< td=""><td>Exon<br/>NO:         ORF SEQ<br/>Signal         Expression<br/>Fignal         Moet Similar<br/>Public         Top Hit Acession<br/>Public         Top Hit Acession<br/>Post Database           26230         2.65         2.0E-67         11438448 NT         Source           24562         38240         2.05         2.0E-67         11418169 NT           23928         37556         2.44         2.0E-67         H418169 NT           23928         37556         2.47         2.0E-67         H418169 NT           23928         37556         2.47         2.0E-67         H418169 NT           13908         26348         0.95         1.0E-67         BF439247.1         EST_HUMAN           13908         26348         0.95         1.0E-67         BF439247.1         EST_HUMAN           17906         30054         0.73         1.0E-67         BF439247.1         EST_HUMAN           25085         3.44         9.0E-68         BE400324.1         EST_HUMAN           17730         30133         5.75         8.0E-68         BE80032.1         EST_HUMAN           17730         30134         5.75         8.0E-68         AAZ09456.1         EST_HUMAN           23700         37310         6.43         6.0E-68         BF10505.1<!--</td--><td>Exon NO:         CNF SEQ Expression Signal ID NO:         Moet Similar SEQ ID NO:         Top Hit Acession Signal ID NO:         Top Hit Acession Signal ID NO:         Top Hit Acession Signal ID NO:         Top Hit Acession Signal ID NO:         Top Hit Acession ID NO:         Top Hit Acession ID NO:         Top Hit Acession ID NO:         Top Hit Acession ID NO:         Top Hit Acession ID NO:         Top Hit Acession ID NO:         Top Hit Acession ID NO:         Top Hit Acession ID NO:         Top Hit Acession ID NO:         Top Hit Acession ID NO:         Top Hit Acession ID NO:         Top Hit Acession ID NO:         Top Hit Acession ID NO:         Top Hit Acession ID NO:         Top Hit Acession ID NO:         Top Hit Acession ID NO:         Top Hit Acession ID NO:         Top Hit Acession ID NO:         Top Hit Acession ID NO:         Top Hit Acession ID NO:         Top Hit Acession ID NO:         Top Hit Acession ID NO:       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37556         2.44         2.0E-67         BF265714.1         EST_HUMAN           23928         3770         2.47         2.0E-67         BF377169.1         EST_HUMAN           23929         25648         0.95         1.0E-67         BF49247.1         EST_HUMAN           24337         1.0E-67         BF49247.1         EST_HUMAN           24337         1.0E-67         BF49247.1         EST_HUMAN           25085         3.44         9.0E-68         BF402045.1         EST_HUMAN           1730         30133         6.75         8.0E-68         BAZ09456.1         EST_HUMAN           21376         3034         6.0E-68         BAZ09456.1         EST_HUMAN           21376         3043         6.75         8.0E-68         AAZ09456.1         EST_HUMAN           23700         3731         6.46         6.0E-68         BF133601.1         NT</td><td>Exon NO:- Signal NO:- Signal NO:- Signal NO:- Signal NO:- Signal NO:- Signal NO:- Signal NO:- Signal NO:- Signal NO:- Signal NO:- Signal NO:- Signal 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        8.0E-68         BE80032.1         EST_HUMAN           17730         30134         5.75         8.0E-68         AAZ09456.1         EST_HUMAN           23700         37310         6.43         6.0E-68         BF10505.1 </td <td>Exon NO:         CNF SEQ Expression Signal ID NO:         Moet Similar SEQ ID NO:         Top Hit Acession Signal ID NO:         Top Hit Acession Signal ID NO:         Top Hit Acession Signal ID NO:         Top Hit Acession Signal ID NO:         Top Hit Acession ID NO:         Top Hit Acession ID NO:         Top Hit Acession ID NO:         Top Hit Acession ID NO:         Top Hit Acession ID NO:         Top Hit Acession ID NO:         Top Hit Acession ID NO:         Top Hit Acession ID NO:         Top Hit Acession ID NO:         Top Hit Acession ID NO:         Top Hit Acession ID NO:         Top Hit Acession ID NO:         Top Hit Acession ID NO:         Top Hit Acession ID NO:         Top Hit Acession ID NO:         Top Hit Acession ID NO:         Top Hit 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BE01032.1         EST_HUMAN           1730         30133         5.75         8.0E-68 BE01032.1         EST_HUMAN           2478         3895         0.56         7.0E-68 AZ08456.1         EST_HUMAN           2478         37310         6.43         6.0E-68 BE01055.1         EST_HUMAN           2576         37310         6.43         6.0E-68 BE01055.1         EST_HUMAN           2576         37310</td> <td>Exon<br/>NO:<br/>10 NO:<br/>10 NO:<br/>10 NO:<br/>10 NO:<br/>10 NO:<br/>10 NO:<br/>10 NO:<br/>10 NO:<br/>10 NO:<br/>10 NO:<br/>10 NO:<br/>10 NO:<br/>10 NO:<br/>10 NO:<br/>10 NO:<br/>10 NO:<br/>10 NO:<br/>10 NO:<br/>10 NO:<br/>10 NO:<br/>10 NO:<br/>10 NO:<br/>10 NO:<br/>10 NO:<br/>10 NO:<br/>10 NO:<br/>10 NO:<br/>10 NO:<br/>10 NO:<br/>10 NO:<br/>10 NO:<br/>10 NO:<br/>10 NO:<br/>10 NO:<br/>10 NO:<br/>10 NO:<br/>10 NO:<br/>10 NO:<br/>10 NO:<br/>10 NO:<br/>10 NO:<br/>10 NO:<br/>10 NO:<br/>10 NO:<br/>10 NO:<br/>10 NO:<br/>10 NO:<br/>10 NO:<br/>10 NO:<br/>10 NO:<br/>10 NO:<br/>10 NO:<br/>10 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BE010038.1         EST_HUMAN           25085         3.44         9.0E-68 BE01032.1         EST_HUMAN           1730         30133         5.75         8.0E-68 BE01032.1         EST_HUMAN           2478         3895         0.56         7.0E-68 AZ08456.1         EST_HUMAN           2478         37310         6.43         6.0E-68 BE01055.1         EST_HUMAN           2576         37310         6.43         6.0E-68 BE01055.1         EST_HUMAN           2576         37310 | Exon<br>NO:<br>10 NO:<br>10 NO:<br>10 NO:<br>10 NO:<br>10 NO:<br>10 NO:<br>10 NO:<br>10 NO:<br>10 NO:<br>10 NO:<br>10 NO:<br>10 NO:<br>10 NO:<br>10 NO:<br>10 NO:<br>10 NO:<br>10 NO:<br>10 NO:<br>10 NO:<br>10 NO:<br>10 NO:<br>10 NO:<br>10 NO:<br>10 NO:<br>10 NO:<br>10 NO:<br>10 NO:<br>10 NO:<br>10 NO:<br>10 NO:<br>10 NO:<br>10 NO:<br>10 NO:<br>10 NO:<br>10 NO:<br>10 NO:<br>10 NO:<br>10 NO:<br>10 NO:<br>10 NO:<br>10 NO:<br>10 NO:<br>10 NO:<br>10 NO:<br>10 NO:<br>10 NO:<br>10 NO:<br>10 NO:<br>10 NO:<br>10 NO:<br>10 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	Top Hit Descriptor	Home canlone mRNA for KIAA0145 protein, partial cds	Homo saplens mRNA for KIAA0145 protein, partial cds	Homo sapiene mBNA for KIAA1485 protein, partial cds	Long serviews profesin tyrosine phosphatase type IVA, member 1 (PTP4A1) mRNA	Homo saplens protein tyrosine phosphatase type IVA, member 1 (PTP4A1) mRNA	The service MRNA for KIAA 1515 protein, partial cds	Homo saprens III w.v. 12 Cerevisiae Hike 2 (SEC14L2), mRNA	Miss misculus G-protein coupled receptor GPR73 (Gpr73) mRNA, complete cds	missing Soares fetal lung_NbHL19W Homo sapiens cDNA clone IMAGE:1950291 3 similar to currents	THR.12 THR repetitive element; THS.22 THR repetitive element; LISPIN 8178 HM3 Homo sapiens cDNA clone s3000023D09	0V1-DT0072-010200-056-h06 DT0072 Homo capiens cDNA	Cricefulus longicaudatus mRNA for EF-1 alpha, complete cds	7414F07 VI NCI CGAP CLL1 Homo saplens cDNA clone IMAGE:3294747 3 similar in 11.000000	HYPOTHETICAL 88.8 KD PROTEIN.:	Homo saptens gene for extrain 1NIB Homo saptens cDNA clone IMAGE:34896 3'	1950-807 1601458514F1 NIH MGC_66 Homo sepiens cDNA clone IMAGE:3862034 6	III 3-CT0534-180900-273-A01 CT0534 Homo saplens cDNA	FORMIN 4 (LIMB DEFORMITY PROTEIN)	10Vo-BT0074-130999-014-g04 BT0074 Homo saplens cDNA	601437367F1 NIH_MGC_72 Home sapiens cDNA clone IMAGE:3922192 3	UI-H-BIO-aam-b-05-0-UI.s1 NCI_CGAP_Sub1 Homo sapiens CUNA GGIE IMAGE	Homo sapiens meningioma (disrupted in balanced translocation) ( (1977),	QV4.ST0234-181199-037-105 S10234 from Septems convinced to the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the 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	Expression Signal		5.39	5.59	3.17	1.64	1.64	1.72	1.17	3.54	3.5	1.35	2.83	29.7	0.79	2.33	9.21				1.49	1.59									2 0.75	2 0 45		
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Top Hit Descriptor	Homo sapiens phosphodlesterase 78 (PDE78), mRNA	Homo sepiens MIF2 suppressor (HSMT3) mRNA complete ods	Homo sapiens myosin IC (MYO1C), mRNA	Human protein kinase C substrate 80K-H /PRKCSH) gene even 4-5	Human protein kinase C substrate 80K-H (PRKCSH) gene, exen 4-8	Homo sapiens CGI-76 protein (LOC51632), mRNA	Homo sapiens CGI-76 protein (LOC51632), mRNA	Homo sapiens meningioma (disrupted in balanced translocation) 1 (MN1), mRNA	Homo saplens low density lipoprotein-related protein 2 (LRP2), mRNA	Homo saplens ADP-ribosylation factor GTPase activating protein 1 (ARFGAP1) mRNA	Homo sapiens pre-B-cell colony-enhancing factor (PBEF) mRNA	Homo saplens pre-B-cell cotony-enhancing factor (PBEF) mRNA	Homo saplens 26S profeasome-associated pad1 homolog (POH1) mRNA	Homo saplens 26S proteasome associated pad1 homolog (POH1) mRNA	Homo saplens v-raf murihe sarcoma viral oncogene homolog B1 (BRAF) mRNA	Homo sapiens glutamate-cysteine ligase (gamma-glutamylcysteine synthetase), regulatory (30.8kD) (GLCLR) mRNA	AU117241 HEMBA1 Home saniens cDNA clane HEMBA100068 8	Homo sapiens RIBIIR gene (partial) exon 12	Homo sapiens actin-related protein 3-beta (ARP3BETA), mRNA	qeS2h01.x1 Scares_fetal_Ling_NbHL19W Homo saplens cDNA clone IMAGE:1743601 3' similar to gb:L11569 60S RIBOSOMAL PROTEIN L18 (HUMAN):	qe82h01.x1 Soares_feba_tung_NbHL19W Homo sapiens cDNA clone IMAGE:1743601 3' similar to	od80803 st NCI CGAP GCR4 Home series cDNA class 1840 CE 19272200 21	wm26h11.x1 NCI CGAP Ut4 Home sablens cDNA clone IMAGE:2427125 3	601344705F1 NIH_MGC 8 Homo sapiens cDNA clone IMAGE:3677641 5	wh57b08x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2384819 3' similar to TR:055137	Homo capiers, after transformitor arouth forter help linding series of the Policy and	Homo sabiens latent transforming growth factor heta hinding protein 2 (LTDT2) mBNA	AU19634 HEMBA1 Homp sapiens aDNA clone HEMBA1006283 5	601110371F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3351352 5	Homo sapiens Smad- and Olf-Interacting zinc finger protein mRNA, partial cds
Top Hit Database Source	Z																T HUMAN	- L		EST_HUMAN	1	Т	Т	Т		NUMBER		T HUMAN	Π	П
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Most Similar (Top) Hit BLAST E Value	1.0E-68	1.0E-68 L76416.1	1.0E-88	1.0E-68 U50319.1	1.0E-68 U50319.1	1.0E-68	1.0E-68	1.0E-88	1.0E-68	1.0E-68	9.0E-69	9.0E-69	9.0E-69	9.0E-69	9.0E-69	9.0E-69	9.0E-69	8.0E-69	7.0E-69	6.0E-69 A	6.P-69	6.0E-69	4.0E-69	4.0E-69 B	4 0F-69 A	4 0F-60	4.0E-69	4.0E-69 A	3.0E-69 B	3.0E-69 A
Expression Signal	2.16	281	1.7	2.83	283	1.81	1.81	2.53	3.05	1.88	2.42	2.42	0.09	0.99	9.0	0.89	7.86	128	4.44	1.85	1.85	1.05	1.18	1.53	4.62	3.17	3.17	0.55	5.24	2.78
ORF SEQ ID NO:	L	37841	38200	38313	38314	38653	38654		31661		26260	26261	27275	27276	30380	30397	-		33011	34649	34650	35795		32378	32467	33315	33316	35739	26672	26834
Exan SEQ (D NO:	24163	24214	24527			24948	24948	13316	26092	25755	13260	13260	14219	14219	17392	17411	24200	16640	19649	21130	21130	22252	13726	25812	19152	19920	19920	22194	13634	13812
Probe SEQ ID NO:	11089	11142	11468	11580	11580	11963	11963	12849	13100	13164	22	2	1063	1053	4246	4268	11128	3473	6482	8047	8047	9174	533	5881	5966	6764	6764	9115	397	627

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Exen SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acesslon No.	Top Hit Database Source	Top Hit Descriptor
47798		1.72	3.0E	-69   780514.1	EST_HUMAN	yd08a02.r1 Soares infant brain 1NIB Homo sepiens cDNA clone IMAGE:24880 5' similar to SP:A48836 A48836 SPEGF II]≕EGF REPEAT-CONTAINING FIBROPELLIN-LIKE PROTEIN - SEA URCHIN ;
21		2.0	305	FN 0166279	ĽN	Homo sepiens lymphatic vesse endoneata nyauridus incopion (Line 1)
//661	00000		0.00		LZ	Homo saplens aconitase 2, mitochandria (ACO2), mKNA
18400	<u>_</u>		<u> </u>	AF0957	Ł	Homo sapiens short chain L-3-hydroxyacyl-CoA dehydrogenase precursor (n.h.d.) 10-0, gunc, name: generalized to september of the configuration of the configuration of the configuration of the configuration of the configuration of the configuration of the configuration of the configuration of the configuration of the configuration of the configuration of the configuration of the configuration of the configuration of the configuration of the configuration of the configuration of the configuration of the configuration of the configuration of the configuration of the configuration of the configuration of the configuration of the configuration of the configuration of the configuration of the configuration of the configuration of the configuration of the configuration of the configuration of the configuration of the configuration of the configuration of the configuration of the configuration of the configuration of the configuration of the configuration of the configuration of the configuration of the configuration of the configuration of the configuration of the configuration of the configuration of the configuration of the configuration of the configuration of the configuration of the configuration of the configuration of the configuration of the configuration of the configuration of the configuration of the configuration of the configuration of the configuration of the configuration of the configuration of the configuration of the configuration of the configuration of the configuration of the configuration of the configuration of the configuration of the configuration of the configuration of the configuration of the configuration of the configuration of the configuration of the configuration of the configuration of the configuration of the configuration of the configuration of the configuration of the configuration of the configuration of the configuration of the configuration of the configuration of the configuration of the configuration of the configuration of the configuration of the configuration of the configu
2002				3.0E-69 U52351.1	F	Homo sapiens arm-repeat protein NPRAP/neurojungin (C INNUZ) IIINNY, parusi CC.
20788	L			3.0E-69 AF268075.1		Homo sapiens 1 KAPP-bittally protein 1 doi: 10.000 July 2000 July 10.000 July 2000 July 2000 July 2000 July 2000 July 2000 July 2000 July 2000 July 2000 July 2000 July 2000 July 2000 July 2000 July 2000 July 2000 July 2000 July 2000 July 2000 July 2000 July 2000 July 2000 July 2000 July 2000 July 2000 July 2000 July 2000 July 2000 July 2000 July 2000 July 2000 July 2000 July 2000 July 2000 July 2000 July 2000 July 2000 July 2000 July 2000 July 2000 July 2000 July 2000 July 2000 July 2000 July 2000 July 2000 July 2000 July 2000 July 2000 July 2000 July 2000 July 2000 July 2000 July 2000 July 2000 July 2000 July 2000 July 2000 July 2000 July 2000 July 2000 July 2000 July 2000 July 2000 July 2000 July 2000 July 2000 July 2000 July 2000 July 2000 July 2000 July 2000 July 2000 July 2000 July 2000 July 2000 July 2000 July 2000 July 2000 July 2000 July 2000 July 2000 July 2000 July 2000 July 2000 July 2000 July 2000 July 2000 July 2000 July 2000 July 2000 July 2000 July 2000 July 2000 July 2000 July 2000 July 2000 July 2000 July 2000 July 2000 July 2000 July 2000 July 2000 July 2000 July 2000 July 2000 July 2000 July 2000 July 2000 July 2000 July 2000 July 2000 July 2000 July 2000 July 2000 July 2000 July 2000 July 2000 July 2000 July 2000 July 2000 July 2000 July 2000 July 2000 July 2000 July 2000 July 2000 July 2000 July 2000 July 2000 July 2000 July 2000 July 2000 July 2000 July 2000 July 2000 July 2000 July 2000 July 2000 July 2000 July 2000 July 2000 July 2000 July 2000 July 2000 July 2000 July 2000 July 2000 July 2000 July 2000 July 2000 July 2000 July 2000 July 2000 July 2000 July 2000 July 2000 July 2000 July 2000 July 2000 July 2000 July 2000 July 2000 July 2000 July 2000 July 2000 July 2000 July 2000 July 2000 July 2000 July 2000 July 2000 July 2000 July 2000 July 2000 July 2000 July 2000 July 2000 July 2000 July 2000 July 2000 July 2000 July 2000 July 2000 July 2000 July 2000 July 2000 July 2000 July 2000 July 2000 July 2000 July 2000 July 2000 July 2000 July 2000 July 2000 July 2000 July 2000 July 2000 Jul
21648		1.33		3.0E-69 AW 138646.1	ш	OF-T-BIT-BOW-9-01-2-01-3-11-10-2-2-1-3-1-1-1-1-1-1-1-1-1-1-1-1-1-1-1-1
22046		0.74		3.0E-69 AA376399.1	ESI HOMAN	15 10000 / 1001 2 curs month observed (beta 1-4)-galactosyltransferase
22668	36238	1.74		X13223.1	Z	In Septembrill MAN 1911 Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of t
2279R	36372	3.15		3.0E-69 X06233.1	TN	(MIF)-related protein to complete A (SEC40) 1 mRNA
23072				5730036 NT	NT.	Homo sapiens official (9. ceravisacy inc. ( (= 0.5%)
23962				11432120 NT	. Ji	Homo sepiens riposoulita protein 519 Protein 518 Ectrason HSC 1905 Protein 518
24155	10	7.68		3.0E-69 AA376399.1	ESI HUMAN	Lance contains mPNA for MFGF8, partial cds
25092	38795	1.77		3.0E-69 AB011541.1	Į,	Home soulens mRNA for MEGF8, partial ods
25092	2 38796	,		AB0115	N	Home services HGC6.2 protein (HGC6.2), mRNA
25223	3	3.1	}	1141915/ N	IN I	Homo sanions KIAA0563 protein gene, complete cds, and alphalib protein gene, partial cds
13612			$\perp$	2.0E-69 AF160252.1	Z	Homo sapiens KIAA0553 protein gene, complete cds, and alphallb protein gene, partial cds
13612			_	9 AF160252.1	Z	Home saplens KIAA0553 protein gene, complete cds; and alphallb protein gene, partial cds
13612			1	9 AF160252.1	Z	Home saniens KIAA0553 protein gene, complete cds; and alphalib protein gene, partial cds
13612				9 AF160252.1	-l⊧	PANA 109444E1 NIH MIGC 16 Homo saplens cDNA clone IMAGE:3350074 5'
15077				9 BE257857.1	EST TOWAN	21/2011 Source tastis NHT Homo sapiens cDNA done IMAGE:781682 5
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21830	35368	38 0.95		2.0E-69 AA114270.1	EST HUMAN	Dos Bulgaria: and Andrews 1405 BN0305 Homo sapiens cDNA
14832	24		1 1.0E-6	1.0E-69 BF330124.1	ESI HUMAN	B-#1 o partial shall sheriff cortactin-binding protein CBP90 mRNA, partial cds
14888	38 27980		2.4 1.0E-6	0E-69 AF053768.1	Į.	CANOMINE IN WASC 21 Homo septens cDNA clone IMAGE:3635781 5
18260	æ	Ö	-	0E-69 BE409094.1	ESI HUMAN	Т
19351	32697		٦	OE-69 BE902501.1	TOT HIMAN	Т
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Top Hit Descriptor	Homo sapiens KIAA0716 gene product (KIAA0716), mRNA	Homo sepiens mRNA for KIAA1147 protein, partial cds	Home septens mRNA for KIAA1147 protein, partial cds	R01278632F1 NIH MGC 39 Homo sapiens cDNA clone IMAGE:3610614 5	1801278532F1 NIH MGC 39 Homo sapiens cDNA done IMAGE:3510614 5	TCBAP1E2678 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project 1 CDA 1 10110 3 april 1 TCBAP1E2678 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project 1 CDA 1 10110 3 april 1 TCBAP1E2678 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project 1 CDA 1 10110 3 april 1 TCBAP1E2678 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project 1 CDA 1 10110 3 april 1 TCBAP1E2678 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project 1 CDA 1 10110 3 april 1 TCBAP1E2678 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project 1 CDA 1 10110 3 april 1 TCBAP1E2678 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project 1 CDA 1 10110 3 april 1 TCBAP1E2678 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project 1 CDA 1 10110 3 april 1 TCBAP1E2678 Pediatric pre-B cell acute lymphoblastic leukemia pre-B cell acute lymphoblastic leukemia pre-B cell acute lymphoblastic leukemia pre-B cell acute lymphoblastic leukemia pre-B cell acute lymphoblastic leukemia pre-B cell acute lymphoblastic leukemia pre-B cell acute lymphoblastic leukemia pre-B cell acute lymphoblastic leukemia pre-B cell acute lymphoblastic leukemia pre-B cell acute lymphoblastic leukemia pre-B cell acute leukemia pre-B cell acute leukemia pre-B cell acute leukemia pre-B cell acute leukemia pre-B cell acute leukemia pre-B cell acute leukemia pre-B cell acute leukemia pre-B cell acute leukemia pre-B cell acute leukemia pre-B cell acute leukemia pre-B cell acute leukemia pre-B cell acute leukemia pre-B cell acute leukemia pre-B cell acute leukemia pre-B cell acute leukemia pre-B cell acute leukemia pre-B cell acute leukemia pre-B cell acute leukemia pre-B cell acute leukemia pre-B cell acute leukemia pre-B cell acute leukemia pre-B cell acute leukemia pre-B cell acute leukemia pre-B cell acute leukemia pre-B cell acute leukemia pre-B cell acute leukemia pre-B cell acute leukemia pre-B cell acute leukemia pre-B cell acute leukemia pre-B cell acute leuke	CONA clone TCBAP2678 TCBA.PGSC project=TCBA Homo sepiens	FOOD OF THE TOTAL TOTAL BUILD HOME SERVICES CON COME IMAGE: 4181325 5	Homo caniens keratin 8 (KRT8) mRNA	ROLL SEPTICE THE MICE 20 Homo Sapiens cDNA clone IMAGE: 4025785 5	LARAAN X1 Sources NFL T GBC S1 Homo sapiens cDNA clone IMAGE:2360390 3' similar to contains Au	repetitive element;contains element MIR repetitive element;	Homo sanions DGS-1 mRNA, 3' end	magnot x1 NCI CGAP Brn25 Homo sapiens cDNA clone IMAGE: 2165305 3	Emisoral v1 NCI CGAP Bri26 Homo sapiens cDNA clone IMAGE:2165305 3	HIGHOALT NOI CGAP GCB1 Homo sapiens cDNA done IMAGE:713239 5	Homo sapians tumor suppressor deleted in oral cancer-related 1 (DOC-1R) money	Homo sapiens adenylate cyclase 3 (ADCY3) mRNA	Homo sapiens MIST mRNA, partial cds	Homo sapiens MIST mRNA, partial cds	Homo sapiens gene encoding splicing factor SF1, exchs 2-6	Homo sapiens titin immunoglobulin domain protein (mydullin) (1112/), 111	Homo sapiens mRNA for KJAA1294 protein, partiel cus	Homo sapiens mRNA for KIAA1294 protein, partial cds	Human displacement protein (CCAAT) mRNA	Human displacement protein (CCAAT) mRNA	Human PBX3 mRNA	Human PBX3 mRNA	Homo sapiens phospholipid scramblase 1 gene, exon 1 and 5 hanking region	Homo sapiens karyopherin beta 2b, transportin (1 KNZ), mKNA	Homo sapiens karyopherin beta 2b, transportin ( FRNZ), mrstva	
Top Hit Database Source			- L	NOVI TOL	EST HOWAIN	LONOL LES	EST_HUMAN	EST HUMAN	ESI HOMBIN	N	EST HUMAIN	EST HUMAN	EST HUMAN	NAM!	NOW TO L	EST HUMAIN	EN TOWAR	120	LZ LZ	Į	Ę	NT NT	ĽΣ	1 2	F	Į.		I-Z		RAINT	NT NT	
Top Hit Acession No.	TIM caccaar	199203	E-69 AB032973.1	E-69 AB032973.1	E-69 BE531007.1	)E-69 BE531007.1	0E-69 BE245070.1	0E-69 BE245070.1	0E-69 BF528429.1	4504918 N I	.0E-69 BF125887.1	0E-69 AI809994.1	8.0E-70 AA230303.1	8.0E-70 L77566.1	.0E-70 AI497807.1	.0E-70 AI497807.1	7.0E-70 AA282955.1 ES		AB02026	7.0E-70 ABOSESSO 1	7.0E-70/ABOSESSOS.1	11417306 NT	VENA77	7.0E-/0 ABOST 15.1	ADM// 10.	7.0E-70 M7 4089.1	7.0E-/0 M/4039.1	A38041.1	7.0E-70 X59841.1	14505084 NT		
Most Similar (Top) Hit BLAST E Value		1.0E-69	1.0E-69 A		<b>-</b> 1	1.0E-69	1.0E-69	1.0E-69	1.0E-69	1.0E-69	1.0E-69	1.0E-69	8.0E-70	8.0E-70	7.0E-70	7.0E-70						1		1		1		1				1010-/
Expression Signal		1.22	2.91	2.91	0.61	0.61	5.01	5.01	0.9	35.41	1.88	3.4	1.56		2.42			5.13	4	5.4					7					0 2.88		1.7
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Exon SEQ ID NO:		20271	20204	20204	20157	20157	23412	23412	23659	24184	25181	1	1	L	1	1_	1_	ì .	1 1	18795	18795	ı		l i		ı	1	8 22433	<u> </u>	5 21078		21102
Probe SEQ ID	:	8968	6078	6976	7021	7021	10377	10377	10625	44412	12237	17673	2400	4493	1856	1856	1984	2125	4340	2800	299	700	794	862	862	8	8919	8	9358	9635	0996	0996

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	Top Hit Descriptor	Homo sapiens glutamate-cysteine ligase (gamma-glutamykysteine synthetase), catalytic (72.8kD) (GLCLC) mRNA	Homo sapiens NDST4 mRNA for N-deacetylase/N-sulfotransferase 4, complete cds	Homo sapions NDST4 mRNA for N-deacetylase/N-sulfotransferase 4, complete cds	Homo sapiens spastic paraplegia 4 (autosomal dominant, spastin) (SPG4), mRNA	Homo sapiens spastic paraplegla 4 (autosomal dominant, spastin) (SPG4), mRNA	Homo sapiens HIR (histone cell cycle regulation defective, S. cerevisiae) homolog A (HIRA), mRNA	Homo sapiens HIR (histone cell cycle regulation defective, S. cerevisiae) homolog A (HIRA), mRNA	Homo sapiens amyloid beta (A4) precursor protein (protease nextr-II, Aizhelmer disease) (APP). mRNA	Human Ku (p70/p80) subunit mRNA, complete cds	Homo sapiens sodium-dependent high-affinity dicarboxylate transporter (NADC3) mRNA, complete ods	Homo sapiens KIAA0792 gene product (KIAA0792), mRNA	Homo sapiens KIAA0792 gene product (KIAA0792), mRNA	MR3-HT0487-150200-115-e06 HT0487 Homo sapiens cDNA	EST03926 Fetal brain, Stratagene (cat#936206) Homo saplens cDNA done HFBDN25	CM4-UM0003-010300-105-g08 UM0003 Homo saplens cDNA	CM4-UM0003-010300-105-g08 UM0003 Homo sapiens cDNA	RC0-BT0522-071299-011-a12 BT0522 Homo sapiens cDNA	RC0-BT0522-071299-011-a12 BT0522 Homo sapiens cDNA	Homo saplens Xq pseudoautosomal region; segment 2/2	Homo sapiens plakophilin 4 (PKP4), mRNA	Homo sapiens plakophilin 4 (PKP4), mRNA	wh90d03.x1 NCI_CGAP_CLT1 Home sapiens cDNA clone IMAGE:2388005.31	602141561F1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4302806 5'	602141561F1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4302806 5'	hz81h02.x1 NCI_CGAP_Lu24 Hamb sapiens aDNA clane IMAGE:32144193'	Homo sapiens phosphatidylinositol 4-kinase 230 (pi4K230) mRNA, complete cds	y,07a10.r1 Sogres melanocyte ZNbHM Homo sapiens cDNA clone IMAGE:270522 5' similer to SW:D3HI_RAT P29266 3-HYDROXYISOBUTYRATE DEHYDROGENASE PRECURSOR;
	Top Hit Database Source	TN	N	NT.	NT	TN	TN	. LN	TN	L	Ę	NT	N	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST HUMAN	EST_HUMAN	EST_HUMAN	NT	LN	NT	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	IN	EST_HUMAN
	Top Hit Acession No.	4557624 NT	0E-70 AB036429.1	0E-70 AB036429.1	11429685 NT	11429685 NT	11526319 NT	11526319 NT	4502166 NT	0E-70 M30938.1	DE-70 AF154121.1	7662307 NT	T662307	0E-70 BE166034.1	4.0E-70 T06037.1	AW 793226.1	AW793226.1	BE071738.1	BE071796.1	AJ271736.1	11430988 NT	11430988 NT	A1831975.1	BF685233.1	3.0E-70 BF685233.1	BE502973.1	AF012872.1	DE-70 N42161.1
	Most Similar (Top) Hit BLAST E Value	7.0E-70	7.0E-70	7.0E-70	7.0E-70	7.0E-70	7.0E-70	7.0E-70	6.0E-70		6.0E-70	5.0E-70	5.0E-70	5.0E-70	4.0E-70	4.0E-70	4.0E-70	3.0€-70	3.0E-70	3.0E-70	3.0E-70	3.0E-70	3.0E-70	3.0E-70	3.0E-70	3.0E-70	2.0E-70	2.0E-70
	Expression Signal	0.53	0.85	0.85	1.77	1.77	237	2.37	2.51	2.29	0.7	1.78	1.78	5	1.03	1.84	1.84	1.71	1.71	1.11	0.59	0.59	1	1.69	1.69	0.62	1.03	15.24
	ORF SEQ ID NO:	36480	37149			38040	38583	38584	27135	28466	30747	28854	28855		33454			27853	27854	31367					33034	38955	26283	26923
	Exan SEQ ID NO:	_	1	23540		24392	24885	24885	14070	15339	17765	15066	15066		20045	. I	- 1	14771	_		_	18930	19248	19669	19669	23349	13277	13890
	Probe SEQ ID NO:	9857	10505	10505	11329	11329	11897	11897	894	2205	4629	2618	2618	12247	6894	6933	6933	1619	1619	5270	5737	5737	9909	6503	6503	10314	39	707

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	Top Hit Descriptor  Top Hit Descriptor  Top Hit Descriptor	MO7410.11 Scares merano yo SW:D3HL RAT P29286 3-HYDROXYISOBUTYRATE DEHYDROGENASE FRECUNOS. SW:D3HL RAT P29286 3-HYDROXYISOBUTYRATE DEHYDROGENASE FRECUNOS. Investinal, XI NCI CGAP Part Homo sepiens cDNA clone IMAGE.2004913.3'	Homo sapiens hypothetical protein FLJ20758 (FLJ20759), minus	Homo saplens KIAA0193 gene product (KIAA0193), min. A	Homo sepiens KIAA0183 gene product (KIAA0183), in Nature 19712758 3'	hz64c12.x1 NCI_CGAP_Lu24 Homo saplens cDNA cione IMAGE:612441 5' similar to	ZD45h05.r1 Stratagene HeLa cell s3 937.215 Homo seprems Community and Stratagene HeLa cell s3 937.215 Homo seprems Community and Stratagene HeLa cell s3 937.215 Homo seprems Community Stratagene HeLa cell s3 937.215 Homo seprems Community Stratagene HeLa cell s3 937.215 Homo seprems Community Stratagene HeLa cell s3 937.215 Homo seprems Community Stratagene HeLa cell s3 937.215 Homo seprems Community Stratagene HeLa cell s3 937.215 Homo seprems Community Stratagene HeLa cell s3 937.215 Homo seprems Community Stratagene HeLa cell s3 937.215 Homo seprems Community Stratagene HeLa cell s3 937.215 Homo seprems Community Stratagene HeLa cell s3 937.215 Homo seprems Community Stratagene HeLa cell s3 937.215 Homo seprems Community Stratagene HeLa cell s3 937.215 Homo seprems Community Stratagene HeLa cell s3 937.215 Homo seprems Community Stratagene HeLa cell s3 937.215 Homo seprems Community Stratagene HeLa cell s3 937.215 Homo seprems Community Stratagene HeLa cell s3 937.215 Homo seprems Community Stratagene HeLa cell s3 937.215 Homo seprems Community Stratagene HeLa cell s3 937.215 Homo seprems Community Stratagene HeLa cell s3 937.215 Homo seprems Community Stratagene HeLa cell s3 937.215 Homo seprems Community Stratagene HeLa cell s3 937.215 Homo seprems Community Stratagene HeLa cell s3 937.215 Homo seprems Community Stratagene HeLa cell s3 937.215 Homo seprems Community Stratagene HeLa cell s3 937.215 Homo seprems Community Stratagene HeLa cell s3 937.215 Homo seprems Community Stratagene HeLa cell s3 937.215 Homo seprems Community Stratagene HeLa cell s3 937.215 Homo seprems Community Stratagene HeLa cell s3 937.215 Homo seprems Community Stratagene HeLa cell s3 937.215 Homo seprems Community Stratagene HeLa cell s3 937.215 Homo seprems Community Stratagene HeLa cell s3 937.215 Homo seprems Community Stratagene HeLa cell s3 937.215 Homo seprems Community Stratagene HeLa cell s3 937.215 Homo seprems Community Stratagene HeLa cell s3 937.215 Homo seprems Community Stratagene HeLa cell s3 937.215 Homo seprems Co	TR:G1041293 G1041223 D2000.21 2245h05.r1 Strategene Hela cell s3 937216 Hamo sapiens cDNA clone IMAGE:612441 5 Similar to	TR:G1041293 G1041283 D2095.5. HTL1A HS21C002 Home septents chromosome 21 segment HS21C002	748004.11 Soares retina N254HR Homo sapiens CDNA cid le livrocares retina N254HR Homo sapiens CDNA cid le livrocare	P03345 GAG POLYPROTEIN;	Novel human gene mapping to chomosome A Navidan) mRNA, partial cds	Human nonmuscle myosin heavy chain to (with 1977)	H. sepiens gene for schwanndmin (USS)	H.sapiens gene for sortwallioning.	Homo saplens NALL I IIINAA, Complete cds (Homo saplens of Sample in the same in the same in the same in the same in the same in the same in the same in the same in the same in the same in the same in the same in the same in the same in the same in the same in the same in the same in the same in the same in the same in the same in the same in the same in the same in the same in the same in the same in the same in the same in the same in the same in the same in the same in the same in the same in the same in the same in the same in the same in the same in the same in the same in the same in the same in the same in the same in the same in the same in the same in the same in the same in the same in the same in the same in the same in the same in the same in the same in the same in the same in the same in the same in the same in the same in the same in the same in the same in the same in the same in the same in the same in the same in the same in the same in the same in the same in the same in the same in the same in the same in the same in the same in the same in the same in the same in the same in the same in the same in the same in the same in the same in the same in the same in the same in the same in the same in the same in the same in the same in the same in the same in the same in the same in the same in the same in the same in the same in the same in the same in the same in the same in the same in the same in the same in the same in the same in the same in the same in the same in the same in the same in the same in the same in the same in the same in the same in the same in the same in the same in the same in the same in the same in the same in the same in the same in the same in the same in the same in the same in the same in the same in the same in the same in the same in the same in the same in the same in the same in the same in the same in the same in the same in the same in the same in the same in the same in the same in the same in the same in the same in the same in the same in the same in the same i	Human mRNA for NF1 protein incommediate chein 1 mRNA, complete cds	Homo saprens of chinamic dynamin termediate chain 1 mRNA, complete cos	Homo sapiens Cympianing Cympianing Compined Compined Compined Compined Compined Compined Compined Compined Compined Compined Compined Compined Compined Compined Compined Compined Compined Compined Compined Compined Compined Compined Compined Compined Compined Compined Compined Compined Compined Compined Compined Compined Compined Compined Compined Compined Compined Compined Compined Compined Compined Compined Compined Compined Compined Compined Compined Compined Compined Compined Compined Compined Compined Compined Compined Compined Compined Compined Compined Compined Compined Compined Compined Compined Compined Compined Compined Compined Compined Compined Compined Compined Compined Compined Compined Compined Compined Compined Compined Compined Compined Compined Compined Compined Compined Compined Compined Compined Compined Compined Compined Compined Compined Compined Compined Compined Compined Compined Compined Compined Compined Compined Compined Compined Compined Compined Compined Compined Compined Compined Compined Compined Compined Compined Compined Compined Compined Compined Compined Compined Compined Compined Compined Compined Compined Compined Compined Compined Compined Compined Compined Compined Compined Compined Compined Compined Compined Compined Compined Compined Compined Compined Compined Compined Compined Compined Compined Compined Compined Compined Compined Compined Compined Compined Compined Compined Compined Compined Compined Compined Compined Compined Compined Compined Compined Compined Compined Compined Compined Compined Compined Compined Compined Compined Compined Compined Compined Compined Compined Compined Compined Compined Compined Compined Compined Compined Compined Compined Compined Compined Compined Compined Compined Compined Compined Compined Compined Compined Compined Compined Compined Compined Compined Compined Compined Compined Compined Compined Compined Compined Compined Compined Compined Compined Compined Compined Compined Compined Compined Compined Compined Compined Compined Comp	in white standing in the standard standard in the standard stands and 5	Human guanine nucleotide binding protein alpha-subunit gene (C-S-atpita), control enzyme, glycogenial Human guanine nucleotide binding enzyme, glycogenial	Homo sapiens amylo-1,6-glucosicase, 1-mpm s		- }	cas	INA	PNO - COURT	Homo saprens righousements in the sector 3, subunit 6 (48kd) (EIF330) moves	Hornto septions consist lipoprotein-related protein 2 (LRP2), mKNA	The section and the section and the section and the section and the section and the section and the section and the section and the section and the section and the section and the section and the section and the section and the section and the section and the section and the section and the section and the section and the section and the section and the section and the section and the section and the section and the section and the section and the section and the section and the section and the section and the section and the section and the section and the section and the section and the section and the section and the section and the section and the section and the section and the section and the section and the section and the section and the section and the section and the section and the section and the section and the section and the section and the section and the section and the section and the section and the section and the section and the section and the section and the section and the section and the section and the section and the section and the section and the section and the section and the section and the section and the section and the section and the section and the section and the section and the section and the section and the section and the section and the section and the section and the section and the section and the section and the section and the section and the section and the section and the section and the section and the section and the section and the section and the section and the section and the section and the section and the section and the section and the section and the section and the section and the section and the section and the section and the section and the section and the section and the section and the section and the section and the section and the section and the section and the section and the section and the section and the section and the section and the section and the section and the section and the section and the section and the section and the section an	
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oligino.	Top Hit Acession No.		٦	8923669 N	7661983 N I	1983	1	-70 AA180093.1	2.0E-70 AA180093.1	2.0E-70 AL163202:2		2.0E-70 AA054010.1	AL 133207.2	2.0E-70 M69181.1	X72662 1	AE340105 1	2.0E-70 D12625.1	AF123074.1	2 0F-70 AF123074.1		11422642 NT	0E-70 (MZ171)	11423599 NT	H47959.1	11526355 NT	0 AF123303.1	89234	2 05-70 89234	4503	11430	
-	Most Similar (Top) Hit BLAST E Value	24 2.0E-70 N42161.1	2.0E-70 AI	2.0E-70	2.0E-70	2.0E-70	2.0E-70B	2.0E-70 A	2.05-70	2.0E-70		2.0E-70	2.0E-70	2.0E-70	Z.05-70	2.0E-70	20E-70	١	1	L	20	127	2.0E-70		1	L	1	$\perp$	$\perp$	$\perp$	
	Expression ( Signal E	15.24	1.85	1.36	2.16	2.16	1.23	1.07	1.07	4.92		9.45	0.71	5.88	8.42		1.23		10.35			2.81	98					3.39		7.70	
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Top Hit Descriptor	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA	Homo sapiens transglutaminase 3 (E polypeptide, protein-glutamine-gamma-glutamytransferase) (1 GM3)	mRNA	zh65g05,r1 Soareo Tetal IIVer spleen TNTLS ST RUITD september 252,444.6	Zv54c03.r1 Soares testis_NHT Homo captens cDNA clone IMAGE:/3/444 3	AV738538 CB Homo sapiens cDNA clone CBLBGB10 5	qe04f01.x1 Soares_testis_NHT Homo sapiens cDNA done IMAGE:1738009 3 similar to 1 K:014045 014045 PHOSPHOTRANSFERASE;	qe04f01x1 Soares_testis_NHT Homo sapiens cDNA done IMAGE:1738009 3 similar to 1 K:U14045	1014045 PHOSPHO (RANSPERASE).	WDSZCOZY NCJ. COD, TODB, TODE, TODE, TODC, CDD1, CDD2, CDD3, AND CDD4 GENES.	wb52c06.x1 NCI_CGAP_GC6 Homo saplens cDNA clone IMAGE:2309268 3 similar to Incit strains 1972; CDU2, CDU3, CDU1, TCDD, TCDB, TCDE, TCDC, TCDC1, CDD2, CDD3, AND CDA GENES:	p21d11.rt Stratagene neuroepithelium (#937231) Homo sapiens cDNA ctone IMAGE:010101 3 similar to	1 K. G1143001 G1143001 G1 MAIN AND 1 CE	WZ40U.K.I OKRIES_14I LCOCA_CITED PROTEIN 1;  054730 TRANSPLANTABILITY ASSOCIATED PROTEIN 1;	z/60h06,r1 Soares testis NHT Homo sapiens cuiva cione livia dell'100/13 3	Zigla06.s1 Soares feta liver spieen invito 31 monto saprans cours cours invitor.	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Top Hit Acession No.	11430460 NT		507476	.0E-70 W85795.1	-	.0E-70 AV738538.1	9.0E-71 A1143870.1		.0E-71 AI143870.1	0E-71 A1654903.1	0E-71 AIB54903.1		.0E-71 AA171451.1	.0E-71 AW273820.1	7.0E-71 AA442230.1		١	5.0E-71 AF056322.1	5.0E-71 AW816405.1	4502740 NT	11641408 NT	7662209 NT	11431590 NT	5.0E-71 M38108.1	11626445 NT	5.0E-71 AF072810.1	5453777 NT	5453777 NT	5.0E-71 X13467.1	5.0E-71 U70968.1
 Most Similar (Top) Hit TELAST E Value	2.0E-70		1.0E-70	1.0E-70 V	1.0E-70	1.0E-70	9.0F-74.A		9.0E-71	9.0E-71	9.0E-71		8.0E-71	8.0E-71	7.0E-71	7.0E-71		5.0E-71					,				5.0E-71			
Expression Signal	2.42		3.72	0.64	0.88	7.61	803		6.03	2.05	3.47		2.88	0.63	7.86	1.34	2.2	7.11		1.59			0.82	1.79	0.8			96.0		
ORF SEQ ID NO:	32051					37877	20573	2122	32574	33751				37484			38353	28548		L	33356			L	L		35335			37124
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Probe SEQ ID S	1.0882	7007	3480	9480	10003	11175	3909	300	6065	7175	707	20	9270	10828	7533	8877	11614	2284	4235	8002	6801	70607	7296	6/9/	7884	7912	8720	8720	10115	10476

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Top Hit Descriptor	Homo sabiens IGF-II mRNA-binding protein 3 (KOCs) mRNA	Homo sapiens similar to transcription factor CA150 (H. senienc) (I. Oceanion) — DA14	Homo saplens similar to transcription factor CA150 (H. saplens) (LOC63170), mRNA	Homo saplens pro-platelet basic protein (includes platelet basic protein, befa-thromboglobulin, connective fissue-activation pening in peninghia proteins peninghia proteins peninghia proteins peninghia proteins peninghia proteins peninghia proteins peninghia proteins peninghia proteins peninghia proteins peninghia proteins peninghia proteins peninghia proteins peninghia peninghia peninghia peninghia peninghia peninghia peninghia peninghia peninghia peninghia peninghia peninghia peninghia peninghia peninghia peninghia peninghia peninghia peninghia peninghia peninghia peninghia peninghia peninghia peninghia peninghia peninghia peninghia peninghia peninghia peninghia peninghia peninghia peninghia peninghia peninghia peninghia peninghia peninghia peninghia peninghia peninghia peninghia peninghia peninghia peninghia peninghia peninghia peninghia peninghia peninghia peninghia peninghia peninghia 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NCI_CGAP_OV/8 Hamo sepiens cDNA clone IMAGE:357/221 3' similar to TR:092165	Homo saplens short chain L-3-hydroxyacyJ-CoA dehydrogenase precursor (HADHSC) gene, nuclear gene encoding mitochondrial protein, complete cds	A dehydrogenase precursor (HADHSC) gene, nuclear gene	bb81a06.y1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3048754 5' similar to SW :R23B_HUMAN P54727 UV EXCISION REPAIR PROTEIN PROTEIN RAD23 HOMO! OG B	Tmul022 Human Epidermal Keratinocyte Subtraction Library- Upregulated Transcripts Homo sapiens cDNA similar to ci 6598881	Tmull022 Human Epidermal Keratinocyte Subtraction Library- Upregulated Transcripts Homo sapiens cDNA 🔛 similar to gi 6598881	W77c11.r1 Soares breast 2NbHBst Homo saniens cDNA clame IMAGE 484772 8	ye43e09.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:120520 5'
Top Hit Database Source	N.	<u>F</u>	N	LZ	Į.	N⊣	۲	١	M	Ψ	Į.	NT	EST HUMAN	FST HIMAN	TAIL TO LO	L L	1	EST HUMAN	EST_HUMAN	LN.	LΝ	EST_HUMAN	EST HUMAN	EST HUMAN	Т	EST_HUMAN
Top Hit Acession No.	5729900 NT	11417012 NT	11417012 NT	11436514 NT	11438069 NT	11418039 NT	4507592 NT	4.0E-71 AF157626.1	4.0E-71 AF157626.1	4505880 NT	4.0E-71 AF056322.1	7657602 NT	3.0E-71 AU135734.1	3.0E-71 AA557683 1	AI 163206 2	387462 1		2.0E-71 AL042439.1	.0E-71 BF195585.1	0E-71 AF095703.1	0E-71 AF095703.1	0E-71 BE018477.1	0E-71 BF149173.1	_		
Most Simitar (Top) Hit BLAST E Value	5.0E-71	5.0E-71	5.0E-71	5.0E-71	5.0E-71	5.0E-71	4.0E-71	4.0E-71	4.0E-71	4.0E-71	4.0E-71	4.0E-71	3.0E-71	3.0E-71	2 0F.74	2 0F-74	2 OF 74	2.0E-71	2.0E-71	2.0E-71	2.0E-71	2.0E-71	2.0E-71 B	2.0E-71 E	2.0E-71 R	2.0E-71 T95489.1
Expression Signal		1.53		3.85	2.1	1.75	1.84	31.91	31.91	1.67	1.97	4.56	1.13	3.32	4 52	7.23	7.23	0.71	0.5	2.12	2.12	4.37	1.46	1.46	2.05	4.88
<u>R</u> □	37584				38199		26370	26601	26602	29141	30667	31200		37646	27481	31614	31615	31489	35826	37467	37468	37647	38545	38546	38567	
()	23955			24295		_{				ı			21305	24013	14416	1	ŀ	11	22285	23846	23846	24015	24848	24848	24870	25231
Probe SEQ ID NO:	10870	10943	10943	11226	11467	12558	106	360	360	2951	4548	5101	8223	10931	1258	5435	5435	7107	9207	10813	10813	10933	11860	11860	11882	12318

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					Single	Single Extil Flores Explored	דאלו מסמס וווי
Probe SEQ ID S	Exan SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Vaiue	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
						7	oy/5e03.s1 Soares_senescent_fibroblests_NbHSF Homo septens cDNA clone IMAGE:1000910.5 Silling to
922	13841	26868	1.55		A1077927	T HUMAN	contains LOR1.bz LOX1 repetitive element. Home, amiens neuronal cell death-related protein (LOC51616), mRNA
964	14137	27198	1.38		7706281 N	Z	Homo saniens dissoled 2 gene, exons 2 through 15 and complete cde
1124	14289	27344	13.07		1.0E-71 AF205890.1	Į.	Homo sagiens phosphatidylinositol 4-kinase 230 (pI4K230) mRNA, complete cds
1371	14526	27600	11.13		1.0E-71 AF012872.1	Z	Trains PMS2L18 mRNA, partial cds
2147	15283				1.0E-71 AB017007.1	- E	Homo sabiens PMS2L16 mRNA, partial cds
2147	15283	28409			1 AB017007.1	2 2	Homo sapiens hairy/enhancer-of-split related with YRPW motif-like (HEYL), mKNA
2757	15874			1	IN SCITCOT	111	Homo sapiens inorganic pyrophosphatase mRNA, complete cds
3590	16754	29769			1.0E-71 AF119665.1	-N	Home seriens SNARE protein kinase SNAK mRNA, complete cds
3685	1	29855	6.57		1.0E-71 AF246219.1	Z	Homo saciens SNARE protein kinase SNAK mRNA, complete cds
3685	1			1.0	E-71 AF246219.1	Z	To 15 Human Enrichmal Keratinocyte Subtraction Library. Upregulated Transcripts Homo septens CUNA
	1_				4 DE422850 1	FST HUMAN	clone 02_15.5' similar to Homo sapiens chromosome 19
3738	16899	3 29902	0.9	2.	E-/1 BE122030.1		02_15 Human Epidermal Keratinocyte Subtraction Library- Opregulated Hansonipus Homen Epidermal Keratinocyte Subtraction Library- Opregulated Hansonipus
i i	46000	20003		0.9 1.0E-7	0E-71 BE122850.1	EST_HUMAN	clone 02, 15 St similar to Homo sapiens chromosome 19
3030	1	١			1.0E-71 AF218904.1	LN.	Homo saprens amagon Process Complete cds
2000	1.				0E-71 D28476.1	_N	יייייייייייייייייייייייייייייייייייייי
4080					TN 28182111	LNC	thesis, yeast, homolog)-like 2 (GCN5L2), mKNA
6881					AB0411	LN	Homo sapiens mRNA for KIAA0559 protein, partial cus
7235	20319				0E-71 ADOL 1 131.1	LN	Home sapiens CAGL79 mRNA, pertral cds
7464	20539				71090735.1	12	Homo sapiens glypican-6 (GPC6) mRNA, complete cds
8340	21421		16 0.82		0E-71 AF 105267.1	TNIO	Homo sapiens myomesin (M-protein) 2 (165kD) (MYOM2), mKNA
8362	21443					TNT	Homo sapiens hypothetical protein FLJ10998 (FLJ10998), mkNA
8641						TNT	Homo sapiens hypothetical protein FLJ10998 (FLJ10995), mixiva
8641					, 00000	LZ.	CSNK2A1-casen kinase !! (OK!!) subunit alpria [human, cenomic, recording
9429	ŀ				11 3/2330.1	Į.	Homo sapiens cytochrome c oxidase subunit VIIa-related protein gene, curithres cus
1021	1 23247	17 36837			.0E-/1/A100/045.	NAM IJ TOB	AV76/1217 MDS Homo sepiens cDNA clone MDSEIAGS 9
10273	1			Ì	AV7612	LONDE ICH	Homo saniens activated leucocyte cell adhesion molecule (ALCAM), mRNA
10759	L	37411			71 1143314Z NI	ECT LIBRAN	Т
11024	ı	23	2	2.49 1.0E-	AV7612	ביייויוסד ביין דואן פספטיי	Home septens coggulation factor XIII, A1 polypeptide (F13A1), mKNA
11121	1_					005 INT	Homo sapiens leucy/cystinyl aminopeptidase (LNPEP), mRNA
11413	3 24474					14417 131 1111 11447404 NIT	
11413	L	74 38139			74 45044900 4	LN	
12709		74	13	10.17 1.0E	0E-/1 ABUT 1388.1	1	

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Expn NO:         ORF SEQ ID NO:         Expression Signal         Most (To Signal           13615         28654         0.77         9           13616         28655         0.77         9           13617         32760         0.86         0.77           17375         30363         1.75           17375         30363         1.75           17375         30363         1.75           13302         26324         1.19           13302         26326         1.19           13302         26326         1.16           13302         26326         1.16           13302         26326         1.16           13302         26326         1.16           13302         26326         1.16           20133         33607         1.62           24576         38263         2.95           24676         38263         2.95           24676         38233         1.55           24631         38634         1.55           24631         38634         1.55           28336         0.91           18073         3415         0.85
SEC   D   ORF SEQ   Signal   Most Similar   Top Hit Acession   Top Hit Acession   Top Hit Acession   Top Hit Acession   Top Hit Acession   Top Hit Acession   Top Hit Acession   Top Hit Acession   Top Hit Acession   Top Hit Acession   Top Hit Acession   Top Hit Acession   Top Hit Acession   Top Hit Acession   Top Hit Acession   Top Hit Acession   Top Hit Acession   Top Hit Acession   Top Hit Acession   Top Hit Acession   Top Hit Acession   Top Hit Acession   Top Hit Acession   Top Hit Acession   Top Hit Acession   Top Hit Acession   Top Hit Acession   Top Hit Acession   Top Hit Acession   Top Hit Acession   Top Hit Acession   Top Hit Acession   Top Hit Acession   Top Hit Acession   Top Hit Acession   Top Hit Acession   Top Hit Acession   Top Hit Acession   Top Hit Acession   Top Hit Acession   Top Hit Acession   Top Hit Acession   Top Hit Acession   Top Hit Acession   Top Hit Acession   Top Hit Acession   Top Hit Acession   Top Hit Acession   Top Hit Acession   Top Hit Acession   Top Hit Acession   Top Hit Acession   Top Hit Acession   Top Hit Acession   Top Hit Acession   Top Hit Acession   Top Hit Acession   Top Hit Acession   Top Hit Acession   Top Hit Acession   Top Hit Acession   Top Hit Acession   Top Hit Acession   Top Hit Acession   Top Hit Acession   Top Hit Acession   Top Hit Acession   Top Hit Acession   Top Hit Acession   Top Hit Acession   Top Hit Acession   Top Hit Acession   Top Hit Acession   Top Hit Acession   Top Hit Acession   Top Hit Acession   Top Hit Acession   Top Hit Acession   Top Hit Acession   Top Hit Acession   Top Hit Acession   Top Hit Acession   Top Hit Acession   Top Hit Acession   Top Hit Acession   Top Hit Acession   Top Hit Acession   Top Hit Acession   Top Hit Acession   Top Hit Acession   Top Hit Acession   Top Hit Acession   Top Hit Acession   Top Hit Acession   Top Hit Acession   Top Hit Acession   Top Hit Acession   Top Hit Acession   Top Hit Acession   Top Hit Acession   Top Hit Acession   Top Hit Acession   Top Hit Acession   Top Hit Acession   Top Hit Acession   Top H
Expn NO:         ORF SEQ ID NO:         Expression Signal         Most Similar (Top) Hit Value         Top Hit Act Value         Top Hit Act Value           13615         26654         0.77         9.0E-72 Al857636.1           13616         26655         0.77         9.0E-72 Al857636.1           17375         30363         1.75         7.0E-72         46           17375         30363         1.75         7.0E-72         46           20357         30363         1.75         7.0E-72         46           17375         30363         1.75         7.0E-72         46           20357         33811         3         7.0E-72         46           20357         33811         3         7.0E-72         46           13302         26324         1.75         7.0E-72         46           13302         26324         1.19         5.0E-72 BF333707.         46           13302         26324         1.19         5.0E-72 BF333707.         46           13302         26324         1.19         5.0E-72 BF333707.         46           13302         26325         1.19         5.0E-72 BF333707.         41045.1           20183         36598         4.16
Exen NO:         ORF SEQ ID NO:         Expression Signal         (Top) Hit PLAST E Nature         Most Similar Value           13615         26654         0.77         9.0E-72           13615         26654         0.77         9.0E-72           17375         30361         1.75         7.0E-72           17375         30363         1.75         7.0E-72           26569         0.77         9.0E-72           13302         26324         1.75         7.0E-72           13302         26324         1.75         7.0E-72           13302         26324         1.76         7.0E-72           13302         26325         1.76         7.0E-72           13302         26325         1.76         7.0E-72           13302         26325         1.76         5.0E-72           13302         26325         1.19         5.0E-72           13302         26325         3.1         5.0E-72           20183         3.3607         1.62         5.0E-72           24575         38253         2.95         5.0E-72           24675         38253         2.95         5.0E-72           24631         38634         1.55
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Page 368 of 550 Table 4 Single Exon Probes Expressed in Placenta

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Top Hit Descriptor	Homo saciens hypothetical protein FLJ20758 (FLJ20758), mRNA	Total Service Service Service (SEC10L1), mRNA	TOTILO SELECTION OF COMPANY TO THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF	RC3-L10023-200100-012-011 L10023 TIGHID Septemble SCHOOL	RC3-L10023-200100-012-011 L1 0023 House squeres conversions to the converse of similar to	qh67c02.xf Soares_fetal_liver_spleen_fNRF.S_S1 Homo sapiens cDNA done invAcE. 10497.50.5 sininga io TR:Q14498 Q14498 SPLICING FACTOR. [1] ;contains Alu repetitive element;contains element L1 repetitive	element;	aa23f09.sf NCL_CGAP_GCB1 Homo sapiens cDNA done IMAGE:314171 3 smillar to SW.CF IN_FLOAT P49131 CHLOROPLAST TRIOSE PHOSPHATE TRANSLOCATOR PREQURSOR.	aa2309.st NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:814121 3. similar to 507.07 11.7 12.11.	P49131 CHLOROPLASI I NOSE TITOSETIMIE Homoseniene CDNA done IMAGE:235084 5	VIZSBOST SOBRES TEIZH IIVEL SPIECH INTECT TO STANDING 2 (BEING SOKO) (EIF2B2), MRNA	Homo sepiens eurençatic densiaduri initiadus (actor 22), ademin 2 (beta 39kD) (EIF2B2), mRNA	Home explicits eukaryote d'ansiation interior les superiors (1906) de la constant de la constant de la constant de la constant de la constant de la constant de la constant de la constant de la constant de la constant de la constant de la constant de la constant de la constant de la constant de la constant de la constant de la constant de la constant de la constant de la constant de la constant de la constant de la constant de la constant de la constant de la constant de la constant de la constant de la constant de la constant de la constant de la constant de la constant de la constant de la constant de la constant de la constant de la constant de la constant de la constant de la constant de la constant de la constant de la constant de la constant de la constant de la constant de la constant de la constant de la constant de la constant de la constant de la constant de la constant de la constant de la constant de la constant de la constant de la constant de la constant de la constant de la constant de la constant de la constant de la constant de la constant de la constant de la constant de la constant de la constant de la constant de la constant de la constant de la constant de la constant de la constant de la constant de la constant de la constant de la constant de la constant de la constant de la constant de la constant de la constant de la constant de la constant de la constant de la constant de la constant de la constant de la constant de la constant de la constant de la constant de la constant de la constant de la constant de la constant de la constant de la constant de la constant de la constant de la constant de la constant de la constant de la constant de la constant de la constant de la constant de la constant de la constant de la constant de la constant de la constant de la constant de la constant de la constant de la constant de la constant de la constant de la constant de la constant de la constant de la constant de la constant de la constant de la constant de la constant de la constant de la constant	yd29d09.s1 Sogres tetal liver spiech innr.3 Hollio sapidis curin cicle innr.	Homo sapiens WEE1 gene for protein kinase and partial ZNF143 gene for zinc finger transcription factor	Homo sapiens pre-B-cell cdony-enhancing factor (PBEF) mRNA	ah63a06.s1 Soares_tests_NHT Homo saptens cDNA clone 13 10250 3	Human chondroitin sulfate proteoglycan varsican V0 splice-variant precursor peptide mRNA, complete cds		Human chondrottin sulfate proteoglycan versican V0 splice-variant precursor peptide mRNA, complete cds	Human gamma-aminobutyi o acid troncaminasa mRNA partial cds	Human gamma-annitobusynu acid daneamingoonii (FAB M1) Baylor-HGSC project=TCAA Homo	I CAAT IE 1232 Fediatile adule in joing in the second in the second in the second in the second in the second in the second in the second in the second in the second in the second in the second in the second in the second in the second in the second in the second in the second in the second in the second in the second in the second in the second in the second in the second in the second in the second in the second in the second in the second in the second in the second in the second in the second in the second in the second in the second in the second in the second in the second in the second in the second in the second in the second in the second in the second in the second in the second in the second in the second in the second in the second in the second in the second in the second in the second in the second in the second in the second in the second in the second in the second in the second in the second in the second in the second in the second in the second in the second in the second in the second in the second in the second in the second in the second in the second in the second in the second in the second in the second in the second in the second in the second in the second in the second in the second in the second in the second in the second in the second in the second in the second in the second in the second in the second in the second in the second in the second in the second in the second in the second in the second in the second in the second in the second in the second in the second in the second in the second in the second in the second in the second in the second in the second in the second in the second in the second in the second in the second in the second in the second in the second in the second in the second in the second in the second in the second in the second in the second in the second in the second in the second in the second in the second in the second in the second in the second in the second in the second in the second in the second in the second in the second in the second in t	Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22, segment 3/3	Homo saplens hypothetical protein FLJ20585 (FLJ20585), mRNA	TOR V data 2.C apha = T-cell receptor delta and C alpha fusion gene (alternatively spliced, splice junction)	[human, precursor B-cell line REH, mRNA Partial, 211 nt]	Homo sapiens hypothetical protein (FLJ1127), mRNA	Homo sapiens protein methyltransferase (JBP1) mRNA, complete cds	Homo sapiens protein methyltransferase (JBP1) mRNA, complete cds	
Top Hit Database Source				- 1	EST_HUMAN		EST_HUMAN	EST HUMAN		EST HUMAN	EST_HOMAN	¥	NT	EST HUMAN	Z	NT	EST_HUMAN	Z		¥	LN.	Į.	FST HUMAN	TN	TN		FZ FZ	BINT	N-	1N	
Top Hit Acession No.	TALCOSCOCO	6923009	<u>\$</u>		4.0E-72 AW836230.1		0E-72 A1248796.1	0E-72 AA465388,1		.0E-72 AA465388.1	.0E-72 H79421.1	7657057 NT	7657057 NT	F81910.1	4 OF. 72 4 1977546 2	5031976 NT	3.0E-72 AA723823.1	05.72 1146306 1		3.0E-72 U16306.1	3.0E-72 U80226.1	.0E-72 U80226.1	2 OF 72 BE242464 1	0.0C-12 DEZ-2101.1	TURESTON	100700	3.0E-72 S77589.1	11416196 NT	A F1675	3.0E-72 A E487572 1	AT 101 VI 6. 1
Most Similar (Top) Hit BLAST E	13.	4.0E-72	4.0E-72	4.0E-72	4.0E-72		4.0E-72			4.0E-72	4.0E-72	4.0E-72	4.0E-72	4.0E-72 T81910.1					_			ေ				3.05-72				1	- [
Expression Signal		0.87	0.57	0.54	0.54		1.04	1.57			6.28	2.19	2.19	1.67	\					6.32		3.98			-	27	25.		2 25		
ORF SEQ ID NO:	}		36953			L	87778	1		38299	L	L	38625		L	32003		<u> </u>	2/380	3 27399	L	L		1	1	4 29539	CBOOK	ł	1	31003	
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Probe SEQ ID		2987	10312	10604	10804		10634	1000	200	11563	11818	11938	11938	11976		12/78	3 000	226	1180	1180	1220	1220		1548	3143	3352		382/	4667	4883	4889

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			gene, exon 5	gene, exon 5				artial cds, neuronal apoptosis Inhibitory	mplete cds	לאניון לפון וויאון)		nox/late transporter), member 2 (SLC13A2),	34131461 5	:4131461 6'	1609 3' similar to gb:X02067 H.saplens	slocator mRNA complete cds	DNA clone IMAGE:1387395 3	41), mRNA	YH13), mRNA	YH13), mRNA		166	Same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same o	spo e	ecds		subfamily member 3) (MPP3) mRNA		GE:2501098 3' similar to TR:Q59050	eptide (PIK3C2A) mRNA
	Top Hit Descriptor	Homo sapiens semaphorin W (SEMAW) mRNA	Homo sapiens growth factor receptor-bound protein 10 (GRB10) gene, exon 5	Homo sapiens growth factor receptor-bound protein 10 (GRB10) gene, exon 5	Homo sapiens mRNA for KIAA1081 protein, partial cdc	Homo eapiens mRNA for KIAA1081 protein, partial cds	Homo sapiens ribosomal protein L3-like (RPL3L) mRNA	Homo sapiens basic transcription factor 2 p44 (btf2p44) gene, partial cds, neuronal apoptosis Inhibitory	Home services mission reasons with family 4 coming the complete cost	Homo sapiens \$100A12 dene for Caldran tin C. exon 2 and initiad ade	Homo sepiens gene for AF-6, complete cds	Homo sapiens solute carrier family 13 (sodium-dependent dicarboxylate transporter), member 2 (SLC13A2), mRNA mRNA	601890419F1 NIH MGC 17 Homo sapiens cDNA clone IMAGE:4131461 5	601890419F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4131461 5	e/28009.s1 Soares_tests_NHT Homo sapiens cDNA clone 1391609 3' similar to gb:X02067 H.sapiens mRNA for 7SL RNA pseudocene (HUMAN):	Rattus norvegicus putative phosphate/phosphoenolpyruyate translocator mRNA complete cds	ai83d02.s1 Soares parathyroid tumor NbHPA Homo sapiens cDNA clone IMAGE:1387395.3	Homo saplens vacuolar protein sorting 41 (yeast homolog) (VPS41), mRNA	Homo sapiens myosin, heavy polypeptide 13, skeletal muscle (MYH13), mRNA	Homo sapiens myosin, heavy polypeptide 13, skeletal muscle (MYH13), mRNA	AV751818 NPD Homo sapiens cDNA clone NPDAIE11 5	RC4-HT0578-170300-012-g02 HT0578 Homo saplens cDNA	RC4-HT0578-170300-012-g02 HT0578 Homo sapiens cDNA	Homo sapiens synaptic glycoprotein SC2 (SC2) mRNA, complete cds	Homo saplens synaptic glycoprotein SC2 (SC2) mRNA, complete cds	MR0-CT0063-071099-002-h11 CT0063 Homo sapiens cDNA	Homo sepiens membrane protein, palmitoviated 3 (MAGUK p55 subfamily member 3) (MPP3) mRNA	Homo sapiens ribosomal protein L13a (RPL13A), mRNA	ws55c08.x1 NCL_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2501098 3' similar to TR:Q59050 Q59050 HYPOTHETICAL PROTEIN MJ1656.;	Homo sapiens phosphatidylinositoi 3-kinase, class 2, alpha polypeptide (PIK3C2A) mRNA
	Top Hit Database Source		- L	Į.	LN			- ·					EST HUMAN 6	Г	EST HUMAN	Г	T HUMAN				Г	EST_HUMAN R	EST_HUMAN R			EST_HUMAN N			T_HUMAN	
216:110	Top Hit Acesslon No.	4759093 NT	3.0E-72 AF073367.1	3.0E-72 AF073367.1		Γ	4826987 NT		5031802		9.1	11426671 NT	2.0E-72 BF308560.1		2.0E-72 AA789277,1	Γ	1.0E-72 AA846225.1	7657676 NT	11321578 NT	11321578 NT	1.0E-72 AV751818.1 E	1.0E-72 BE175434.1 E	1.0E-72 BE175434.1 E		1.0E-72 AF222742.1	9.0E-73 AW374968.1 E	11525883 INT	11424099 NT	8.0E-73 AW071755.1 E	4505798 NT
	Most Similar (Top) Hit BLAST E Value	3.0E-72	3.0E-72	3.0E-72	3.0E-72	3.0E-72	3.0E-72	2 OF 22   180047 4	3.0E-72	3.0E-72 X98289.1	3.0E-72	2.0E-72	2.0E-72	2.0E-72	2.0E-72	2.0E-72	1.0E-72	1.0E-72	1.0E-72	1.0E-72	1.0E-72 A	1.0E-72 B	1.0E-72 B	1.0E-72	1.0E-72 A	9.0E-73 A	9.0E-73	9.0E-73	8.0E-73	8.0E-73
	Expression Signal	1.12	1.94	1.94	4.53	4.53	4.1	200	5.42	1.09	2.18	1.38	0.64	0.64	5.46	3.39	8.14	3.54	1.22	1.22	1.29	3.5	3.5	7.37	7.37	1.17	0.92	24.49	0.73	0.98
	ORF SEQ ID NO:		32613	32614	32822	32823	33286	34307	34973	37290	32018	32590	35923	35924	37691	31999	28394	32384	33237	33238	33319	34366	34367	36408	36409	27723	32687		27285	32184
	Exan SEQ ID NO:	18831	19281				19903	20817	21450	23680	25453	19261	22373	22373	24057	25515	15273	19075	19847	19847	25832	20870	20870	22830	22830	14641	19340	24262	14228	18892
	Probe SEO ID NO:	5637	6101	6101	6295	6295	6747	7758	8369	10646	12678	6029	9297	9297	10978	12772	2137	5887	6899	6899	6269	7815	7815	9790	9790	1488	6164	11183	1063	5698

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Single Exon Probes Expressed in Placenta

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Top Hit Descriptor	Homo sapiens lysozyme homolog (LOC57151) mRNA	Homo sapiens vacuolar ATPase Isoform VA68 mRNA, complete cds	bb62g06.y1 NIH_MGC_9 Home sapiens cDNA clone IMAGE:3030034 5' similar to gb:X04099_cds1 ACTIN	UTIOT LASMIC & (HUMAN); gp:://www.rasp.mouse.cy/cosketetal.gamma-actin mRNA, complete cds (MOUSE);	nomo sapiens interfeukin 12 receptor, beta 1 (L/12KB1), mKNA Homo sapiens interfeukin 12 receptor, beta 1 (II 1908), mDNA	H. sabiens mRNA for WNT-88 protein	Homo saplens transition protein 1 (during historie to profamine replacement) (TNP4) mRNA	Homo saplens brefeldin A-inhibited quanine nucleotide exchange profes 1 mRNA complete cds	Homo saplens DNA for Human P2XM, complete cds	Homo sepions thyroid autoentigen 70kD (Ku antigen) (G22P1), mRNA	Homo sapiens hypothetical protein FLJ20309 (FLJ20309), mRNA	Homo saplens chromosome 21 segment HS21C006	Homo saplens chromosome 21 segment HS21C082	Homo saplens chromosome 21 segment HS21C018	QV0-HT0494-020300-137-d03 HT0494 Homo sapiens cDNA	Homo sapiens HELG protein (FAM4A1), mRNA	Homo sapiens heme-binding protein (HEBP), mRNA	Homo saplens heme-binding protein (HEBP), mRNA	2055604.c1 Stratagene fetal retina 937202 Homo sapiens cDNA clone IMAGE.565950 3' similar to ob. 223064. edst HFTEROGENE OILS NIICE FAR RIBORITOR ECODOCTEM O CULLARAY.	AV729428 HTC Homo sapiens cDNA clone HTCAAF071 5'	AV729428 HTC Homo saplens cDNA clone HTCAAF071 5'	H.sapiens SH3GLP2 pseudogene, 5' end	RC8-HT0678-290600-013-H10 HT0678 Homo saplens cDNA	RC6-HT0678-290600-013-H10 HT0678 Homo sapiens cDNA	au11d02.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1625956.3	Homo saplens chromosome 21 segment HS21C046	RC3-NN0066-270400-011-c04 NN0066 Homo saplens cDNA	Homo saplens BASS1 (BASS1) mRNA, partial cds	RC3-NN0066-270400-011-c04 NN0066 Homo sapiens cDNA	Human beta globin region on chramosome 11	Homo sapiens caspase θ, apoptosis-related cysteine protease (CASP8) mRNA
Top Hit Database Source	N	NT	TO LO	FIGURES FIN	Z	LN	ŢN	TN	TN	Lz	N <sub>T</sub>	LN	L	N⊤	EST HUMAN	N	N-	N	EST HUMAN	7	EST HUMAN	LN.	EST HUMAN	EST_HUMAN	EST_HUMAN	ΝŢ	EST_HUMAN		EST_HUMAN		
Top Hit Acession No.	11426469 NT	8.0E-73 AF113129.1	8 0E.73 RE040000 4	44 EDENOTINE	11526037 NT	K91940.1	4507628 NT	8.0E-73 AF084520.1	8.0E-73 AB002059.1	11418189 NT	TN 0923290	.0E-73 AL163206.2	.0E-73 AL163282.2		6.0E-73 BE166574.1	11422159 NT	11435913 NT	11435913 NT	3.0E-73 AA136403.1						Γ						4502582 NT
Most Similar (Top) Hit BLAST E Value	8.0E-73	8.0E-73	8 0E.73	B OF 72	8.0E-73	8.0E-73 X91940.1	8.0E-73	8.0E-73	8.0E-73	8.0E-73	7.0E-73	7.0E-73	7.0E-73 /	6.0E-73	6.0E-73	4.0E-73	3.0E-73	3.0E-73	3.0E-73	3.0E-73	3.0E-73	3.0E-73	3.0E-73	3.0E-73	3.0E-73 A	3.0E-73 A	3.0E-73 A	2.0E-73	2.0E-73 µ	2.0E-73 U01317.1	2.0E-73
Expression Signal	6.29	2.1	4 35	1 76	1.76	0.51	0.47	1.49	12	4.55	1.61	0.7	1.29	3.04	3.42	2.05	1.34	1.34	0.73	0.73	0.73	1.45	1.41	1.41	1.82	3.04	2.05	1.57	29'6	1.49	2.03
ORF SEQ ID NO:		34890	36188		36571	36770	37490	38690	32044	31986	27376	29559			, 33867	31439	28165	28166	33398	35578	35579		37970	37971				27115			29440
Exon SEQ ID NO:		21369	22618	22980	22980				- 1	25560	14321	16545	18187			- 1		15054	19990	22037	22037	24010	24330	24330	24897	25730	25732	14050	15141	15502	16423
Probe SEQ ID NO:	6702	8287	9553	9941	9941	10134	10834	12001	12598	12842	1157	3373	5059	162	7323	2368	1911	1911	6837	8928	8928	10927	11261	11261	11910	13118	13122	874	2000	2371	3249

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				_	_	_	_	_	_	_		_	_	_	_	_	- 1	P	444	쓩	<del>- 1</del>	731.5	-	- 14		rated i	-	i e	14.10	4.5	413
Top Hit Descriptor	Homo sapiens Parkinson disease (autosomal recessive, juvenile) 2, parkin (PARK2), transcript varlant 3, mRNA	Homo sapiens Parkinson disease (autosomal recessive, juverlie) 2, parkin (PARK2), transcript variant 3, mRNA	Homo sapiens chromosome 21 segment HS21C083	Mus musculus morteo-interacting citron kinase (Crik) mRNA, complete cds	Mus musculus rho/rac-interacting cliron kinase (Crik) mRNA, complete cds	Homo sapiens mRNA for KIAA1591 protein, partial cds	Homo sapiens interleukin 4 receptor (IL4R), mRNA	Homo sapiens interleukin 4 receptor (IL4R), mRNA	Human peripheral myelin protein 22 mRNA, complete cds	Gallus gallus Dach2 protein (Dach2) mKNA, complete cds	Gallus gallus Dach2 protein (Dach2) mRNA, complete cds	Homo sapiens glutathione synthetase (GSS) mRNA	Homo sapiens supervilin (SVIL), transcript variant 1, mRNA	Homo saplens supervillin (SVIL), transcript variant 1, mRNA	Homo sapiens galactosylceramidase (Krabbe disease) (GALC), mRNA	Homo saplens galactosylceramidase (Krabbe disease) (GALC), mRNA	Homo saplens mRNA for KIAA1059 protein, partial cds	RC3-NN0066-270400-011-c04 NN0066 Homo sapiens cDNA	AU121585 MAMMA1 Homo sapiens cDNA clone MAMMA1000490 5	CM1-HT0282-111199-042-h10 HT0282 Homo sepiens cDNA	gg61b07.rf Soares_testb_NHT Homo sapiens cDNA done IMAGE:1839837 5 smilar to contains element . MER2z repetitive element ;	601276071F1 NIH_MGC_20 Homo saplens cDNA clone IMAGE:3617105 5	H.sapiens mRNA for TFIIA	H.saplens mRNA for TFIIA	Homo sapiens CD39-like 4 (CD39L4) mRNA	Ca2+/calmodulin-dependent protein kinase IV kinase Isoform [rats, brain, mRNA, 3429 nt]	Ca2+/calmodulin-dependent protein kinase IV kinase isoform [rats, brain, mRNA, 3429 nt]	Homo sapiens NKG2D gene, exon 10	Homo sapiens chromosome 21 segment HS21C046	601649284F1 NIH_MGC_73 Homo sapiens cDNA clone IMAGE:3932997 5	601191927F1 NIH_MGC_7 Homo sepiens cDNA clone IMAGE:3535855 5
Top Hit Database Source	IN	Ę	LN	L	NT	NT	NT	LN	Z	NT	IN	LN	NT	TN	. IN	NT	IN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST HUMAN	EST HUMAN	Z	F	Z	LN.	N	L	N L	EST_HUMAN	EST_HUMAN
Top Hit Acession No.	7669539 NT	7669539 NT	20E-73 AL163283.2		2.0E-73 AF086824.1	2.0E-73 AB046811.1	11431471 NT	11431471 NT	2.0E-73 M94048.1	2.0E-73 AF198349.1	2.0E-73 AF198349.1	4504168 NT	11496380 NT	11496980 NT	4557612 NT	4557612 NT	2.0E-73 AB028982.1	2.0E-73 AW 898081.1	1.0E-73 AU121585.1	1.0E-73 BE151283.1	1.0E-73 A1147427.1	1.0E-73 BE385477.1	9.0E-74 X77225.1		4557426 NT	8.0E-74 S83194.1	8.0E-74 S83194.1	7.0E-74 AJ001589.1	7.0E-74 AL163246.2	7.0E-74 BE967432.1	7.0E-74 BE266305.1
Most Similar (Top) Hit BLAST E Value	2.0E-73	20E-73	2.0E-73	2.0E-73	2.0E-73	2.0E-73	2.0E-73	2.0E-73	2.0E-73	2.0E-73	2.0E-73	2.0E-73	1	2.0E-73	]	2.0E-73	2.0E-73	2.0E-73	1.0E-73									_		L	Ш
Expression Signal	0.68	0.68	1.31			5.46	1.87	1.87	1.01	0.54	0.54					2.91	1.44	4.32	3.52		1.22										
ORF SEQ ID NO:	29816			33106						36370	36371					38018			28068										L	L	
Exan SEQ ID NO:	16804	16804	17693	19729	19729	19770	19992	19992	21033	22797	22797	23671	23748	23748	24374	24374	24402	15141	14973	19656	22748	L	L	L	L		L	,	1	1	1 .
Probe SEQ ID NO:	3640	3840	4555	6567	9567	98.10	6839	6839	7984	9732	9732	10637	10715	10715	11309	11309	11339	12599	1824	9490	0090	11736	12045	12045	750	8036	9039	2004	3407	944	12841

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Table 4
Single Exon Probes Expressed in Placenta

Chigo Lyon Capacita Capacita Capacita Capacita Capacita Capacita Capacita Capacita Capacita Capacita Capacita Capacita Capacita Capacita Capacita Capacita Capacita Capacita Capacita Capacita Capacita Capacita Capacita Capacita Capacita Capacita Capacita Capacita Capacita Capacita Capacita Capacita Capacita Capacita Capacita Capacita Capacita Capacita Capacita Capacita Capacita Capacita Capacita Capacita Capacita Capacita Capacita Capacita Capacita Capacita Capacita Capacita Capacita Capacita Capacita Capacita Capacita Capacita Capacita Capacita Capacita Capacita Capacita Capacita Capacita Capacita Capacita Capacita Capacita Capacita Capacita Capacita Capacita Capacita Capacita Capacita Capacita Capacita Capacita Capacita Capacita Capacita Capacita Capacita Capacita Capacita Capacita Capacita Capacita Capacita Capacita Capacita Capacita Capacita Capacita Capacita Capacita Capacita Capacita Capacita Capacita Capacita Capacita Capacita Capacita Capacita Capacita Capacita Capacita Capacita Capacita Capacita Capacita Capacita Capacita Capacita Capacita Capacita Capacita Capacita Capacita Capacita Capacita Capacita Capacita Capacita Capacita Capacita Capacita Capacita Capacita Capacita Capacita Capacita Capacita Capacita Capacita Capacita Capacita Capacita Capacita Capacita Capacita Capacita Capacita Capacita Capacita Capacita Capacita Capacita Capacita Capacita Capacita Capacita Capacita Capacita Capacita Capacita Capacita Capacita Capacita Capacita Capacita Capacita Capacita Capacita Capacita Capacita Capacita Capacita Capacita Capacita Capacita Capacita Capacita Capacita Capacita Capacita Capacita Capacita Capacita Capacita Capacita Capacita Capacita Capacita Capacita Capacita Capacita Capacita Capacita Capacita Capacita Capacita Capacita Capacita Capacita Capacita Capacita Capacita Capacita Capacita Capacita Capacita Capacita Capacita Capacita Capacita Capacita Capacita Capacita Capacita Capacita Capacita Capacita Capacita Capacita Capacita Capacita Capacita Capacita Capacita Capacita Capacita Capacita Capacita C	Top Hit Top Hit Descriptor No. Source	Homo saplens S164 gene, partial cds; PS1 and hypothetical protein genes, complete cds; and S171 gene, partial cds	EST HUMAN	EST HUMAN	EST HUMAN	EST_HUMAN	EST HUMAN	EST_HUMAN	EST HUMAN	213 NT	EST_HUMAN	EST_HUMAN	117 NT	N		X07866 NT	131471 NT	11431471 NT Homo seplens interieukin 4 receptor (IL4R), mRNA	7662263 NT Homo sapiens KIAA0716 gene product (KIAA0716), mRNA	45483 NT			5729766 NT Homo sapiens cell adhesion molecule with homology to L1CAM (close homologue of L1) (CHL1), mRNA	FZ	N-	Ļ	Homo saplens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, 1 complete octs)	06192 NT		LN.	
dol i llovi olgino	ession		EST	EST	Π	Г	Γ		Γ	13			417 NT	Γ		4507866 NT	11431471 NT	11431471 NT	7662263 NT	11345483 NT			5729766 NT					26192	4506192 NT		
	Most Similar (Top) Hit Top BLAST E Value	6.0E-74 AF109907.1	6.0E-74 AW263177.1	6.0E-74 BE3	6.0E-74 BE3	6.0E-74 AW014039.1	6.0E-74 AW	6.0E-74 BE0	6.0E-74 BE0						1	5.0E-74 46	5.0E-74				5.0E-74 Y09	5.0E-74 Y09	\$.0E-74	4.0E-74 D87675.1	4.0E-74 AB028942.1	4.0E-74 AB026898.1	4.0E-74 AB026898.1	4	4	4.0E-74 AB032994.1	
	Expression Signal	3.65	1.03	15,52	15.52	26.0	76.0	1.22	1.22	3.49		4.96	1.92				2.94	2.94		2.33	1.67	1.67	1.36	3.31	10.3	3.07	3.07		96.6	1.32	
	ORF SEQ ID NO:	27368	L	L					29969				31736	32413		$\perp$						37687	37801	26542	27116	28262	28263		L		
	Exon SEQ ID NO:	6 14311	14809	15521	1		1	5 16965			1		3 18720	0 19099	_		j	1				3 24053		13507	14051	15158	8 16168	1	4 15270	l`	
	Probe SEQ ID NO:	1146	1656	2390	2390	2927	292	380	380	548	928	2767	5623	5910		5961	88	9030	703	8224	10973	10973	11090	230	876	2018	2018	2134	213	2201	

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	Т	Т	Т	Т	Т	Т	Т	Т	Т	Т	Т	Т	Т	Т	Ŧ	Т	Т	Т	i i	١.,	-1	1	T''.	- 4	Ŧ	T,	7	74.	Ť	Ties	l ii	4.41 4.
Top Hit Descriptor	Hamo saplens chromosome 21 segment HS21C004	zp96a06.s1 Stratagene muscle 937209 Homo saziens cDNA clone IMAGE:628018 3'	7g50a08.x1 NCI_CGAP_Pr28 Homo sapiens cDNA clone IMAGE:3309878 3'	Homo sapiens Misshapen/NIK-related kinase (MINK), mRNA	QV4-ST0234-181199-037-105 ST0234 Homo sapiens cONA	Homo sapiens hypothetical protein FLJ11026 (FLJ11026), mRNA	Homo sapiens beta 2 gene	Homo saplens zinc finger protein 259 (ZNF259) mRNA	Homo sapiens mRNA for KIAA0833 protein, partial cds	Homo saplens chromosome 21 segment HS21C048	Homo sapiens DNA for Human P2XM, complete cds	Homo sapiens mannosidase, alpha, class 24, member 1 (MAN2A1), mRNA	260c01.r1 Soares_NHHMPu_S1 Homo sapiens cDNA clone IMAGE:687776 5	zr80c01.r1 Soares NhHMPu, S1 Homo saplens cDNA clone IMAGE:687776 5'	Homo saplens glutamate receptor, ionotropic, kainate 1 (GRIK1) mRNA	Homo saplens glutamate receptor, tonotropic, kainate 1 (GRIK1) mRNA	Homo sapiens chromosome 21 segment HS21C068	RC2-BT0642-270300-019-006 BT0642 Homo sapiens cDNA	hz/3h08.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3213663 3' similar to WP:B0511.12 CE17351 :	Human neurofibromin (NF1) gene, complete cals	Homo sapiens KIAA0852 protein (KIAA0852), mRNA	601070088F1 NIH_MGC_12 Homo sapiens cDNA clane IMAGE:3456260 5'	601070088F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3456260 5'	Homo sapiens tracheal eplithelium enriched protein (PLUNC) gene, complete cds	MR0-HT0559-230500-021-e03 HT0559 Homo sapiens cDNA	Homó saplens partial AK155 gene for AK155 protein, exons 1-3 and joined CDS	Homo sapiens partial AK155 gene for AK155 protein, exons 1-3 and joined CDS	Homo sapiens hypothetical protein FLJ10783 (FLJ10783), mRNA	Homo sapiens glutathione S-transferase theta 2 (GSTT2), mRNA	Homo sapiens glutathione S-transferase theta 2 (GSTT2), mRNA	Homo sapiens DNA for Human P2XM, complete cds	Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds
Top Hit Database Source	NT	EST HUMAN	EST HUMAN		EST_HUMAN		Į.	Ł	N.	E	ĮN.	Z,	EST HUMAN	EST HUMAN		L	N.	EST_HUMAN	Г	Т		EST HUMAN	EST_HUMAN		T_HUMAN	Г	¥				LN L	NT
Top Hit Acession No.	2.0E-74 AL163204.2	2.0E-74 AA196181.1	2.0E-74 BF002855.1	7657334 NT	1.0E-74 AW816405.1	8922829 NT		4508020 NT	1.0E-74 AB020640.1	1.0E-74 AL163246.2		4758697 NT	1.0E-74 AA258549.1	1.0E-74 AA258549.1	4116	4504116 NT	1.0E-74 AL163268.2	1.0E-74 BE083080.1	1.0E-74 BE467769.1		11417977 NT	1.0E-74 BE549105.1			1.0E-74 BF351951.1	1.0E-74 AJ251550.1	1.0E-74 AJ251550.1	11420549 NT	11417856 NT	11417856 NT	1.0E-74 AB002059.1	1.0E-74 AF240786.1
Most Similar (Top) Hit BLAST E Value	2.0E-74	2.0E-74	2.0E-74	1.0E-74	1.0E-74	1.0E-74	1.0E-74 X02344.1	1.0E-74	1.0E-74	1.0E-74 /	1.0E-74	1.0E-74	1.0E-74 /	1.0E-74 /	1.0E-74	1.0E-74	1.0E-74 /	1.0E-74	1.0E-74	1.0E-74 M89914.1	1.0E-74	1.0E-74 E	1.0E-74	1.0E-74 /	1.0E-74	1.0E-74 /	1.0E-74	1.0E-74	1.0E-74	1.0E-74	1.0E-74/	1.0E-74 A
Expression Signal	5.27	2.87	1.16	1.5	3.71	1.8	2.59	1.28	0.86	2.26	6.03	2.82	1.29	1.29	0.84	0.84	5.41	0.85	0.87	1.29	1.05	1.27	1.27	7.81	0.67	0.65	0.65	1.77	1.94	4.97	1.61	1.38
ORF SEQ ID NO:	36294			26308	26586	26734	26739	26823	27036	27253	28566	29394	29646	29647	30197	30198	30237	30316	30508	33404	34353	34844	34845	35627	35656	37086	37087	37337	38826		28586	
Exan SEQ ID NO:	L		H	13293	13558	13706	13712	13803	13984	14195	15433	16383	16627	16627	17187	17187	17231	17326	17525	19997	20860	l		- 1	22113	23480	23480	23732	25124	25182	15433	25610
Probe SEQ ID NO:	9582	12526	13169	54	347	512	519	614	804	1024	2301	3209	3460	3460	4031	4031	4075	4175	4382	6844	7804	8246	8246	9005	9034	10445	10445	10699	12154	12238	12386	12925

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	F		A				
Probe SEQ ID NO:	SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
2709			5.1	8.0E-75	8.0E-75 AF176228.1	LN	Homo saplens DNA cytosine-6 methylitensferase 3B (DNMT3B) mRNA, complete cds
12552	25375		3.07	8.0E-75		TN	Homo sapiens chromosome 21 segment HS21C002
2395	15526	28654	1.25	6.0E-75	6.0E-75 AI817415.1	EST HIMAN	wk38a08.x1 NCI_CGAP_Pr22 Homo sapiens cDNA done IMAGE:2417654.3' similar to gb:M14123_cds4 RFTROVIRI IS.REI ATED POI DOI YOROTTEIN /HIMANN
11780	L	38466	1.39	6.0E-75	6.0E-75 BE791831.1	EST HUMAN	601586109F1 NIH MGC 7 Home sapiens cDNA clone IMAGE:3840130 5
9109		35731	1.09	5.0E-75	BE272325.1	EST HUMAN	601126068F1 NIH_MGC_9 Homo sepiens cDNA clone IMAGE:2989865 5
9317		35944	0.77	5.0E-75	5.0E-75 AA132611.1	EST HUMAN	zo17e08.r1 Stratagene colon (#937204) Homo sapiens cDNA clone IMAGE:587174 S
9395		36034	0.47	5.0E-75		EST HUMAN	601346909F1 NIH_MGC_8 Homo saplens cDNA clone IMAGE:3687458 5'
9395		36035	0.47	5.0E-75	Γ	EST HUMAN	601346909F1 NIH_MGC_8 Homo sapiens cDNA done IMAGE:3687458 5'
9573	22715	36283	1.1	5.0E-75	5.0E-75 BF890254.1	EST_HUMAN	602186616T1 NIH_MGC_49 Homo sapiens cDNA clone IMAGE:4298738 3'
10439	23474	37078	2.64	5.0E-75		EST HUMAN	#31c12x1 NCI_CGAP_GC9 Homo sapiens cDNA clone IMAGE:2242390 3' similar to TR:P97361 P97361 HYPOTHETICAL 20.1 KD PROTEIN:
115	13346	26373	2.1	4.0E-75		EST HUMAN	QV1-BT0632-210200-079-e02 BT0632 Homo saplens cDNA
. 471	13666		1.68	4.0E-75	0E-75 N36757.1	EST HUMAN	yx90h08.r1 Soares melanocyte 2NbHM Homo sapiens cDNA clone IMAGE 269055.57
1805	14954	28048	1.08	4.0E-75	0E-75 AW 897230.1	EST HUMAN	CM0-NN0057-150400-335-a11 NN0057 Homo sapiens cDNA
2910		29101	5.64	4.0E-75	.0E-75 BE409464.1	EST_HUMAN	601303866F1 NIH_MGC_21 Homo saplens cDNA clone IMAGE:3638344 5
5646		32120	0.68	4.0E-75	11417946 NT	N-	Homo sapiens NIPSNAP, C. elegans, homdog 1 (NIPSNAP1), mRNA
5646	_ [	32121	0.68	4.0E-75	11417946 NT	LN L	Homo sapiens NIPSNAP, C. elegans, homolog 1 (NIPSNAP1), mRNA
838	[	32929	5.18	4.0E-75	5579457 NT	F	Homo saplens eukaryotic translation initiation factor 3, subunit 8 (110kD) (EIF3S8), mRNA
6898		33458	1.4	4.0E-75	11417946 NT	FZ	Homo saplens NIPSNAP, C. elegans, homolog 1 (NIPSNAP1), mRNA
8689	- [	33459	1.4	4.0E-75	11417946 NT	TN.	Homo sapiens NIPSNAP, C. elegans, homolog 1 (NIPSNAP1), mRNA
10924	- {	37642	10.52	4.0E-76	69505	NT	Homo sapiens mycsin, heavy polypeptide 1, skeletal muscle, adult (MYH1), mRNA
1027	ı	27256	3.6	3.0E-75		NT	Homo sapiens HTRA serine protease (PRSS11) gene, complete cds
1028	f	27256	3.59	3.0E-75		IN	Homo sapiens HTRA serine protease (PRSS11) gene, complete cds
1883		28134	2.23	3.0E-75	3.0E-75 AB011153.1	LN	Homo saplens mRNA for KIAA0531 protein, partial cds
2180		28444	1.44	3.0E-75	4507334 NT		Homo sapiens synaptojanin 1 (SYNJ1), mRNA
2494	1	28740	4.39	, 3.0E-75	4759153 NT	 	Homo saplens synaptosomal-associated protein, 28kD (SNAP29) mRNA
3086	_ [	29279	96.0	3.0E-75		IN	Hamo sapiens chromosome 21 segment HS21C001
3258	_[	29449	1.09	3.0E-75	3.1	LN	Homo sapiens mRNA for KIAA0581 protein, partial cds
3431		29616	0.93	3.0E-75			Human calclum-dependent phospholipid-binding protein (PLA2) mRNA, complete ods
3431	[	29617	0.93	3.0E-75		LN	Human calcium-dependent phospholipid-binding protein (PLA2) mRNA, complete cds
883	_[	29995	9.0	3.0E-75			Human calclum-dependent phospholipid-binding protein (PLA2) mRNA, complete cds
4283	$\perp$	30418	2.92	3.0E-75	D87675.1		Homo saplens DNA for amylold precursor protein, complete cds
5365	18568	31434	1.15	3.0E-75	11420956 NT		Homo sapiens adaptor-related protein complex 1, sigma 2 subunit (AP1S2), mRNA

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פונולום בעמו בו מספי בילה מספי ויין ויין ויין ויין ויין ויין ויין וי	Top Hit Descriptor	Homo saniens adaptor-related protein complex 1, sigma 2 subunit (AP1S2), mRNA	Association of the series of the series of the series of the series of the series of the series of the series of the series of the series of the series of the series of the series of the series of the series of the series of the series of the series of the series of the series of the series of the series of the series of the series of the series of the series of the series of the series of the series of the series of the series of the series of the series of the series of the series of the series of the series of the series of the series of the series of the series of the series of the series of the series of the series of the series of the series of the series of the series of the series of the series of the series of the series of the series of the series of the series of the series of the series of the series of the 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Top Hit Descriptor	Human ferritin Heavy subunit mRNA, complete cds	Homo canients H factor 1 (complement) (HF1) mRNA	Tronic agricus II factor ( complement) (HF1) mRNA	HOMO SQUEIS IN IBOURT (COUR) COURS OF THE COURS OF THE COURS OF THE COURS OF THE COURS OF THE COURS OF THE COURS OF THE COURS OF THE COURS OF THE COURS OF THE COURS OF THE COURS OF THE COURS OF THE COURS OF THE COURS OF THE COURS OF THE COURS OF THE COURS OF THE COURS OF THE COURS OF THE COURS OF THE COURS OF THE COURS OF THE COURS OF THE COURS OF THE COURS OF THE COURS OF THE COURS OF THE COURS OF THE COURS OF THE COURS OF THE COURS OF THE COURS OF THE COURS OF THE COURS OF THE COURS OF THE COURS OF THE COURS OF THE COURS OF THE COURS OF THE COURS OF THE COURS OF THE COURS OF THE COURS OF THE COURS OF THE COURS OF THE COURS OF THE COURS OF THE COURS OF THE COURS OF THE COURS OF THE COURS OF THE COURS OF THE COURS OF THE COURS OF THE COURS OF THE COURS OF THE COURS OF THE COURS OF THE COURS OF THE COURS OF THE COURS OF THE 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Top Hit Database Source	Į.			ĻN.	LN	NT	NT	LN	LN	뉟	Ż	Ł	Ŀ	Į.	1	2	N.	-N	EST HUMAN	EST HOMAN	Z.	Z	IN.	TOWAR TOWAR	ESI HUMAN	ESI HUMAN	EST HUMAN	EST HOMAN	EST HUMAN	LN 9	LN 9	EST HUMAN	EST HUMAN	EST HOMAN
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Most Similar (Top) Hit BLAST E Value		21	8.0E-76	8.0E-76	8.0E-76	8.0E-76	8.0E-76	8.0E-76	8.0E-76	8.0E-76 M13792.1	8.0E-78	8.0E-76	1	7.0E-76	2	7.0E-78	7.0E-76				5.0E-76		۳.	4	4	4				``				
Expression Signal		5.44	1.18	1.18	96.0	5.84	1.17	1.05	0.69	1.28	4.29	2.51		1.69			5.52		,									2.01	2.01	8.04				1.82
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Page 378 of 550 Table 4 Single Exon Probes Expressed in Placenta	
Page T T Single Exon Probe	

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	Top Hit Descriptor  Top Hit Descriptor  Top Hit Descriptor  Top Hit Descriptor  Top Anno Sapiens CDNA clone IMAGE:592524 5' similar to	26/360/11 STANDER RINASE 1 (HUMAN); gbt.1280/8 MIXED LINEAGE KINASE 1 (HUMAN); marans XI Somes thymus NHFTh Homo septems odna marans XI Somes thymus NHFTh Homo septems odna	Homo saplens anglostatin binding protein 1 mRNN, Company clone IMAGE:271842 5'	Jy20g10.r1 Soares melandove 21 cm. Sapiens oDNA done IMAGE:2773009 3	xe4gh01.x1 NCI_CCAT_ Null Homo sapiens cDNA clone IMAGE:75/461 5	ZV54011.11 Scares, Testis_NHT Homo sapiens cDNA clone IMAGE. CO.		- 1	1	Human mRNA for possible protein in the constitution of the constitution of the constitution of the constitution of the constitution of the constitution of the constitution of the constitution of the constitution of the constitution of the constitution of the constitution of the constitution of the constitution of the constitution of the constitution of the constitution of the constitution of the constitution of the constitution of the constitution of the constitution of the constitution of the constitution of the constitution of the constitution of the constitution of the constitution of the constitution of the constitution of the constitution of the constitution of the constitution of the constitution of the constitution of the constitution of the constitution of the constitution of the constitution of the constitution of the constitution of the constitution of the constitution of the constitution of the constitution of the constitution of the constitution of the constitution of the constitution of the constitution of the constitution of the constitution of the constitution of the constitution of the constitution of the constitution of the constitution of the constitution of the constitution of the constitution of the constitution of the constitution of the constitution of the constitution of the constitution of the constitution of the constitution of the constitution of the constitution of the constitution of the constitution of the constitution of the constitution of the constitution of the constitution of the constitution of the constitution of the constitution of the constitution of the constitution of the constitution of the constitution of the constitution of the constitution of the constitution of the constitution of the constitution of the constitution of the constitution of the constitution of the constitution of the constitution of the constitution of the constitution of the constitution of the constitution of the constitution of the constitution of the constitution of the constitution of the constit	Human mRNA for poscible protein   PRO!!, Company 1 (IGBP1) mRNA	Homo saptens intriungalcous (CD/SA) princing in Homo saptens intriungalcous (CD/SA)	Hamo sapiens glucagon (GCG) mKNA hinding protein 1 (CREB1) mRNA	Homo sapiens cAMP responsive element binding processing in RNA	Home sapiens GM2 ganglioside activatur process (AM2A) mRNA	Homo sapiens GM2 gangilloside activator protein (GM2A) IIII	T	Т	T		T	$\neg$		П	7	1		Gorilla gonilla University of Klad 1081 protein, partial cds	Homo sapiens minary in the product (KIAA0783), mRNA	Homo sapletto titro and PRKA and or protein 10 (AKAP10), micro	Homo sapleiro A miser		
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+	<u>m</u> + m	3 0E-76 AA	3.0E-76 AW027705.1	3.0E-76 AF286598.1	3.0E-76 N426/1.1	3.0E-70	3.0E-76A	3.0E-76	3.0E-76 A	2.0E-76	2.0E-76 D84295.1	20E-76	2.0E-78	2.0E-76	2 0F-76	2 OF-76	2 0F-76	2 OE-76	20E-76		2.0E-76	2.0E-7		1				1		. }		9 2.05-75	l
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Page 379 of 550 Table 4 Single Exon Probes Expressed in Pla

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Single Exon Probes Expressed in Placenta	Top Hit Descriptor		Homo sapiens TPCR86 protein (HSTPCR86P), mRNA	Homo saplens similar to ribosomal protein \$26 (H. sapiens) (I. OCE2450)	Homo sapiens HIRA interacting protein 4 (dnsJ-ijke) (HIRIPA) mRNA	Human mRNA for HMG-1, complete cdc	Human mRNA for HMG-1, complete cds	601589896F1 NIH_MGC_7 Homo sapiens cDNA clone IMA CE 3944262 El	EST37301 Embryo, 8 week I Homo sapiens cDNA 5 and	601512435F1 NIH_MGC_71 Homo saplens cDNA clone IMAGE 3042737 El	60/302333F1 NIH_MGC_21 Homo saplens cDNA done IMACE.3661753 5' yp11h02.r1 Soares breast 3NbH8st Homo senlene cDNA	SP.ANKB HUMAN 001484 ANKYRIN, BRAIN VARIANT 1	60/1866926F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE;4109803 5: Homo eaplens professions (homo magnetics)	mRNA mRNA homolog) (PSMD1), Indicionality, Indicionality, Indicionality, Indicionality, Indicionality, Indicionality, Indicionality, Indicionality, Indicionality, Indicionality, Indicionality, Indicionality, Indicionality, Indicionality, Indicionality, Indicionality, Indicionality, Indicionality, Indicionality, Indicionality, Indicionality, Indicionality, Indicionality, Indicionality, Indicionality, Indicionality, Indicionality, Indicionality, Indicionality, Indicionality, Indicionality, Indicionality, Indicionality, Indicionality, Indicionality, Indicionality, Indicionality, Indicionality, Indicionality, Indicionality, Indicionality, Indicionality, Indicionality, Indicionality, Indicionality, Indicionality, Indicionality, Indicionality, Indicionality, Indicionality, Indicionality, Indicionality, Indicionality, Indicionality, Indicionality, Indicionality, Indicionality, Indicionality, Indicionality, Indicionality, Indicionality, Indicionality, Indicionality, Indicionality, Indicionality, Indicionality, Indicionality, Indicionality, Indicionality, Indicionality, Indicionality, Indicionality, Indicionality, Indicionality, Indicionality, Indicionality, Indicionality, Indicionality, Indicionality, Indicionality, Indicionality, Indicionality, Indicionality, Indicionality, Indicionality, Indicionality, Indicionality, Indicionality, Indicionality, Indicionality, Indicionality, Indicionality, Indicionality, Indicionality, Indicionality, Indicionality, Indicionality, Indicionality, Indicionality, Indicionality, Indicionality, Indicionality, Indicionality, Indicionality, Indicionality, Indicionality, Indicionality, Indicionality, Indicionality, Indicionality, Indicionality, Indicionality, Indicionality, Indicionality, Indicionality, Indicionality, Indicionality, Indicionality, Indicionality, Indicionality, Indicionality, Indicionality, Indicionality, Indicionality, Indicionality, Indicionality, Indicionality, Indicionality, Indicionality, Indicionality, Indicionality, Indicionality, Indicionality, Indicionality, Indicion	2662902.r1 Soares retina N2b4HR Homo saniens cDNA Accession	Ze6Ze02.r1 Soares retina NZP4HR Homo sanlens CDNA All HAR SE	969904.81 Soares fetal liver spiesen INFLS Homo sapiens cDNA clane IMAGE 423047 2011	MERTO repetitive element;	Abril 2018 Scares Tests NHT Homo sepiens cDNA clone IMAGE:745392 3'	Home services (MMA) II (DNA directed) polypeptide E (25kD) (POLR2E) mRNA	Homo septients parymetrase (RNA) II (DNA directed) polypeptide E (25kD) (POLR2E) mRNA	FSTREEPS MACE	CONTROL I September MAGE Homo sapiens CDNA	7 Homo sabiens attrackhase 700Km.	Homo saplens disinfecting and matellanders.	Homo sapiens tousied-like kinase 1 (71 K4) mRNA	Homo sapiens cullin 1 (CUL1) mRNA	Homo sapiens ubiquitin specific protesse 18 (1 SP1a) BNA	Homo saplans EGF-like repeats and discordin Ulike domana 3 (75). 2	Homo sapiens EGF-like repeats and discoidin Like domains 3 (EDIL3), mRNA	DKFZp434G1728_11 434 (smonvm: https://doi.org/10.1016/10.1016/10.1016/10.1016/10.1016/10.1016/10.1016/10.1016/10.1016/10.1016/10.1016/10.1016/10.1016/10.1016/10.1016/10.1016/10.1016/10.1016/10.1016/10.1016/10.1016/10.1016/10.1016/10.1016/10.1016/10.1016/10.1016/10.1016/10.1016/10.1016/10.1016/10.1016/10.1016/10.1016/10.1016/10.1016/10.1016/10.1016/10.1016/10.1016/10.1016/10.1016/10.1016/10.1016/10.1016/10.1016/10.1016/10.1016/10.1016/10.1016/10.1016/10.1016/10.1016/10.1016/10.1016/10.1016/10.1016/10.1016/10.1016/10.1016/10.1016/10.1016/10.1016/10.1016/10.1016/10.1016/10.1016/10.1016/10.1016/10.1016/10.1016/10.1016/10.1016/10.1016/10.1016/10.1016/10.1016/10.1016/10.1016/10.1016/10.1016/10.1016/10.1016/10.1016/10.1016/10.1016/10.1016/10.1016/10.1016/10.1016/10.1016/10.1016/10.1016/10.1016/10.1016/10.1016/10.1016/10.1016/10.1016/10.1016/10.1016/10.1016/10.1016/10.1016/10.1016/10.1016/10.1016/10.1016/10.1016/10.1016/10.1016/10.1016/10.1016/10.1016/10.1016/10.1016/10.1016/10.1016/10.1016/10.1016/10.1016/10.1016/10.1016/10.1016/10.1016/10.1016/10.1016/10.1016/10.1016/10.1016/10.1016/10.1016/10.1016/10.1016/10.1016/10.1016/10.1016/10.1016/10.1016/10.1016/10.1016/10.1016/10.1016/10.1016/10.1016/10.1016/10.1016/10.1016/10.1016/10.1016/10.1016/10.1016/10.1016/10.1016/10.1016/10.1016/10.1016/10.1016/10.1016/10.1016/10.1016/10.1016/10.1016/10.1016/10.1016/10.1016/10.1016/10.1016/10.1016/10.1016/10.1016/10.1016/10.1016/10.1016/10.1016/10.1016/10.1016/10.1016/10.1016/10.1016/10.1016/10.1016/10.1016/10.1016/10.1016/10.1016/10.1016/10.1016/10.1016/10.1016/10.1016/10.1016/10.1016/10.1016/10.1016/10.1016/10.1016/10.1016/10.1016/10.1016/10.1016/10.1016/10.1016/10.1016/10.1016/10.1016/10.1016/10.1016/10.1016/10.1016/10.1016/10.1016/10.1016/10.1016/10.1016/10.1016/10.1016/10.1016/10.1016/10.1016/10.1016/10.1016/10.1016/10.1016/10.1016/10.1016/10.1016/10.1016/10.1016/10.1016/10.1016/10.1016/10.1016/10.1016/10.1016/10.1016/10.1016/10.1016/10.1016/10.1016/10.1016/10.1016/10.1016/10.1016/10.1016/10.1016/10.1016/10.1016/10.1016/10.1016/	Homo sapiens protein kinase Chefaul has Zepticon as each als CDNA done DKFZp434G1728 5:	H.sapiens mRNA for ubiquitin hydrotese	
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	Top Hit Descriptor	H, sapiens mRNA for ubfquitin hydrolase	Homo sapiens 3-hydroxy/sobutyryl-Coenzyme A hydrolase (HIBCH), mKNA	Hamo sapiens 3-hydroxylsobutyryl-Coenzyme A hydrolase (HIBCH), mRNA	Homo sapiens sorting nexin 6 (SNX5), mRNA	Homo saplens scriting nexin 5 (SNX5), mRNA	Human mRNA for KIAA0299 gene, partial cds	Human mRNA for KIAA0299 gene, partial cds	Homo sapiens SET domain and mariner transposase tustori gene (SET MARY) misus	Homo sapiens SET domain and mariner transposase rusion gene (SET whith) Illinum	yu64g01.r1 Welzmann Olfactory Epithellum Homo saplans CUNA corte invoce	yu64g01.r1 Weizmann Oifactory Epithelium Homo sapiens cDNA done iMAGE:239905 o sumiar to SP:S17447 S17447 PROBABLE LIGAND-BINDING PROTEIN RY2G5 - ;	PM3-MT0078-080800-005-g03 MT0078 Homo sapiens cDNA	AV764617 MDS Hamo sapiens cDNA cone MDSB I F10 3	RC3-BN0053-170200-011-h01 BN0053 Home sapiens culvin	Homo sepiens CYP17 gane, 5' end	Homo sapiens CGI-79 protein (LOC31634), mRNA	Homo sapiens mRNA for KIAA1415 protein, partial cus	Homo sapiens mKNA for KIAA1415 protein, parties dus	ho43b05.x1 Soares_NFL_T_GBC_S1 flomo saplens dDNA cighe INACE.3040113 5 similar is switched to the same is switched by SW:GAG2_HUMAN P10294 RETROVIRUS-RELATED GAG POLYPROTEIN:	IW22g02.x1 NCI_CGAP_Brn52 Homo sapiens cDNA done IMAGE:2280466 3' similar to 1 K:C05246 [065245 F21E10.7 PROTEIN ;	w22g02x1 NCI CGAP Bm52 Homo sapiens cDNA clone IMAGE:2260466 3' similar to TR:065245	065245 F21E10.7 PROTEIN.;	ns68g12.s1 NCI_CGAP_Pr2 Homo sapiens cDNA clone IMACE:1188838 similar to SW:RL29_HUMAN p47914 60S RIBOSOMAL PROTEIN L29. [1] ;contains element MSR1 repetitive element ;	EN1110852E1 NIH MCC 17 Homo saniens cDNA clone IMAGE:3029436 5.	001 I SSOZET NIN LEW CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE	0014700251111 Line DB2 Lines capiene cDNA rieme IMAGE:2377720 3 similar to TR:013311	61/4803.11 Dersted Cudi III Livo I I I I I I I I I I I I I I I I I I I
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	Expression Signal	0.72	121	121	2.61	2.61	0.97	76.0	1.30	1.30	80	6.0	2.83	1.74	9.74	1.1	275		1.69	1.98			0.67			2.08		15.02
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Most Similar (Top) Hit BLAST E Value	2.0E-77 AI362707.1	2.0E-77 U	2.0E-77	2.0E-77 B	2.0E-77 B	1.0E-77	1.0E-77	1.0E-77	1.0E-77	1.0E-77	1.0E-77	1.0E-77	1.0E-77	1.0E-77	1.0E-77	1.0E-77	1.0E-77	1.0E-77 /	1.0E-77 /	1.0E-77	1.0E-77	1.0E-77	1.0E-77	1.0E-77	1.0E-77	1.0E-77	1.0E-77		
Expression Signal	0.86	5.68	5.68	0.47	0.47	2.62	2.62	1.68	1.68	3.4	3.4	1.30	1.17	2.28		,					1.72	1.1	15.97	0.82					
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Probe         Exon           SEQ ID         SEQ ID           NO:         NO:           10773         23806           6576         16738           8677         19738           8676         16738           87         1323           3389         1655           6690         19848           224         13472           1669         1675           3472         16639           5693         18887           7304         20369           9284         22361           1547         14699           1544         17582           4442         17582           4896         18026           4896         18026           4896         18026           6703         19476           6703         20727           9568         22710           10660         23694           10660         23694           10660         23694
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	Τ	I	Γ	Γ	Γ	Τ	Г	Γ	Γ	Τ	Γ	Γ	Γ	Г	Γ	Τ	Γ	Γ	13-	Tü,	Γ	1	扎	11 4	201, 21:	- Fills	il	7		4	1
Top Hit Descriptor	Human transforming growth factor-beta precursor gene exons 4-5 (and joined mature peptide)	Ното sapiens gene for AF-6, complete cds	Homo sapiens eRF1 gane, complete cds	Homo sapiens eRF1 gene, complete cds	Homo saplens SH3 and PX domain-containing protein SH3PX1 (SH3PX1), mRNA	AU140604 PLACE3 Homo sapiens cDNA clone PLACE3000373 5	Homo sapiens synaptojanin 1 (SYNJ1), mRNA	Homo sapiens synaptojantn 1 (SYNJ1), mRNA	CM0-HT0180-041099-065-c07 HT0180 Homo sapiens cDNA	QV0-HT0367-150200-114-g09 HT0367 Homo sapiens cDNA	Homo sapiens type IV collagen alpha 5 chain (COL4A5) gene, exon 20	EST182583 Jurkat T-cells VI Homo sapiens cDNA 5 end	UI-HF-BK0-aaj-g-10-0-UI:-1 NIH_MGC_36 Homo capiens cDNA clone IMAGE:3054139 6'	UI-HF-BK0-aaj-g-10-0-UI.r1 NIH_MGC_36 Homo sapiens cDNA clone IMAGE:3054139 5/	602186529F1 NIH_MGC_49 Homo sapiens cDNA clone IMAGE:4298599 5'	AV714177 DCB Homo sapiens cDNA clone DCBAWF09 5'	Pt2.1_16_B07.r tumor2 Homo sapiens cDNA 3'	Pt2.1_16_B07.r tumor2 Homo saplens oDNA 3'	qisoho5x1 NCL_CGAP_Brn25 Homo sepiens cDNA clone IMAGE:1859961 3' similar to WP:R90,1 CE06325 PROTEIN KINASE;	HTM1-025F1 HTM1 Homo sapiens cDNA	za48f12.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:295823 3'	Hamo sapiens GAP-like protein (LOC51306), mRNA	AV648699 GLC Homo sapiens cDNA clone GLCBMCO13'	Human serine/threonine kinase MNB (mnb) mRNA, complete cds	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA	Homo sapiens similar to lymphocyte activation-associated protein (H. saplens) (LOC63140), mRNA	Homo sapiens peptide YY (PYY), mRNA	RC2-BN0074-090300-014-612 BN0074 Homo sapiens cDNA	Homo sapiens mRNA for activator of S phase Kinase, complete cds	Homo sapiens ubiquitin-conjugating enzyme E2E 3 (homologous to yeast UBC4/5) (UBE2E3) mRNA	Homo sapiens hypothetical protein FLJ11294 (FLJ11294), mRNA
Top Hit Database Source	NT	IN	LZ LZ	N FA	LN FN	EST_HUMAN	LN	F	EST_HUMAN	EST_HUMAN	Г	EST_HUMAN	EST_HUMAN .	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST HUMAN	EST_HUMAN	EST_HUMAN	Į	EST_HUMAN	IN				EST_HUMAN	TN		
Top Hit Acession No.	.0E-78 X05844.1	1.0E-78 AB011399.1	3.0E-78 AF095901.1	3.0E-78 AF095901.1	7706705 NT	:0E-78 AU140604.1	4507334 NT	4507334 NT	3.0E-78 BE144758.1		.0E-78 U04489.1	.0E-78 AA311872.1	.0E-78 AW 402306.1	.0E-78 AW 402306.1	.0E-78 BF689800.1	.0E-78 AV714177.1	.0E-78 AI557509.1	.0E-78 AI657509.1	2.0E-78 AI197837.1	2.0E-78 BE439409.1	.0E-78 N66951.1	11417304 NT	.0E-78 AV648699.1		11430460 NT	11435903 NT	11525891 NT	9.0E-79 BE000837.1	.0E-79 AB028070.1	6454145 NT	11430822 NT
Most Similar (Top) Hit BLAST E Value	4.0E-78	4.0E-78	3.0E-78	3.0E-78	3.0E-78	3.0E-78	3.0E-78	3.0E-78	3.0E-78	3.0E-78	2.0E-78	2.0E-78	2.0E-78	2.0E-78	2.0E-78	2.0E-78	2.0E-78	2.0E-78	2.0E-78	2.0E-78	2.0E-78	1.0E-78	1.0E-78	1.0E-78 U52373.1	1.0E-78	1.0E-78	9.0E-79	9.0E-79	9.0E-79	9.0E-79	9.0E-79
Expression Signal	6.72	3.93	1.69	1.69	1.01	0.81	0.78	0.82	5,44	2.5	2.49	1.99	1.09	1.09	3.36	2.49	1.72	1.72	9.58	1.47	3.01	3.16	0.82	1.81	1.83	2.44	4.04	1.6	16.98	2.52	0.98
ORF SEQ ID NO:	L		26417				30074	30074		37937			34177	34178			35262	35263	38048		38108	31597	31514		32107	32086	30938	31093	31781	32996	
SEQ ID NO:	24842	25568	L	13390	15615		17077	17077	23528	H			[.	20700			21726	21726	24389	1	-24447	18621	18521	21434	25234	25299	17953	18115	18746	19637	[ [
Probe SEQ ID NO:	11854	12855	.165	165	2488	3860	3918	4221	10493	11227	3191	4122	7631	7631	7908	8230	8646	8646	11336	11358	11386	5420	7094	8353	12324	12422	4820	4986	5549	6470	6752

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Top Hit Descriptor	Homo sapiens hypothetical protein FLJ20345 (FLJ20345), mRNA	Homo sapiens cAMP response element-blinding protein CRE-BPa (H GS165L15.1), mRNA	Homo saplens cAMP response element-binding protein CRE-BPa (H_GS165L15.1), mRNA	Homo sapiens threonyl-tRNA synthetase (TARS), mRNA	Homo sapiens threonyl-tRNA synthetase (TARS), mRNA	Homo sapiens casein kinase II alpha subunit mRNA, complete cds	Homo sapiens cesein kinase II alpha subunit mRNA, complete cds	Homo saplens DNA for amyloid precursor protein, complete ods	Homo sapiens hypothetical protein FLJ20535 (FLJ20535), mRNA	Homo sapiens zinc finger protein 216 splice variant 1 (ZNF216) mRNA, complete cds	Homo sapiens zlnc finger protein 216 splice variant 1 (ZNF216) mRNA, complete cds	Homo saplens TRAF6-regulated IKK activator 1 beta Uev1A mRNA, complete cds	Homo saplens suppressor of white apricot homolog 2 (SWAP2), mRNA	Homo sapiens suppressor of white apricot homolog 2 (SWAP2), mRNA	Homo sapiens gamma-glutamytransferase 1 (GGT1), mRNA	Hamo sapiens chromosome 21 segment HS21C010	601472766T1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3875657 3'	Homo saplens chromosome 21 segment HS21C046	294604.st Soares, fetal liver_spleen_1NFLS_St Home sapiens cDNA done IMAGE:462568 3' similar to TR:Q15408 Q15408 NEUTRAL PROTEASE LARGE SUBUNIT;	Homo sapiens chromosome 21 segment HS21C082	Homo sapiens intersectin short isoform (ITSN) mRNA, complete cds	Homo sapiens cell-line tsA201a chloride ion current inducer protein I(Cin) gene, complete cds	Human zinc finger protein ZNF131 mRNA, partial cds	Homo sapiens MSTP016 (MST016) mRNA, complete cds	Homo sapiens mRNA for KIAA0892 protein, partial cds	601482143F1 NIH_MGC_68 Homo saplens cDNA clone IMAGE:3884554 5	601482143F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3884564 5'	Homo sapiens netrin 1 (NTN1), mRNA	Homo saplens netrin 1 (NTN1), mRNA	601112055F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3352885 5'	Homo sapiens mRNA for KIAA0620 protein, partial cds	Homo sapiens mRNA for KIAA0620 protein, partial cds	Homo saplens guanine nucleotide exchange factor for Rap1 (KIAA0277), mRNA
Top Hit Detabase Source	F	F	Į.	NT	LN	TN	LN	LN LN	N.	N T	LΝ	Ę	Ę	N	TN	ĽN LN	EST HUMAN	N	EST_HUMAN	LN	FZ	LΝ	IN	FZ	۲	EST HUMAN	EST_HUMAN	LΝ	FZ	EST_HUMAN	LN.	LN	TN
Top Hit Acession No.	11424427 NT	11421735 NT	11421735 NT	11417250 NT	11417260 NT	E-79 J02853.1	JE-79 J02853.1	E-79 D87675.1	11438643 NT	IE-79 AF062346.1	IE-79 AF062346.1	E-79 AY008273.1	11423827 NT	11423827 NT	11417877 NT	DE-79 AL163210.2	E-79 BE619648.1	E-79 AL163246.2	DE-79 AA699829.1		Г	3.0E-79 AF232708.1				E-79 BE789470.1	E-79 BE789470.1	11426770 NT	11426770 NT	0E-79 BE256893.1	IE-79 AB014520.1	JE-79 AB014520.1	6912455 NT
Most Similar (Top) Hit BLAST E Value	9.0E-79	9.0E-79	9.0E-79	9.0E-79	9.0E-79	9.0E-79	9.0E-79	9.0E-79	9.0E-79	9.0E-79	9.0E-79	9.0E-79	9.0E-79	9.0E-79	9.0E-79	8.0E-79	7.0E-79	6.0E-79	6.0E-79	5.0E-79	3.0E-79	3.0E-79	3.0E-79	3.0E-79	3.0E-79	3.0E-79	3.0E-79	3.0E-79	3.0E-79	3.0E-79		3.0E-79	3.0E-79
Expression Signal	0.99	0.63	0.63	29.0	0.52	4.78	4.78	99.0	0.82	1.05	1.05	1.61	2.94	2.94	4.1	1.18		0.62	5.44	3.63	1.74	1.22	1.74	7.05	1.69	0.93	0.93	3.87			- 2.58		0.87
ORF SEQ ID NO:		34298	34299	35158	35/59	35890	35891			37274		38029		38490	31967		29516				26569		ı		32337								34574
Exan SEQ ID NO:	25846	20808	20808	21622	21622	.22340	22340	22722	23609	23666	23666	24385	24792	24792	25711	16996	16498	21923	25132	24776	13537	14172	16343	1	19031		19056			20036	H		21062
Probe SEQ ID NO:	7505	7748	7748	8541	8541	9263	9263	9580	10574	10632	10632	11322	11802	11802	13088	3836	3325	8844	12169	11786	323	1001	3168	5477	5841	5866	5866	5889	5889	6884	7206	7206	8012

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	Top Hit Description	Homo serians Bcl-2-associated transcription factor short form mRNA, complete cds	Homo sepiens tetratricopertide repeat domain 3 (TTC3), mRNA	AVROB115 GKC Homo saplens cDNA clone GKCAHE11 5	vyasing 31 Sogres fetal liver spleen 1NFLS Homo saplens cDNA clone IMAGE:208341 3	601159415F2 NIH_MGC_53 Homo saplens cDNA clone IMAGE:3511107 5	Homo sapiens BCL2-like 2 (BCL2L2) mRNA	Homo sapiens Gardner-Rasheed feline sarcoma viral (v-fgr) oncogene homolog (r GR) mixivo	Homo sapiens Gardner-Rasheed feline sarcoma viral (v-fgr) oncogene homolog (r-Gr) minum	th18h07.x1 NCI_CGAP_Pr28 Homo saplens cDNA clone IMAGE:2118655	Homo sapiens phosphodiesterase 6A, cGMP-specific, rod, alpha (PDE6A), mixing hosphodiesterase 6A, cGMP-specific, rod, alpha (PDE6A), mixing hosphodiesterase 6A, cGMP-specific, rod, alpha (PDE6A), mixing hosphodiesterase 6A, cGMP-specific, rod, alpha (PDE6A), mixing hosphodiesterase 6A, cGMP-specific, rod, alpha (PDE6A), mixing hosphodiesterase 6A, cGMP-specific, rod, alpha (PDE6A), mixing hosphodiesterase 6A, cGMP-specific, rod, alpha (PDE6A), mixing hosphodiesterase 6A, cGMP-specific, rod, alpha (PDE6A), mixing hosphodiesterase 6A, cGMP-specific, rod, alpha (PDE6A), mixing hosphodiesterase 6A, cGMP-specific, rod, alpha (PDE6A), mixing hosphodiesterase 6A, cGMP-specific, rod, alpha (PDE6A), mixing hosphodiesterase 6A, cGMP-specific, rod, alpha (PDE6A), mixing hosphodiesterase 6A, cGMP-specific, rod, alpha (PDE6A), mixing hosphodiesterase 6A, cGMP-specific, rod, alpha (PDE6A), mixing hosphodiesterase 6A, cGMP-specific, rod, alpha (PDE6A), mixing hosphodiesterase 6A, cGMP-specific, rod, alpha (PDE6A), mixing hosphodiesterase 6A, cGMP-specific, rod, alpha (PDE6A), mixing hosphodiesterase 6A, cGMP-specific, rod, alpha (PDE6A), mixing hosphodiesterase 6A, cGMP-specific, rod, alpha (PDE6A), mixing hosphodiesterase 6A, cGMP-specific, rod, alpha (PDE6A), mixing hosphodiesterase 6A, cGMP-specific, rod, alpha (PDE6A), mixing hosphodiesterase 6A, cGMP-specific, rod, alpha (PDE6A), mixing hosphodiesterase 6A, cGMP-specific, rod, alpha (PDE6A), mixing hosphodiesterase 6A, cGMP-specific, rod, alpha (PDE6A), mixing hosphodiesterase 6A, cGMP-specific, rod, alpha (PDE6A), mixing hosphodiesterase 6A, cGMP-specific, rod, alpha (PDE6A), mixing hosphodiesterase 6A, cGMP-specific, rod, alpha (PDE6A), mixing hosphodiesterase 6A, cGMP-specific, rod, alpha (PDE6A), mixing hosphodiesterase 6A, cGMP-specific, rod, alpha (PDE6A), mixing hosphodiesterase 6A, cGMP-specific, rod, alpha (PDE6A), mixing hosphodiesterase 6A, cGMP-specific, rod, alpha (PDE6A), mixing hosphodiesterase 6A, cGMP-specific, rod, alpha (PDE6A), mixing hosphodiesterase	Homo sapiens phosphodiesterase 6A, cGMP-specific, rod, alpha (PDEOA), ill. 100	Homo sapiens mRNA for Fas-associated factor, FAF1 (Faf1 gene)	Home seniers hepatocellular carcinoma-associated antigen 88 (HCA88) mRNA, complete cus	Homo sapiens mRNA for KIAA0937 protein, partial cds	Lumo saniens chloride chennel CLC4 (ClC4) mRNA, complete cds	Home samens mRNA for Fas-associated factor, FAF1 (Faf1 gene)	Homo saplens chromosome 21 segment HS21C006	Technology Inket T-cells VI Homo saptens cDNA 6 end similar to similar to C. elegans hypometical protein,	posmid B0303.15	Homo sepiens X transporter protein a (A.1.), illustration	Homo saplens mRNA for KIAA0830 protein, perida cus	ment of the complete cds	Home seplens membrane-associated deficient interpretation of (ARHGAP6), transcript variant 4, mRNA	Homo canians Rho GTPase activating protein 6 (ARHGAP6), transcript variant 4, mRNA	trains separate retine attended (1907) (RBL1) mRNA	mRNA			Homo sapiens hypothetical protein Fuzzar ( Caraman Amerikan motivin mump) membrane soctor	Homo sepiens similar to ATP ase, H+ transporting, lysosomal (vacuoral procession)	11				
	Top Hit Database Source			MANAGE	Т	EST HIMAN	101		= =	TOT LIMAN	_4	1		Z	ž	z!	Į.	Z	Z	EST_HUMAN	LZ	Ė		LN.	Z	INT	NT NT	NT NT	NT	IN		4 NT	Z	N	EST_HUMAN	
3	Top Hit Acession	T	7	8	T	T	7	4/5/841	4685234 NT	\$	8	00000	3	1	T	T		2.0E-79 AJ271408.1	2.0E-79 AL163206.2	2 OF-79 AA312223.1	11181769 NT	201-70 AB030637 1	I DOZDOJ.	2.0E-79 AF263613.1	7382479 NT	7382479 NT	4506442 NT	11427428 NT	8923248 NT	R023248 NT		11432184 NT	2.0E-79 S72869.1	2.0E-79 S72869.1	2.0E-79 BE064386.1	
-	jg '''	value	3.0E-79 AF	3.0E-79 10835	3.0E-79 AV	2.0E-79 He	2.0E-79 BE	2.0E-79	2.0E-79	2.0⊏-79	2.0E-79 AI523/4/.1	2.0E-/8	2.0E-79	2.0E-79 A	2.0E-79 A	2.0E-79 A	2.0E-79 A	2.0E-79 A	2.0E-79 A	2.05-79	205.70	205-79	Z0E-19/	2.0E-79	2.0E-79	2.0E-79	2.0E-79	2.0E-79	1	L						
	Expression ( Signal E		0.78	0.59	0.62	1.4	1.05	1.14	4.97	4.97	2.15	6.17	6.17	1.35	1:1	1.2	0.69	1.25	0.83	40	2	S. C.	1.19	0.69	_	2.09				30.0		69.0				
	ORF SEQ ID NO:		34961	36230	-		26864	27186	27239	27240		28478	١			L	L				1	32340		34.540		l	Ì.				4 35588	35823		1	20020	١
	SEO ID	<u>.</u>	21439	22658	23590	13515	13837	14124	14178	14178	14226	15349	١.	15399	L	L	L	l	1	1	- 1		19542		┸	1	2600	- 1	.1		55 22044	22283	1	1	23332	- 1
	00	j Z	8358	3	10555	208	651	951	1007	1007	1060	2215	2215	2268	23.87	2780	402	4280	4813		5788	5844	873		3 2	2 3		8282	87.	8965	8965	8	2000	2	2	1128

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	·					R:Q26623 Q26623		R:Q26623 Q26623						ber 8 (SLC7A8),		nber 8 (SLC7A8),	mRNA, partial cds				J		to SW:NUEM_HUMAN	π. - 1	NA SNA					
	Top Hit Descriptor	RC4-BT0310-110300-015-f10 BT0310 Homo sapiens cDNA	Homo sapiens KIAA0879 prolein (KIAA0879), mRNA	Homo sepiens mRNA for KIAA0833 protein, pertial cds	Homo saplens oadherin EGF LAG seven-pass G-type receptor 1 (CELSTV), III.	MR0-4NN0087-260600-017-b10 NN0087 Homo sapiens CLINA GE-2281286 3' similar to TR: Q26623 Q26623	1637e08.x1 NCI_CGAP_Ut2 Homo sapiens culva cione livia ci-	TEKTIN C1.; ty37e08.X1 NCI_CGAP_U12 Homo septiens cDNA clone IMAGE:2281286 3' similar to TR:Q26623 Q26623	TEKTIN C1.: 601311517F1 NIH_MGC_44 Homo saplens oDNA clone IMAGE:3632909 5	QV2-HT0540-120900-358-a05 HT0540 Homo sapiens CD14A	ar7Ba04 X1 Barstead colon HPLRB7 Homo sapiens culva cigine ilva cin.	er23e05.s1 Scares testis NHT Homo seplens cDNA clone 1343646 3	lai23e05.s1 Soares testis NHT Homo sapiens cDNA clone 1343046 3	601581652F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3930001 3	Homo sapiens solute carrier family 7 (cationic amino acid transporter, yt system,	mRNA Homo saplens solute carrier family 7 (cationic amino acid transporter, y+ system), member 8 (SLC7A8),	mRNA meandonare	Homo sapiens Y chromosome spermatogenesis candidate brown (Now,) posesses Homo sapiens KIAA0724 gene product (KIAA0724), mRNA	Homo sapiens KIAA0724 gene product (KIAA0724), mKIVA	Homo sapiens triple functional domain (PTPRF Interacting) (TRIO), malva	Homo saplens triple functional domain (PTPRF interacting) (TRIO), Illumin	Callithrix jacchus diactory receptor (CJA80) gene, partial cas	INAGE:2103459 3' similar to SW:NUEM_HUMAN		Homo sapiens NKD Collidates IIII (S. cerevisiae) 3 (MCM3), mRNA	Homo sapiers minoring maintenance deficient (S. cerevisiae) 3 (MCM3), mRNA	Homo sapiens minicinomoscino manage 2 NAD (mitochondrial) (MDH2), mRNA	Homo saplens malate derrydroger lase 2, 1, 1, 2 (minute)	Homo sapiens mknA to gynein neary stem.	
	Top Hit Detabase Source	Т	NOMOL	FZ.		EST HUMAN		EST_HUMAN	EST HUMAN	EST HIMAN	NAAN TOTAL	TO LOUGH	TO LONG	NAME TO FOLL	EST	TN 4	TN 4	F	100	N N	1212	2 2		EST_HUMAN	N.	6631094 NT	6631094 NT	11421462 NT	۲	
Single	Top Hit Acession No.		79 BE064386.1	TN 1052001	79 ABUZU640.1	79 1141632	130307 1.	79 AI613480.1	-79 AI613480.1	79 BE394211.1	-79 BF08/405.1	1.0E-79 AI460115.1	9.0E-80 AA725848.1	9.0E-80 AA725848.1	-80 BE798603.1	11433924 NT	11433924 NT	8.0E-80 U94387.1				NI LZGCOCO	7.0E-80 AF12/802.1	A1422197.1	6.0E-80 U64898.1	6631	9631	11421	A 14044	
	ğ III	Value	2.0E-79 BE	2.0E-79	2.0E-79 A	20E-79	1.05-79.0	1.0E-79 A	1.0E-79 A	1.0E-79	1.0E-79 E	1.0E-79 /	9.0E-80 /	9.0E-80 /	9.0E-80	9.0E-80	9.0E-80	8.0E-80	8.0E-80				1		1	L	L	L	ع اد	
	Expression (Signal		2.94	. 4.27	2.3	3.08	3.28	0.65	0.65	0.9	1.9	1.44	6.95	6.95	1.3	7.63	7.63	1.01	2.82	2.82	22	2.2	0.61	0.77					1.40	
	ORF SEQ E)		37988	31534	32100	32067		33394	33395	35049	١			29400		38288	Ì		34328				31497			1	1	1		75 327.20
		Ö Z	24350	1	١.	L	<u> </u>	19986	19986	21520	L	丄	L	ł	L	1	1	1	L	┸	22857	١.	١.			_1		1	1	6200 19375
	Probe SEQ ID	ö Z	11284	12208	12298	12531	6718	6833	6833	8439	1,1000	42228	202	32.13	10217	11554	11554	369.	1780	2017		9602	7114		5	<b>#</b>	×	×	ซั	œ G

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	Top Hit Descriptor	Homo sapiens tubby like protein 3 (TULP3), mRNA	Homo sapiens KIAA0941 protein (KIAA0941), mRNA	Homo saziens dystrophin (DMD) mRNA, complete cds	Liberton Convoluin, controlled recentor 51 (GPR51), mRNA	Trust Saprato Cardein Animaled receptor 51 (GPR51) mRNA	Torro septens of procent country and the septens of the septens of the septens of the septens of the septens of the septens of the septens of the septens of the septens of the septens of the septens of the septens of the septens of the septens of the septens of the septens of the septens of the septens of the septens of the septens of the septens of the septens of the septens of the septens of the septens of the septens of the septens of the septens of the septens of the septens of the septens of the septens of the septens of the septens of the septens of the septens of the septens of the septens of the septens of the septens of the septens of the septens of the septens of the septens of the septens of the septens 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Page 388 of 550 Table 4 Single Exon Probes Expressed in Placenta

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mRNA	Homo saplans gene for AF-6, complete cds	
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	Most Similar (Top) Hit To BLAST E		2.0E-80 R3	2.0E-80 AI	2.0E-80 AL043116.2	2.0E-80 A	2.0E-80	2.0E-80 T	2.0E-80 A	2.0E-80 A	2.0E-80 A		1.0E-80 A		1.0E-80 A	1.0E-80 A	1.0E-80.1	1.0E-80 E	1.0E-80 L	1.0E-80	1.0E-80												
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Page 389 of 550 Table 4 Single Exon Probes Expressed in Placenta

Top Hit Descriptor	PAIL - HAADE AGE 91	qh30g05.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE: 1804.595 3	qh90g06.x1 Soares_NFL_T_GBC_S1 home sapiens culve done invested to	601310531F1 NIH MGC 44 Homo capiens curva cione Invace: 3022/10 5	zez1d10.r1 Soares_fetal_hear_ubHH19W Homo sepiens cDNA clone IMAGE:359635 5 simitar to SW:KRHA_RABIT Q02957 KERATIN, GLYCINE/TYROSINE-RICH OF HAIR. 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Most Similar (Top) Hit BLAST E	Value	8.0E-81	8.0E-81	8.0E-81		7.0E-81	7.0E-81	6.0E-81	6.0E-81	6.0E-81	6.0E-81	6.0E-81	6.0E-81	6.0E-81	5.0E-81	5.0E-81	5.0E-81	5.0E-81	5.0E-81	5.0E-81	70 40 7	4.0E-01	4	4		4							`
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Homo sapiens pleiotrophin (heparin binding growth factor 8, neurite growth-promoting factor 1) (PTN) mRNA Homo sapiens pleiotrophin (heparin binding growth factor 8, neurite growth-promoting factor 1) (PTN) mRNA z185408.r1 Scares\_NhHMPu\_S1 Homo sapiens cDNA clone IMAGE:682475 5' similar to SW;PRI2\_HUMAN P49643 DNA PRIMASE 58 KD SUBUNIT : hg85c01.xi NCI\_CGAP\_Kid11 Homo sepiens cDN4 clone IMAGE:2952384 3'
zk45h09.t1 Scares\_pregnant\_uterus\_NbHPU Homo sapiens cDNA clone IMAGE:495825 5' similar to
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Page 391 of 550 Table 4 Single Exon Probes Expressed in Placenta

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	Top Hit Descriptor	Homo sapiens arm-repeat protein NPRAP/neurojungin (CTNND2) mRNA, partial ods	enganates All MCC 83 Home saplens CDNA clone IMAGE:4274535 5	00213/004F1NIT NO. CO. LIGHT SEPTEMBER OF ANY (exons 1 29 and 2h) CAV1 (exons 1 8n	Hamo saplens cavedin-1/-2 locus, Contg1, D/SOZZ, genes CAVZ (exclus 1, ze, and ze), COV (care and ze)	2) Lambers and merses (DNA directed), gamma (POLG), mRNA	Homo aghieris poyiliea asc (Lora a general) as	Homo sapiens GLI3 gene for GLI3 protein	601645051F1 NIH_MGC_56 Homo sapiens clink done IMMAGE 3930226 3	601645051F1 NIH MGC 56 Home sapiens conv done invoce 3505220 5	601343180F1 NIH MGC 35 nome september of the control of the last of the last of the last of the last of the last of the last of the last of the last of the last of the last of the last of the last of the last of the last of the last of the last of the last of the last of the last of the last of the last of the last of the last of the last of the last of the last of the last of the last of the last of the last of the last of the last of the last of the last of the last of the last of the last of the last of the last of the last of the last of the last of the 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ממון ומאיין	Top Hit Database Source	FX	100	EST_HUMAN	. !		Į.	NT	EST_HUMAN	EST_HUMAN	EST_HUMAN		EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST HUMAN	N	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST HUMAN	EST HUMAN	2 !	Z.	Į.	Ł	Į.	NT	N		N.	LNE	IN 2
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	Most Similar (Top) Hit BLAST E Value	10.0	1.05-20.1	1.0E-81 B			1.0E-81	1.0E-81 A	1.0E-81 B	1.0E-81 B	1.0E-81 B		1.0E-81	1.0E-81 B	1.0E-81 B	1.0E-81	1.0E-81	1 OF-81	1.0E-81	1.0E-81	1.0E-81	1.0E-81 /	1.0E-81	1.0E-81	1.0E-81	8.0E-82	8.0E-82	8.0E-82 U08988.1	8.0E-82 U08988.1	8.0E-82	8			1	8.0E-82
	Expression Signal		3.18	1.81		1.09	7.94	0.61	68.0,	0.89	5.13		0.81	3.72	3.72	141	0.49	1 97	1.56	1.56	2.93	2.93	2.46	1.89	3.6	1.59	1.35	1.58		49.					0.83
	ORF SEQ ID NO:		32265	32797		33439	34509	34535	38610	36611	36804		36948)	36950	36951	37367	37510	32070	38064	38062	38068					26251	26251		27070					30339	_
	Exan SEQ ID NO:		18983	19448		2002	20999	24022	23017	23017	23211		23343	23.45	23345	L	1.	2000	00777	24409	ı	1	1_	l.		13251	_	L	L	1_		L	14842	L	١
	Probe EQ ID NO:		5771	6274		222	7949	707	4700 8700	878	10174		10308	10370	2 6	20704	107/01	1000	111102	11347	11352	11352	11550	11812	12417	13	109	274	837	910	1520	1	1690	4198	4358

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Single Exon Probes Expressed in Placenta	Top Hit Descriptor	601458531F1 NIH_MGC_66 Homo sapiens cDNA clane IMAGE:3862086 5'	AU144050 HEMBA1 Homo sepiens cDNA clone HEMBA1000752 3'	Homo sepiens alpha-tubulin isoform 1 mRNA, complete cds	QV2-HT0540-120900-362-f08 HT0540 Homo sapiens cDNA	QV2-HT0540-120900-362-t08 HT0540 Homo sapiens cDNA	Human von Willebrand factor gene, exon 9	wp75e09.x1 NCI_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2487624 3' similar to TR:O73276 O75276 PKD1;	Homo sapiens presentiin-1 gene, exons 1 and 2	Homo sapiens amyloid beta (A4) precursor protein (protease nextn-II, Alzheimer disease) (APP). mRNA	RC2-BN0120-010400-013-f02 BN0120 Homo saplens cDNA	Homo sapions transforming growth factor beta-activated kinase-binding protein 1 (TAB1), mRNA	Homo sapiens amyloid beta (A4) precursor protein (protease nedn-li, Abzheimer disease) (APP), mRNA	al23e05.s1 Soares_testis_NHT Homo sepiens cDNA clone 1343648 3'	RC8-PT0001-190100-021-B02 PT0001 Homo sapiens cDNA	Homo sapiens chromosome 21 segment HS21C085	RC1-BN0005-260700-018-g04 BN0005 Homo saplens cDNA	Homo sapiens adenyate cyclase activating polypeptide 1 (cituitary) receptor type ( ADCYAP1R1) mRNA	Homo sapiens neurotrophic tyrosine kinase, receptor, type 2 (NTRK2) mRNA	Homo sapiens ankyrin-like with transmembrane domains 1 (ANKTM1), mRNA	Homo sapiens contactin 6 (CNTN6), mRNA	Homo sapiens contactin 6 (CNTN6), mRNA	Homo sapiens mRNA for KIAA1077 protein, partial cds	Homo sapiens mRNA for KIAA1077 protein, partial cds	Homo saplens mRNA for KIAA0999 protein, partial cds	Homo sapiens mRNA for KIAA0999 protein, partial cds	DKFZp434M117_r1 434 (oynonym: htes3) Homo sapiens oDNA clone DKFZp434M117 5'	Homo sapiens DNA for amyold precursor protein, complete cds	Human integral membrane serine protease Seprase mRNA, complete cds	Homo sapiens glutamate receptor, ionotropic, kainate 1 (GRIK1) mRNA	Homo sapiens mRNA for KIAA1096 protein, partial cds
Exon Propes	Top Hit Database Source	EST_HUMAN 6	EST_HUMAN A	T	EST_HUMAN C	HUMAN	Г	EST HUMAN O	T		T HUMAN			EST_HUMAN a	EST_HUMAN R	Г	EST_HUMAN R							N F		Г	r_HUMAN	H TN			H
Sirigie	Top Hit Acesslon No.	7.0E-82 BF035327.1	7.0E-82 AU144050.1	4.0E-82 AF081484.1	4.0E-82 BF351691.1	,	4.0E-82 M25833.1	4.0E-82 A1937300.1		4502166 NT		3.0E-82 5174702 NT	4502166 NT	3.0E-82 AA725848.1	3.0E-82 AW875073.1	3.0E-82 AL163285.2	3.0E-82 BE813232.1	4501922 NT	5453811 NT	11425206 NT	11432889 NT	11432889 NT			2.0E-82 AB023216.1		1.		2.0E-82 U76833.1	4116	2.0E-82 AB029019.1
	Most Similar (Top) Hit BLAST E Value	7.0E-82	7.0E-82	4.0E-82	4.0E-82	4.0E-82	4.0E-82	4.0E-82	4.0E-82	3.0E-82	3.0E-82	3.0E-82	3.0E-82	3.0E-82 /	3.0E-82	3.0E-82]/	3.0E-82	3.0E-82	3.0E-82	3.0E-82	3.0E-82	3.0E-82	3.0E-82/	3.0E-82	2.0E-82	2.0E-82/	2.0E-82	2.0E-82	2.0E-82	2.0E-82	2.0E-82
	Expression Signal	1.18	1.62	22.54	0.87	0.87	1.1	4.71	3.78	15.3	2.5	8.44	5.31	15.73	1.22	69.9	2.14	1.11	2.42	2.66	0.89	0.89	4.01	4.01	2.49	2.49	2.23	0.93	0.68	0.0	1.52
	ORF SEQ ID NO:		28049	27944	31874		32374	38702		26540	26944	27043	27134		27617	27729	28194	28318	-	34952		35372		36666	26818			30104	30279		30803
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	Probe SEQ ID NO:	1481	2825	1705	5613	5613	5876	12016	12683	288	721	810	893	1086	1386	1494	1950	2062	3345	8346	8753	8753	10029	10029	610	610	1720	3949	4131	4348	4680

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
				200	T	L.	Homo sapiens mRNA for KIAA1096 protein, partial cds
4680	17815	30804	1.62	Z.UE-82	-02 AB028019.1		Homo septens weser1 (WBSCR1) and wescr5 (WBSCR5) genes, complete cds, alternatively spliced and
4002	18121	31100	2.86	2.0E	-82 AF045556.1	LN	replication factor C subunit 2 (RFC2) gene, complete cds
5191			1.56	2.0E		LZ	Homo saprens union morroes factor recentor superfemily, member 5 (TNFRSF5) mRNA
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7858	<u></u>	S.	1.19	2.0E	A)47642	EST HUMAIN	uniz 1993 XI Con Con Con Con Con Con Con Con Con Con
7988	L	34550				Z	Homo sapiens slit (Drosophila) homolog 3 (SLIT3), mRNA
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18	L	35483	3 0.58		7657340 N	z!	nound september referrings-K LTR U5 and gag gene
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12230	<u>ا</u> ا	1	2,81		2 N94950.1	EST HUMAN	And a Source fetal liver spleen (NFLS S1 Homo sapiens cDNA clone IMAGE:429568 5
12818	8 25545	5	3.72		AA0112	ESI HUMAN	Home sanisms melanoma differentiation associated protein-5 (MDA5), mRNA
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1315	L.				1.0E-82 AB011110.2	Z !	Lione serviors mRNA for KIAA1417 protein, partial cds
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7004	┸	37698		1.0	E-82 AL163209.2	μ	Homo sapiens critoring of segment HS010046
11258	上	L		1.0	E-82 AL163246.2	LN.	Homo sapiens chromosodine 21 segment (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3
1	1		101	Œ	0E-83 AF224669.1	Þ	(UBE2D3) genes, complete cds
2	1	24 3 33		6	PE-83 BF672220.1	EST HUMAN	602150403F1 NIH MGC 81 Homo sapiens clurk cigne IMACE 2357724 F
8912					IS BE253347.1	EST HUMAN	601117160F1 NIH_MGC_16 Homo sapiens clund digner invace: 3507134
1948	┙	1	0.12		0 OF 92 BE283073 1	FST HUMAN	601273346F1 NIH_MGC_20 Homo sapiens CDNA clone IMAGE.3014302 5
4	1446 14599	99 2/6/0					

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Page 396 of 550 Table 4 Single Exon Probes Expressed in Placenta

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Top Hit Descriptor	Homo sablens regulatory factor X 3 (influences HI A class II expression) (DEYs) DNA	Homo sapiens mRNA for KIAA1131 protein, partial cds	Homo sapiens mRNA for KIAA1131 protein, partial cds	Homo saplens mRNA for KIAA1314 protein, partial cds	wa76c04.x1 Scares_NFL_T_GBC_S1 Home sapiens cDNA clone IMAGE:2302086 3' similar to SW:NRDC_HUMAN 043847 NARDII VSIN PREFI IRSOID	Homo sapiens polymerase (DNA-directed), alpha (70kD) (POLA2), mRNA	Homo saplens mycsin light chain kinase isoform 2 (MLCK) mRNA, complete cds	Homo sapiens multidiug resistance protein (MRP), excn 13	Homo sapiens protein brosine phosphatase, recenting the G (PTPRG) mRNA	Homo sapiens protein trosine phosphatase, mentor than G (PTPRG), mRNA	Homo saplens histone deacet/dase 3 (HDAC3) gene, complete cds	Homo septens KIAA0783 gene product (KIAA0783), mRNA	Homo sapiens discs, large (Drosophila) homolog 2 (chapsyn-110) (Dr. G.2) mRNA	Homo sapiens discs, large (Drosophila) homolog 2 (chapsyn-110) (Dl G2) mRNA	Homo sapiens mRNA for KIAA1130 protein partial cds	Homo sapiens Bach1 protein homolog mRNA, partial cals	Homo sapiens chondroitin sulfate proteoglycan 2 (versican) (CSPC2) mRNA	Homo sapiens pericentridar material 1 (PCM1) mRNA	Novel human mRNA containing Zinc finger C2H2 type domains	Homo saplens X-linked juvenile retinoschisis precursor protein (XLRS1) mRNA, complete odo	wu20405.x1 Scares_Dieckgreefe_colon_NHCD Homo sapiens cDNA clone IMAGE:2520585 3' similar to gb:L05083 60S RIBOSOMAL PROTEIN L18A (HUMAN):	CM1-BT0785-190600-272-b08 BT0795 Homo sapiens cDNA	CM1-BT0795-190800-272-b08 BT0795 Homo sapiens cDNA	Homo sapiens myelin transcription factor 1-like (MYT14) mRNA, connoiste cds	H. sapiens DNA for endogenous retroviral like element	UI-H-BI4-ad-ta-02-0-UI.s1 NCL CGAP Sub8 Homo sapiens cDNA clone IMAGE:3084963.3	UI-H-BI4-aol-e-02-0-UI:s1 NCI_CGAP_Sub8 Homo saplens cDNA clone IMAGE:3084963.3	yr58e11.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE 209324.31	qm87c09.x1 NCL CGAP_Lu5 Homo saplens cDNA clone IMAGE:1895728.3'	Homo sapiens chromosome 21 segment HS21C004	Homo sapiens chromosome 21 segment HS21C004	AU120280 HEMBB1 Homo sapiens cDNA clone HEMBB1000339 5'
Top Hit Database Source			LN	Ę		4505928 NT	Т	. LN			± E					E				L	EST HUMAN 9	Г	Г	Γ	Į.	EST_HUMAN U	Г	EST HUMAN	EST HUMAN Q	Ī	Г	EST_HUMAN A
Top Hit Acession No.	11428740 NT	5.0E-84 AB032957.1	5.0E-84 AB032957.1	4.0E-84 AB037735.1	4.0E-84 AI685321.1	4505928	4.0E-84 AF069601.2	4.0E-84 AF022835.1	11386168 NT	11386168 NT	4.0E-84 AF059650.1	11421326 NT	4557526 NT	4557526 NT	4.0E-84 AB032956.1	3.0E-84 AF026200.1	4758081 NT	5453855 NT		3.0E-84 AF014459.1		2.0E-84 BE695397.1	2.0E-84 BE695397.1	2.0E-84 AF036943.1		2.0E-84 BF511675.1	2.0E-84 BF511575.1		2.0E-84 A1298674.1	2.0E-84 AL163204.2		2.0E-84 AU120280.1 E
Most Similar (Top) Hit BLAST E Value	5,0E-84	5.0E-84	5.0E-84	4.0E-84	4.0E-84	4.0E-84	4.0E-84	4.0E-84	4.0E-84	4.0E-84	4.0E-84	4.0E-84	4.0E-84	4.0E-84	4.0E-84	3.0E-84	3.0E-84	3.0E-84	3.0E-84	3.0E-84	3.0E-84	20E-84	2.0E-84	2.0E-84 /	2.0E-84 X89211.1	2.0E-84	2,0E-84 E	2.0E-84 H63370.1	2.0E-84	2.0E-84	2.0E-84 A	2.0E-84 A
Expression Signal	2.85	1.99	1.99	1.34	4.47	99.0	1.52	1.62	1.8	1,8	2.14	13.68	1.12	1.12	4.76	2.16	1,53	2.39	2.36	5.53	5.78	6.46	6.46	9.21	1.22	0.93	0.93	0.92	1.55	0.58	0.58	1.24
ORF SEQ ID NO:	38516	38640	38641	27635	27672	31167	31168	31448	32162	32163	32928	34381	35735	35736	37859	26572	27395	28260	28319	30005		28435	28436	29209	29226	31914	31915	33325		35200	35201	36179
SEQ (D NO:	24827	24938	24938	14561	14596	18192	18193	18579	18874	18874	19567	20880	22191	22191	24229	13540	14341	15155	15203	17002	24190	15307	15307	16185	16203	18837	18837	19929	21329	21660	21660	22611
Probe SEQ ID NO:	11838	11952	11952	1407	1443	5064	5065	5377	2680	5680	6398	7825	9112	9112	11158	326	1178	2015	2063	3843	11118	2172	2172	3009	3027	5643	5643	6774	8247	8579	8579	9546

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	Top Hit Descriptor	ym49e11.r1 Soares Infant brain 1NIB Home sapiens cDNA clone IMAGE:51383 5 striller to construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the	P26644 BETA-2-GLYCOPKOLEIN I. paestant 2 xt Lubeki sympathetic_trunk Homo sapiens cDNA clone IMAGE:4090251 3' similar to	TR.09UGS3 Q9UGS3 DJ756G23.1; TR.09UGS3 Q9UGS3 DJ756G23.1; TR.09UGS3 Q9UGS3 LJ756G23.1; TR.09UGS3 Q9UGS3 DJ756G23.1;	TR: OBUGS3 OBUGS3 DJ786023.1; TR: OBUGS3 OBUGS3 DJ786023.1; TR: OBUGS3 OBUGS3 DJ786023.1;	Homo sapiens intersecting around a property of the monoxygenase activation protein, zeta polypeptide Homo sapiens (vrosine 3-monoxygenase/trypfophan 5-monoxygenase)	Homo septions complement component 5 (C5), mRNA	James 2011, S1 Stratagene schizo brain S11 Homo sapiens cDNA clone INACE. 1020000	601308006F1 NIH MGC 44 Homo caplens cDNA clone IMAGE:3020237 0	Homo sapiens pericentrolar material 1 (PCM1), mKNA	my 2206.51 NOI_CGAP_SS1 Homo sapiens cDNA clone IMAGE: 1239 1003	Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21422, segment	IDKFZ0434N0323 11 434 (synonym; https://doi.o/gotiens.cip/na/cone.ph/220434N0323 11 434 (synonym; https://doi.o/gotiens.cip/na/cone.ph/220434N0323 51	DKFZp434N0323_r1 434 (synorym: htes3) Homo saplens cDNA clone DA 2p12m 3022	Homo sagiens 959 kb contig between AML1 and CBK1 on chickings and a sagient 959 kb contig between AML1 and CBK1 on chickings and a sagient 950 kb contig between AML1 and CBK1 on chicking a sagient 950 kb contig between AML1 and CBK1 on chicking a sagient 950 kb contig between AML1 and CBK1 on chicking a sagient 950 kb contig between AML1 and CBK1 on chicking a sagient 950 kb contig between AML1 and CBK1 on chicking a sagient 950 kb contig between AML1 and CBK1 on chicking a sagient 950 kb contig between AML1 and CBK1 on chicking a sagient 950 kb contig between AML1 and CBK1 on chicking a sagient 950 kb contig between AML1 and CBK1 on chicking a sagient 950 kb contig between AML1 and CBK1 on chicking a sagient 950 kb contig between AML1 and CBK1 on chicking a sagient 950 kb contig between AML1 and CBK1 on chicking a sagient 950 kb contig between AML1 and CBK1 on chicking a sagient 950 kb contig between 950 kb contig between 950 kb contig between 950 kb contig between 950 kb contig between 950 kb contig between 950 kb contig between 950 kb contig between 950 kb contig between 950 kb contig between 950 kb contig between 950 kb contig between 950 kb contig between 950 kb contig between 950 kb contig between 950 kb contig between 950 kb contig between 950 kb contig between 950 kb contig between 950 kb contig between 950 kb contig between 950 kb contig between 950 kb contig between 950 kb contig between 950 kb contig between 950 kb contig between 950 kb contig between 950 kb contig between 950 kb contig between 950 kb contig between 950 kb contig between 950 kb contig between 950 kb contig between 950 kb contig between 950 kb contig between 950 kb contig between 950 kb contig between 950 kb contig between 950 kb contig between 950 kb contig between 950 kb contig between 950 kb contig between 950 kb contig between 950 kb contig between 950 kb contig between 950 kb contig between 950 kb contig between 950 kb contig between 950 kb contig between 950 kb contig between 950 kb contig between 950 kb contig between 950 kb co	Home sepeckle-type POZ protein (SPOP), mRNA	uterine water channel=28 kda erythrocyte integral membrane protein nornoug trustics.	nt) Novel human gene mapping to chomosome 13	Novel human gene mapping to chomosome 13	Novel human gene mapping to chomosome 13	Homo sapiens polymerase (DNA directed), alpha (POLY), minyry	Homo saplens NGFI-A binding protein 1 (EKG1 pinding protein 1) (NAR1), mRNA	Homo sapiens NGFI-A binding protein 1 (ERG1 pinding protein 15) (PP16) mRNA	Homo sapiens nuclear transport tactor 2 (placetial protein to your form)	Homo sapiens Ca2+-binding protein CABP 3 (CAC) 1991 C. CAP 3 (USP 13) (USP 13) (MRNA	Homo sapiens ubiquitin specific protease 13 (1904) Homo sapiens ubiquitin specific protease 13 (18013) mRNA	Homo sapiens ubiquitin specific protease 13 (Isopephrusas 1977) mRNA	Homo sapiens purinergic receptor PZA-like 1, old lant occur.	Homo sapiens aconitase 2, mitochonana (ACCE), micros	Homo sapiens chromosome 21 segment noznoso	
-	Top Hit Database Source		EST_HUMAN	EST_HUMAN	EST_HUMAN	LN	FZ.	TOT LINAAN	EST HOWAIN	101	INAMA IL	-1	NOT TOT	EST HIMAN		- N	\ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \	Ę,	Z	Z LZ	T.N. Y	NT	LN 8	NT NT	Z	4507848 NT	AE078ABINT	12 NT	85 NT	<u></u>	
	Top Hit Acession No.		22841.1	2.0E-84 BF448000.1	2.0E-84 BF448000.1	1.0E-84 AF114488.1	4507952 NT	1142/031 114	DE-84 AA984379.1	0E-84 BE392137.1	1142/19/10	0E-84 AA720851.1	0E-84 AJ229041.1	.0E-84 AL043314.2	0E-84 AL043314.2	AJ2290	11434422 14	.0E-84 S73482.1	.0E-84 AL049784.1	1.0E-84 AL 049784.1	0E-84 AL049/04: 1				A E 22 A E 4	A5078				AI 1832	
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	Probe SEQ ID		5500		12448	12449	563	738	1321	2114	2268	3845	4538	482	4821	503	6043	83.10	2 2	202	7256	7637	7737	E	9736	66	8	9894	12325	12438	6

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Top Hit Descriptor	Homo sapiens nuclear protein Skip mRNA, complete ods	Homo sapiens nuclear protein Skip mRNA, complete cds	Human plasminogen gene, exon 7	Human plasminogen gene, exon 7	Homo sapiens DKFZp434P211 protein (DKFZP434P211), mRNA	Homo sapiens chromosome 21 segment HS21C009	Homo sapiens chromosome 21 segment HS21 C080	Homo sapiens heat shock franscription factor 2 binding protein (HSF2BP), mRNA	Homo sapiens chromosome 21 segment HS21C068	Homo sapiens DKFZp434P211 protein (DKFZP434P211), mRNA	Homo sapiens ribosomal protein L27 mRNA, complete cds	Homo sapiens MSTP030 mRNA, complete cds	Homo sapiens DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 10 (RNA helicase) (DDX10), mRNA	Homo sapiens DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 10 (RNA helicase) (DDX10), mRNA	zl62b01.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:726889 5' similar to TR:G1335769 G1335769 GAG-POL POLYPROTEIN	Homo saplens chromosome 21 segment HS21C084	Homo sapiens T-type calcum channel alpha1 subunit Alpha1Le Isoform (CACNA1I) mRNA, complete cds	801458646F1 NIH_MGC_65 Homo saplens cDNA clone IMAGE:3862402 5/	601458646F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3862402 5	Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D3) genes, complete cds	Homo sapiens T-type calcum channel alphat subunit Alphat I-a Isoform (CACNA1I) mRNA, complete cds	602084730F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4249087 5'	602084730F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4249087 5'	601505022F2 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3906940 5'	RC1-BT0623-120200-011-c07 BT0623 Homo sapiens cDNA	Homo sapiens protein phosphatase 2A BR gamma subunit gene, exon 6	ye53g09.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:121504 5'	Homo sapiens F-box only protein 24 (FBXO24), mRNA
Top Hit Database Source	TN	LN	ĮN.	N	TN	TN	NT	LN	NT	۲	IN	TN	NT	LΝ	EST_HUMAN	NT	뒫	EST_HUMAN	EST_HUMAN	NT	LN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	NT	EST_HUMAN	NT
Top Hit Acessian No.	9.0E-85 U51432.1	9.0E-85 U51432.1	9.0E-85 M33282.1	9.0E-85 M33282.1	7657020 NT	9.0E-85 AL163209.2	9.0E-85 AL163280.2	5901979 NT	9.0E-85 AL163268.2	7657020 NT	L05094.1	7.0E-85 AF113210.1	11438573 NT	11438573 NT	6.0E-85 AA403053.1	5.0E-85 AL163284.2	5.0E-85 AF211189.1	5.0E-85 BF035674.1	5.0E-85 BF035874.1	5.0E-85 AF224869.1	5.0E-85 AF211189.1	4.0E-85 BF677910.1	4.0E-85 BF677910.1	4.0E-85 BE882304.1	4.0E-85 BE079263.1	3.0E-85 AF096157.1	3.0E-85 T97495.1	11024695 NT
Most Similar (Top) Hit BLAST E Value	9.0E-85	9.0E-85	9.0E-85	9.0E-85	9.0E-85	9.0E-85	9.0E-85	9.0E-85	9.0E-85	9.0E-85	7.0E-85 L05094.1	7.0E-85	6.0E-85	6.0E-85	6.0E-85	5.0E-85	5.0E-85	5.0E-85	5.0E-85	5.0E-85 /	5.0E-85	4.0E-85	4.0E-85	4.0E-85	4.0E-85	3.0E-85	3.0E-85	3.0E-85
Expression Signal	2.89	2.89	1.12	1.12	3.59	0.8	0.92	0.99	1.16	1.78	4.64	5.61	2.56	2.56	8	4.09	0.71	1.59	1.59	2.31	1.72	1.39	1.39	3.43	1.8	0.91	4.8	1.03
ORF SEQ ID NO:		27320						31105	31137	27949	27378		38391	38392	38750	28668		31804	31805	38101		32798	32799	34586		27551	28062	31125
Exan SEQ ID NO:	14263	14263	14762	14762		1		ľ	18160	14860	14323	24929	24699	24699	25041		17690	18764	18764	24442	17690	1 1	i	1	23831	[		18148
Probe SEQ ID NO:	1098	1098	1609	1609	1709	3870	4366	5001	2032	13046	1159	11943	11702	11702	12060	2410	4552	2999	5567	11381	13127	6276	6276	8021	10798	1327	1821	5019

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READ DRIVERS         Most Shiller         Top HR         Top HR         Top HR         Top HR         Top HR         Top HR         Top HR         Top HR         Top HR         Top HR         Top HR         Top HR         Top HR         Top HR         Top HR         Top HR         Top HR         Top HR         Top HR         Top HR         Top HR         Top HR         Top HR         Top HR         Top HR         Top HR         Top HR         Top HR         Top HR         Top HR         Top HR         Top HR         Top HR         Top HR         Top HR         Top HR         Top HR         Top HR         Top HR         Top HR         Top HR         Top HR         Top HR         Top HR         Top HR         Top HR         Top HR         Top HR         Top HR         Top HR         Top HR         Top HR         Top HR         Top HR         Top HR         Top HR         Top HR         Top HR         Top HR         Top HR         Top HR         Top HR         Top HR         Top HR         Top HR         Top HR         Top HR         Top HR         Top HR         Top HR         Top HR         Top HR         Top HR         Top HR         Top HR         Top HR         Top HR         Top HR         Top HR         Top HR         Top HR         Top HR						_	_	-т	_	_	_	_	_	_	- T	_	т	Т	Т	Т	- 1	7	Τ	٣	Τ,	٠,	T	Τ	7	T	T	Ţ <del>'</del>	4	134	4	ا	•
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cDNA clone IMAGE:4126440 5	SO1897003F1 NIH MGC 19 Homo sapiens cDNA clone IMAGE: 4128440 S	rafeao7 x1 NCi CGAP Brn25 Homo saplens cDNA clone IMAGE:1860468 3'	Home satisfies calcineurin binding protein 1 (KIAA0330), mRNA	Home carleins celcineurin binding protein 1 (KIAA0330), mRNA	ANA 2017 RE1 NIH MIGC 20 Homo sapiens cDNA clone IMAGE: 2967690 5	Unione sanians similar to CDC28 protein kinase 1 (H. sapiens) (LOC63041), mRNA	Home saniens KIAA0680 cene product (KIAA0680), mRNA	Spares Spares parathroid fumor NbHPA Homo sapiens cDNA clone IMAGE:1403559 3	apoliticus i compositione de la Norda de la Norda de la Company de la Company de la Company de la Company de la Company de la Company de la Company de la Company de la Company de la Company de la Company de la Company de la Company de la Company de la Company de la Company de la Company de la Company de la Company de la Company de la Company de la Company de la Company de la Company de la Company de la Company de la Company de la Company de 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sapiens similar to transcription factor CA150 (H. sapiens) (LOC63170), mkNA	Homo saplens similar to transcription factor CA150 (H. saplens) (LOC63170), mrNA	Homo sapiens coagulation factor XIII, A1 polypeptide (F13A1), mKNA	Homo sapiens oxoglutarate dehydrogenase (lipoamide) (OGDH) mRNA	601072594F1 NIH MGC_12 Homo sapiens cDNA done IMAGE:3458830 6	And 176865F1 NIH MGC 17 Homo sepiens cDNA clone IMAGE:3531953 5	601072594F1 NIH MGC 12 Homo sapiens cDNA clone IMAGE:3458830 5	601443262F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3847455 5	xz92h12.x1 NCI_CGAP_Lu24 Homo sapiens cDNA done IMAGE:28717193	AV722329 HTB Homo seplens cDNA clone HTBBSD04 5	801509696F1 NIH_MGC_71 Home sapiens cDNA clone IMAGE:3911303 5	
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Francis)	hd87g08.x1 NCI CGAP GCO nomo sapiens con a configuración con control de	Homo sapiens cAMP-specific phosphodiesterase an (PDCoA) IIINNA, Palua cas	H.sapiens mRNA encoding phospholipase c	H.sapiens mRNA encoding phospholipase c	Homo sapiens similar to ectonucleotide pyrophosphatase/phosphodiesterase 3 (H. saplens) (LOC63214),	mRNA	Human Chediak-Higashi syndrome protein short isoform (LYSI) mKNA, complete cus	Homo sapiens butyrobetaine (gamma), 2-oxoglutarate clioxygenase (gamma-butyrobetaine hydroxylase)	(BBOX), mRNA	Homo sapiens butyrobetaine (gamma), 2-oxogiutarate dioxygenase (gamina-butyrobetaine nyuloxyrase)	(BBOX), mRNA	Homo sapiens phospholipid scramblase 1 (PLSCR I), middin	Homo sapiens chromosome segregation 1 (yeast nomolog) hitse (Commission and Commission and Commission and Commission and Commission and Commission and Commission and Commission and Commission and Commission and Commission and Commission and Commission and Commission and Commission and Commission and Commission and Commission and Commission and Commission and Commission and Commission and Commission and Commission and Commission and Commission and Commission and Commission and Commission and Commission and Commission and Commission and Commission and Commission and Commission and Commission and Commission and Commission and Commission and Commission and Commission and Commission and Commission and Commission and Commission and Commission and Commission and Commission and Commission and Commission and Commission and Commission and Commission and Commission and Commission and Commission and Commission and Commission and Commission and Commission and Commission and Commission and Commission and Commission and Commission and Commission and Commission and Commission and Commission and Commission and Commission and Commission and Commission and Commission and Commission and Commission and Commission and Commission and Commission and Commission and Commission and Commission and Commission and Commission and Commission and Commission and Commission and Commission and Commission and Commission and Commission and Commission and Commission and Commission and Commission and Commission and Commission and Commission and Commission and Commission and Commission and Commission and Commission and Commission and Commission and Commission and Commission and Commission and Commission and Commission and Commission and Commission and Commission and Commission and Commission and Commission and Commission and Commission and Commission and Commission and Commission and Commission and Commission and Commission and Commission and Commission and Commission and Commission and Commission and Commission and Commission and Commission and Commi	Homo sapiens basic-helix-toop-helix-PAS protein (NPASS), mrnvA	Homo sapiens basic-hefix-kop-hefix-PAS protein (NPASS), mrivA	Homo sapiens hypothetical protein FLJ20125 (FLJ20125), mRNA	Homo sapiens mRNA for KIAA141 protein, partial cds	Hamo sapiens ribosomal protein S6 kinase, 90kD, polypeptide 5 (RPS6KA5) mRNA	Home serviens thyroid autoantiden 70kD (Ku amigen) (G22P1), mRNA	Lower series can for AF-8 complete cds	Truction sequences generally appropriate and the protein 1 (75kD) (NADH-coenzyme Q reductase)	(NDUFS1) mRNA	
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	Top Hit Descriptor	y80f10.r1 Soares placenta Nb2HP Homo saplens cDNA clone IMAGE:146579 5' similar to contains Alu repetitive element.	y80f10,r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:1455/9 5 similar to contains Aiu	repetitive element;	Homo sapiens CGI-60 protein (LOC3) oct.	Homo saplens CGI-60 protein (LOC31626), mKNA	Homo saplens myeloid/lymphdid or mixed-lineage leukemia (mimdax (Linosophila) noinolog), uansiooaaca is, a (MLLT4) mRNA	ETS-RELATED PROTEIN 71 (ETS TRANSLOCATION VARIANT 2)	Human transcription factor NFATX3 mRNA, complete cas	TCBAP1E4051 Pediatric pre-B cell acute lymphoblastic leukemia bayid +1GSV prigotal CDA 11GH 12GH 12GH 12GH 12GH 12GH 12GH 12GH	Homo saplens KIAA1072 protein (KIAA1072), mRNA	Homo sapiens KIAA1072 protein (KIAA1072), mKNA	Homo saplens tuberin (TSC2) gene, exon 10	Human von Willebrand factor pseudogene corresponding to exorts 23 uniquities	Homo sapiens calcineutin binding protein 1 (NAAUSSU), minna	Homo saplens calcineum binding protein 1 (KIAA0339), mKNA	Homo saplens purinergic receptor rizzanti i dipliani receptor (rizzanti), in assi	Home sapiens high-mobility group (homistone citi di losottian) protest + (highest) him to the citi di losottian de la citi di losottian de la citi di losottian de la citi di losottian de la 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Page 405 of 550 Table 4 Single Exon Probes Expressed in Placenta

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Top Hit Descriptor	Homo sapiens putative glycolipid transfer protein (LOC51054), mRNA	PM2-CT0265-141099-001-904 CT0265 Homo sapiens cDNA	PM2-CT0265-141099-001-904 CT0265 Homo sapiens cDNA	Human mRNA for T-cell cyclophilin	Homo saplens neurexin III (NRXN3) mRNA	Homo sapiens growth factor receptor-bound protein 10 (GRB10) gene, exon 8	Homo sapiens growth factor receptor-bound protein 10 (GRB10) gene, exon 8	Homo sapiens IQ motif containing GTPase activating protein 1 (IQGAP1) mRNA	Homo sapiens protein kinase C, beta 1 (PRKCB1), mRNA	Homo sapiens IQ motif containing GTPase activating protein 1 (IQGAP1) mRNA	Homo sapiens tracheal epithelium enriched protein (PLUNC) gene, complete cds	Homo sapiens mRNA for alpha2,3-sialytransferase ST3Gal VI, complete cds	Hamo paplens mRNA for alpha2,3-sialytransferase ST3Gal VI, complete cds	RC6-BN0276-050700-012-E02 BN0278 Homo sapiens cDNA	RCS-BN0276-050700-012-E02 BN0278 Homo sapiens cDNA	Human L-plastin mRNA, 5' end	Homo sapiens hect domain and RLD 2 (HERC2), mRNA	Homo sapiens RGH1 gene, retrovirus-like element	Homo sapiens sulfotransferase-related protein (SULTX3), mRNA	Homo sapiens beta-vreidopropionase (BUP1) gene, exon 9	Homo sapiens beta-ureidopropionase (BUP1) gene, exon 9	Homo sapiens double stranded RNA activated protein kinase (PKR) gene, exon 12	Hamo sapiens mRNA for KIAA1399 protein, partial cds	Homo sapiens mRNA for KIAA1399 protein, partial cds	Homo saplens DKFZP596P1522 protein (DKFZP586P1522), mRNA	Homo saplens chromosome 21 segment HS21C009	H.sapiens ECE-1 gene (exon 9)	H. sapiens ECE-1 gene (exon 9)	Homo sapiens X-linked anhidroitic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat	regions	Homo sapiens KIAA0063 gene product (KIAA0063), mRNA	K9719F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA clone K9719 5' similar to ZINC FINGER PROTEIN H7F1	Through interacting the delination (ITAN) and A complete add	בים ווס פקופוני ווופן פפקון פוים ניפסים ווי סיין וויצואלי כסווים פים
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Page 406 of 550 Table 4 Single Exon Probes Expressed in Placenta

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	Expression Signal		0.71	0.71	2.78	0.75	27.0	2.67	2.67	0.53	0.96	0.96	0.65	1.7	1.54	1.72	1.72	1.25	3.09			0.81		2.79						1	3 6.63	60		7 1.58
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Top Hit Descriptor	Homo sapiens v-ets avkan erythroblastosis virus E26 oncogene related (ERG), mRNA	Homo sapiens mRNA for RALDH2-T, complete cds	Homo sapiens mRNA for RALDH2-T, complete cdc	Homo saplens acyl-Coenzyme A dehydrogenase family, member 8 (ACAD8), mRNA	Homo saplens transcobalamin II; macrocytic anemia (TCN2), mRNA	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA	Homo sapiens protease, serine, 7 (enterokinase) (PRSS7), mRNA	Homo sapiens Calsenilin, presenilin-binding protein, EF hand transcription factor (CSEN), mRNA	Homo sapiens SNARE protein kinase SNAK mRNA, complete cds	Homo seplens SNARE protein kinase SNAK mRNA, complete cds	Homo sapiens SNARE protein kinase SNAK mRNA, complete ods	Homo sapiens dynein, axonemal, light polypeptide 4 (DNAL4), mRNA	UI-H-BI1-asa-d-04-0-UI.s1 NCI_CGAP_Sub3 Homo capiens cDNA olone IMAGE:2718760 3'	UI-H-BI1-aea-d-04-0-UI.s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2718750 3'	Homo sapiens KIAA0417 mRNA, complete cds	Homo saplens KIAA0417 mRNA, complete cds	wq70a12.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2476606 3	ae54a11.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:824732 3' similar to WP:80272.2 CE00851 ;	Homo sapiens Reoq helicase 5 (RECQ5) gene, alternative splice products, complete cds	zp87c02.r1 Stratagene HeLa cell s3 937216 Homo sapiens cDNA done IMAGE:627170 5' similar to SW:POL1_HUMAN P10266 RETROVIRUS-RELATED POL POLYPROTEIN	DKFZp434N0323_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434N0323 5'	os91g03.s1 NCI_CGAP_GC3 Homo saplens cDNA cione IMAGE:1612756 3' similar to gb:M16342 HETEROGENEOUS NJCLEAR RIBONUCLEOPROTEINS C1/C2 (HUMAN);	Homo sapiens chromosome 21 segment HS21 C046	UI-H-BI3-alk-b-03-0-UI:s1 NCI_CGAP_Sub5 Hamo septens cDNA clone IMAGE:2737084 3'	Homo sapiens transgelin 2 (TAGLN2), mRNA	601142409F1 NIH_MGC_14 Homo sapiens cDNA clone IMAGE:3506186 5'	Homo sapiens similar to sema domain, immunoglobulin domain (1g), short basic domain, secreted, (semaphorin) 3A (H. sapiens) (LOC63232), mRNA	Homo sapiens hormonally upregulated neu tumor-associated kinase (HUNK), mRNA	Homo septens hormonally upregulated neu fumor-associated kinase (HUNK), mRNA	Homo sapiens complement component 8, beta polypeptide (C8B) mRNA
Top Hit Database Source	TN	NT	NT	NT	N⊤	TN	NT	LN	IN	LN.	Z	LN	EST HUMAN	EST_HUMAN	ΙN	FZ	EST HUMAN	EST HUMAN	N	EST HUMAN	EST_HUMAN	EST HUMAN	N	EST_HUMAN	F	EST_HUMAN	NT	Z	NT	L
Top Hit Acession No.	11526262 NT	3.0E-88 AB015228.1	3.0E-88 AB015228.1	11439065 NT	11417974 NT	11430460 NT	11528140 NT	7305198 NT	2.0E-88 AF246219.1	2.0E-88 AF246219.1	2.0E-88 AF246219.1	5031666 NT	1.0E-88 AW139565.1	1.0E-88 AW 139565.1	1.0E-88 AB007877.1	1.0E-88 AB007877.1	1.0E-88 AI969034.1	1.0E-88 AA488981.1	1.0E-88 AF135183.1	1.0E-88 AA190368.1	1.0E-88 AL043314.2	1.0E-88 AA991479.1	1.0E-88 AL163246.2	1.0E-88 AW451790.1	21238	8.0E-89 BE311557.1	11421514 NT	7657213 NT	7657213 NT	4557390 NT
	3.0E-88	3.0E-88/	3.0E-88 /	3.0E-88	3.0E-88	3.0E-88	3.0E-88	2.0E-88	2.0E-88	2.0E-88	2.0E-88	2.0E-88	1.0E-88	1.0E-88	1.0E-88	1.0E-88/	1.0E-88	1.0E-88	1.0E-88	1.0E-88	1.0E-88	1.0E-88	1.0E-88	1.0E-88	9.0E-89	8.0E-89	8.0E-89	7.0E-89	7.0E-89	7.0E-89
Expression Signal	2.14	0.76	0.76	9.0	2.49	1.63	1.31	6.85	4.24	6.83	2.9	1.93	4.98	4.98	21.66	21.66	1.52	3.7	0.51	0.76	2.83	3.35	4.28	1.54	8.14	1.75	1.14	1.41	1.41	2.74
ORF SEQ ID NO:	34589	36767		36794						28031	29733	30665	32636	32537	33334	33335	33807	33877	34939	36122		37541		31850	37898		33541			31108
Exan SEQ ID NO:	21077	23170	23170	23199	25301	26030	25796	14227	14806	14938	16719	17683	19215	19215	19938	16938	20354	20415	21413	22559	22818	23916	25442	25800		15910	20125	13642	13642	18134
	9834	10132	10132	10162	12424	12439	13223	1061	1653	1789	3554	4545	6032	6032	6783	6783	7271	7334	8331	9443	97.78	11730	12665	13232	11194	2795	7072	446	446	5005

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	Top Hit Descriptor	Target A 424 (sunanym; htes3) Homo septens cDNA clone DKFZp434E248 5	DKFZp434E249 11 37 137 137 137 137 137 137 137 137 1	H.sapiens CLN3 geno, complete CU3	Homo sepiens plastin 3 (Tisoforn) (1-50) mRNA	Homo satiens plastin 3 (T isdorm) (T LS3),	Horno saplens actin related protein 2/3 Control MRNA	Homo sapiens KIAA0433 protein (KIAA0433), mRNA	Homo saplens NAMULA promoter (1965) mRNA, complete cds	Human 85-kilodatton prospring	H, sapiens West rin year	H.sapiers West hu gene	Homo sepiens mRNA for NANAVALET (AND AND AND AND AND AND AND AND AND AND	Homo sapiens mRNA for niverse rement 2	Human aldose reductase (AR) gene, segment minochondrial (mitofilin) (IMMT), mRNA	Homo saplens liner membrane process, in the process of PRP4 homolog (PRP4) mRNA	Homo saplens serine/threonine-process in the Paragram (UBE2I.3) mRNA	Homo sapiens ubiquitin-conjugating of 2013 (UBE2L3) mRNA	Homo sablens ublquitin-conjugating entation cas	Homo sapiens mRNA for KIAA0406 protein, partial cds	Homo saplens mRNA for KINALULY in Instantal protein 2 (LRP2), mRNA	Homo capiens low density (poprotein active control of (LRP2), mRNA	Homo sapiens low density (popposer) in the homopopiestic leukemia Baylor-HGSC project	TCBAP2E0383 Pediatric pre-B cell acute 1977-		1				Γ	Г	w86e11.r1 Soares placenta Stoswerns From North North 4-KINASE ALTIN 1			ı	
110	Top His		HOMAN				-			12	I.V	2 2	14		Z.	Z	Z	Z	Z	IZ !	Į.	Z.	N.S.	z z	Per LIMAN	101	EST HUMAN	EST HUMAN	EST HUMAN	EST HUMAN	1		EST HUMAN	EST HUMAN	EST_HUMAN	
Single Exult 1		rop Hit Acesslon No.	-			7549808 NI	7549808 N I	11420754 NT	LNGVICE	41/110		T		٦		9783.1	5803114 N	4506124 N	4507788 NI	4507788 NT	-89 AB007866.2	6.0E-89 AB007866.2	6806918 <sub>N</sub> I	6806918 N		-89 BE244323.1	4 50001.00	5.0E-89 BE 244323.1	4.0E-89 BE / 02/43:	3.0E-89 AW976181.1	E-89 AI217359.1			3.0E-89 N57357.1	3.0E-89 AV705749.1	
	-		89 AL045748.1		-89 X99832.1	68-	7.0E-89	7.0E-89	7.0E-89		7.0E-89 J0Z9Z3.1	7.0E-89 X62048.1	7.0E-89 X62048.1	7.0E-89 AB020630.1	DE-89 ABC	0E-89 M5	0E-89	6.0E-89	98-75	60E-89	6.0E-89 AE	3.0E-89 AE	S.0E-89	60E-89		5.0E-89B		5.0E-89	4.0E-89	3.0E-89	3.0E-89			3.0E-89	3.05.00	3.05-00
	in o	Most Similar (Top) Hit BLAST E	7.0E-89	7.0E-89	2.0E-89	7.0E-89	Š		L					L		L	1	L	1	1.6.1			L		$\perp$	3.36	-	3.36	1.02	1.83	1.3	+		2.29	1.52	1.82
	+	Expression Signal	7.20	18	13	15.	5 15	1.84	99.0	0.68	130	1.34	1.34	1 35	1 35	20.0	۱	٦	1	-	1										1			34	83	92
	-		+	34151	31778	31779	33000	33001	ASSA.	34665	00030	30702	3/320	980/2	37423	37424	38260	27271	28551	28750	28751	30873	30874	31379	31380	24273	2	21774	34310	1	١	33828	L	37751	1	
	-	ORF SEQ ID NO:	_		18744	١	1			1	١	21754	23783	23783	23801	23801	24572	14214	15419	15631	15631	17894	17894	18413	18413			000	18300	28820	16118	20372	<u> </u>	24118	-1-	L
	-	- 0	<u> </u>	5046 181			L	Ш	_1	L	1	8674 2	- 1	10750 2		乚	١_	L	L	4-	2504	4759	4759	5295	5235		5186		5188	7761	2941	7290			11039	72/30
	Ì	Probe SEQ ID	<u>ğ</u>	) N	Š	فقا	Ø		_			Ĺ	Ľ			Ľ	L	L	1		1_	ــــــــــــــــــــــــــــــــــــــ	ــــــــــــــــــــــــــــــــــــــ	1		<b></b>	لــــ		_							

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	Top Hit Descriptor	Horno saniens PXR2b protein (PXR2b), mRNA	Home satiens PXR2b protein (PXR2b), mRNA	Homo sapiens PXR2b protein (PXR2b), mRNA	Home saplens PXR2b protein (PXR2b), mRNA	Homo sapiens mRNA for KIAA1342 protein, partial cds	Standardinia to coccess and an initial to the standard and standard to the standard and standard and standard and standard and standard and standard and standard and standard and standard and standard and standard and standard and standard and standard and standard and standard and standard and standard and standard and standard and standard and standard and standard and standard and standard and standard and standard and standard and standard and standard and standard and standard and standard and standard and standard and standard and standard and standard and standard and standard and standard and standard and standard and standard and standard and standard and standard and standard and standard and standard and standard and standard and standard and standard and standard and standard and standard and standard and standard and standard and standard and standard and standard and standard and standard and standard and standard and standard and standard and standard and standard and standard and standard and standard and standard and standard and standard and standard and standard and standard and standard and standard and standard and standard and standard and standard and standard and standard and standard and standard and standard and standard and standard and standard and standard and standard and standard and standard and standard and standard and standard and standard and standard and standard and standard and standard and standard and standard and standard and standard and standard and standard and standard and standard and standard and standard and standard and standard and standard and standard and standard and standard and standard and standard and standard and standard and standard and standard and standard and standard and standard and standard and standard and standard and standard and standard and standard and standard and standard and standard and standard and standard and standard and standard and standard and standard and standard and standard and standard and standard and standard and standard	4996-08.x1 Soares_NFL_T_GBC_S1 Home septens cDNA clone IMAGE:1843-02.5 strintal to septent oggettive element; GAMMA-GLUTAMYLTRANSPEPTIDASE 1 PRECURSOR (HUMAN);combins Alu repetitive element; GAMMA-GLUTAMYLTRANSPEPTIDASE 1 PRECURSOR (HUMAN);combins Alu repetitive element;	Homo saplens topolsomerase-related function protein (11x14-2) military.	H.sapiens HCK gene for tyrosine kinase (PTK), exons 10-11	H.sapiens HCK gene for tyrosine kinase (PTK), exons 10-11	Homo saptens chromosome 21 segment HS21C003	Homo saplens GGT gene, exon 5	AN1065996F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3432423 3	Homo sapiens gene for LECT2, complete eds	Human N-ethytmaleimide-sensitive factor mRNA, partial cds	Homo sapiens chromosome 21 segment HS21C085	Himan GT24 (GT24) mRNA, partial cds	indition of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the	Homo sapiens solute carrier family 24 (sodium)podassuring asserting asserting asserting the solute carrier family 24 (sodium)podassuring asserting asserting asserting asserting asserting asserting asserting asserting asserting asserting asserting asserting asserting asserting asserting asserting asserting asserting asserting asserting asserting asserting asserting asserting asserting asserting asserting asserting asserting asserting asserting asserting asserting asserting asserting asserting asserting asserting asserting asserting asserting asserting asserting asserting asserting asserting asserting asserting asserting asserting asserting asserting asserting asserting asserting asserting asserting asserting asserting asserting asserting asserting asserting asserting asserting asserting asserting asserting asserting asserting asserting asserting asserting asserting asserting asserting asserting asserting asserting asserting asserting asserting asserting asserting asserting asserting asserting asserting asserting asserting asserting asserting asserting asserting asserting asserting asserting asserting asserting asserting asserting asserting asserting asserting asserting asserting asserting asserting asserting asserting asserting asserting asserting asserting asserting asserting asserting asserting asserting asserting asserting asserting asserting asserting asserting asserting asserting asserting asserting asserting asserting asserting asserting asserting asserting asserting asserting asserting asserting asserting asserting asserting asserting asserting asserting asserting asserting asserting asserting asserting asserting asserting asserting asserting asserting asserting asserting asserting asserting asserting asserting asserting asserting asserting asserting asserting asserting asserting asserting asserting asserting asserting asserting asserting asserting asserting asserting asserting asserting asserting asserting asserting asserting asserting asserting asserting asserting asserting asserting asserting asserting	Homo sapiens partial incly in incly in the sapiens sapiens partial rds	Homo saplens mRNA for KIRA 1933 protein, pariting	Homo saplens CaBP's (CABP's) gene, exen 5	Homo saplens CaBP5 (CABP3) gaile, dwill 5		Homo sapiens integrin, apriled (1988) Homo sapiens formed on the CHL1), mRN.	Homo saplens cell adhesion molecule with homology to L1CAMI (close nondegode 17)	Human MAGE-7 antigen (MAGE) pseudogene, compression and complete cds	Homo sapiens human endogenous retrovirus W gaglos 37 G gag (3/3/1897) Similar to TR:054778 C	hr81d09.x1 NCI_CGAP_Kid11 Homo sapiens clone living care. 3131331 c	$\neg$	1
	Top Hit Database Source	إ	-  -				Z	EST HUMAN	LZ	12	12/2	FIN	PIA PIA	NOT THE PARK	F31 TOWNS		Z		Ę.	NT	LN	N.	NT L	NT TN		LN.	E NT	¥	Į.		EST_HUMAN	EST_HUMAN
Signio	Top Hit Acession No.		1706870 NI	7708870 N	7708670 N	3	1		T	T	Т	Т	Т	Т	7	B007540.1	103985.1	L163285.2	2.0E-89 UB1004.1	11,428801 NT	1,1245503.1	2 0F-89 AB037754.1	1F170814.1	AF170814.1		11434411 NT	11433673 NT	1110602 1	2.0E-891010092.1	Z.0E-88 AF 130901.1	.0E-89 BF196052.1	1.0E-89 BF196052.1
	=====	Value	2.0E-89	2.0E-89	2.0E-89	2.0E-89 770t	2.0E-89 At	u co	2.0E-09 A	2.0E-89 A	2.0E-89 X	2.0E-89 X	2.0E-89 A	2.0E-89 A	2.0E-891B	2.0E-89 A	2.0E-89 L	2.0E-89/	2.0E-89 (	2.0E-89	205.80	20 E B9	98-30-6	205	7,7	2.0E-89	2 OF-89					
	Expression (Signal	<u>.</u>	0.73	0.73	0.89	0.80	0.63		1.53	1.18	5.14	5.14	1.13	T	1.39	3.55	1.5	0.79	6.28			0.70	3 5	77.		2.63		3.02		4.25	6.88	5 6.88
	ORF SEQ ID NO:		26658	26657	26656	26667	26760		29135	30394	30402	30403	30587	30738		31842						1			36648	38425			38703	4	5 38561	38562
	SE OF C		13816	13616	13616	13616	13736		16122	17408	17414	17414	17609	17756	l l	l	1	L	1_	_	ı			. [	23053	5 24734	_		7 25001	1_	7 24865	1
	7.0	<del></del>	130	18	424	421	543		2945	4283	4269	4269	4469	4619	5459	5508	5909	6230	7847		8119	8612	9453	10015	10015	11655		11871	12017	12877	11877	11877

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
8422	21503		1.07	9.0E-90	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
8422	21503		1.07	9.0E-90	AL163246.2	Z	Homo sapiens chromosome 21 segment HS21C046
1088	14254		4.38	8.0E-90	AL163246.2	N	Homo saplens chromosome 21 segment HS21C046
1089			2.91	8.0E-90	AL163246.2	N T	Homo sapiens chromosome 21 segment HS21C046
1361			3.26	8.0E-90	BE670561.1	EST_HUMAN	7e36f08x1 NCI_CGAP_Lu24 Homo sepiens cDNA clone IMAGE:3284583 3'
1361	16035		3.26	8.0E-90	8.0E-90 BE670561.1	EST_HUMAN	7e36f08xf NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3284583 3'
8757	21836		9.0	8.0E-90	BE177830.1	EST_HUMAN	RC1-HT0598-120400-022-b08 HT0598 Homo sapiens cDNA
10939	24021	37654	1.38	8.0E-90	8.0E-90 AI222095.1	EST_HUMAN	qg96c08.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA done IMAGE:1843022.3' similar to gb:J04131 GAMMA-GLUTAMYLTRANSPEPTIDASE 1 PRECURSOR (HUMAN);contains Atu repetitive element;
10939	24021	37655	1.38	8.0E-90	.0E-90 AI222095.1	EST_HUMAN	qg98c08.x1 Soares_NFL_T_GBC_S1 Homo saplens cDNA clone IMAGE:1843022.3' similar to gb.J04131 QAMMA-GLUTAMYLTRANSPEPTIDASE 1 PRECURSOR (HUMAN);contains Alu repetitive element;
869	14036		6.81	7.0E-90	0E-90 AF223391.1	LΝ	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spiced
8619	21699		2,14	7.0E-90	.0E-90 AA782977.1	EST_HUMAN	al63d08.s1 Soares_testis_NHT Homo sapiens cDNA clone 1375503 3'
9166			2,13	7.0E-90	.0E-90 BE962525.2	EST_HUMAN	601656837R1 NIH_MGC_66 Homo sepiens cDNA clone IMAGE:3855824 3'
9166	22244		2.13	7.0E-90	7.0E-90 BE962525.2		601655837R1 NIH_MGC_66 Homo sapiens cDNA done IMAGE:3855824 3'
10220	23256	36844	0.46	7.0E-90	.0E-90 AW273794.1	EST_HUMAN	xx24a02.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2814026 3'
10340	23375	36985	4.2	7.0E-90	0E-90 H68849.1	EST_HUMAN	yя86604.s1 Soares fetal liver spleen 1NFLS Homo sepiens cDNA done IMAGE:212190 3' similar to SP:C1TC_HUMAN P11586 C-1-TETRAHYDROFOLATE SYNTHASE, CYTOPLASMIC;
10340	23375	36986	4.2	7.0E-90	7.0E-90 H68849.1	EST_HUMAN	y86e04.s1 Soares fetal liver spleen 1NFLS Hono sepiens cDNA done IMAGE:212190 3' similar to SP:C1TC_HUMAN P11586 C-1-TETRAHYDROFOLATE SYNTHASE, CYTOPLASMIC;
10672		37314	0.62	7.0E-90	7.0E-90 BF526089.1	EST_HUMAN	602071208F1 NCI_CGAP_Brn64 Homo saplens cDNA done IMAGE:4214257 5'
3136			1.16	6.0E-90	6.0E-90 X91926.1	NT	H.sapiens ECE-1 gene (exon 6)
3136			1.16	6.0E-90	X91926.1	NT	H.sapiens ECE-1 gene (exon 6)
4342	17485		11.21	6.0E-90	IN 8652268	NT	Homo sapiens hypothetical protein FLJ10388 (FLJ10388), mRNA
4342			1	6.0E-90	IN 86522388	M	Homo sapiens hypothetical protein FLJ10388 (FLJ10388), mRNA
6105				6.0E-90	U77700.1	NT	Homo sapiens HsGCN1 mRNA, partial cds
6105	- 6			6.0E-90	U777700.1	NT	Homo sapiens HsGCN1 mRNA, partial cds
8522	1		4.01	6.0E-90	4504794 NT	LΝ	Homo sepiens Incistol 1,4,5-triphosphate receptor, type 3 (ITPR3) mRNA
8522	[	35141		6.0E-90	6.0E-90 4504794 NT	NT	Homo sepiens inositol 1,4,5-triphosphate receptor, type 3 (ITPR3) mRNA
159	- 1			5.0E-90		IN	Homo sapiens TCL6 gene, exon 1-10b
1219	14380	27439	6.22	5.0E-90	U80226.1	LN L	Human gamma-aminobutyric acid transaminase mRNA, partial cds

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Top Hit Descriptor		qg98c08.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1843022.3' similar to gb:J04131 GAMMA-GLUTAMYLTRANSPEPTIDASE 1 PRECURSOR (HUMAN);contains Alu repetitive element;	qg96c08 x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1843022 3' similar to gb:J04131 GAMMA-GLUTAMYLTRANSPEPTIDASE 1 PRECURSOR (HUMAN);contains Alu repetitive element;	Homo sapiens intersectin long isoform (ITSN) mRNA, complete ods	Homo sapiens pregnancy-zone protein (PZP) mRNA	Homo saplens chromosome 21 segment HS21C001	H.sapiens mRNA encoding phospholipase o	Homo saplens EVI5 homdog mRNA, complete cds	Homo sapiens ELKS mRNA, complete cds	H.sapiens mRNA encoding phospholipase c	Homo sapiens Carbonic anhydrase-related protein 10 (LOC56934), mRNA	Homo sapiens Carbonic anhydrase-related protein 10 (LOC56934), mRNA	Homo sapiens anglopoletin 4 (ANG4) mRNA, partial cds	Homo sapiens angiopoietin 4 (ANG4) mRNA, partial cds	Homo sapiens adenylate cyclase 9 (ADCY9) mRNA	Homo sapiens hypothetical protein FLJ13222 (FLJ13222), mRNA	Homo sapiens similar to ectronucleotide pyrophosphatase/phosphodiesterase 3 (H. sapiens) (LOC63214), mRNA	Homo sapiens calcium-binding transporter mRNA, partial cds	Homo sapiens ATPase, aminophospholipid transporter-like, Class I, type 8A, member 2 (ATP8A2), mRNA	Homo sapiens KIAA0317 gene product (KIAA0317), mRNA	Homo sapiens KIAA0317 gene product (KIAA0317), mRNA	Homo sapiens gene for AF-6, complete cds	ar 78h05.x1 Barstead aurta HPLRB6 Homo sapiens cDNA clone IMAGE:2128761 3'	Homo saplens chromosome 21 unknown mRNA	Homo sapiens chromosome 21 unknown mRNA	Homo sapiens myosin phosphatase, target subunit 1 (MYPT1), mRNA	H.sapiens gene encoding discoidh receptor tyrosine kinase, exon 16	Homo saplens low density lipoprotein-related protein 2 (LRP2), mRNA	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
	Source	EST_HUMAN	EST HUMAN	LN	FZ	TN	NT	LN	ΗN	LN	NT	NT	LN	INT	LN	LN	k	ΙN	Į	LN	NT	TN	EST HUMAN	NT	TN	LN	NT	LN-	Ę
Top Hit Acession		5.0E-90 AI222095.1	5.0E-90 A1222095.1	5.0E-90 AF114487.1	4506354 NT	5.0E-90 AL163201.2	5.0E-90 Z16411.1	5.0E-90 AF008915.1	5.0E-90 AB015617.1	5.0E-90 Z16411.1	9910365 NT	9910365 NT	5.0E-90 AF113708.1	5.0E-90 AF113708.1	4557258 NT	11345483 NT	11419429 NT	5.0E-90 AF123303.1	11433721 NT	7662051 NT	7662051 NT	5.0E-90 AB011399.1	5.0E-90 A1523366.1	4.0E-90 AF231920.1	4.0E-90 AF231920.1	4505316 NT	4.0E-90 X99033.1	6806918 NT	6806918 NT
Most Similar (Top) Hit BLAST E	Value	5.0E-90	5.0E-90	5.0E-90	5.0E-90	5.0E-90	5.0E-90	5.0E-90	5.0E-90	6.0E-90	5.0E-90	5.0E-90	5.0E-90	5.0E-90	5.0E-90	5.0E-90	5.0E-90	5.0E-90	5.0E-90	5.0E-90	5.0E-90	5.0E-90	5.0E-90	4.0E-90	4.0E-90	4.0E-90	4.0E-90	4.0E-90	4.0E-90
Expression Signal		1.07	1.07	2.37	4.51	0.78	2.85	0.72	1.32	1.88	0.95	0.95	2.04	2.04	7.98	4.89	1.17	0.71	99.6	0.53	0.53	1.77	4.54	2.04	2.04	4.36	13.42	0.74	0.74
ORF SEQ ID NO:		28116	28117		30784		32186	L	32307	32196	33430	33431	33905		34286	35107	36506	37133	37306		37363				59293			29114	29115
Exan SEQ ID	Š	15010	15010	15745	17797	17818	18901		19000			1			20797	21569	22922	23523	23697		23756	25659	Ш	13529	13529	14275	14874	16101	16101
Probe SEQ ID	Š	1864	1864	2622	4662	4683	5708	5726	5810	5886	6869	6869	7364	7364	7736	8488	9882	10488	10663	10723	10723	12948	13000	313	313	1110	1724	2923	2923

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	Top Hit Descriptor	Homo sepiens low density il poprotein-related protein 2 (LRP2), mRNA	Homo saniens law density lipoprotein-related protein 2 (LRP2), mRNA	11 consideration DNA for amylaid precursor protein, complete cds	Horing Salderia Crist in direction of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the se	United Sapirate 111 V.Y. C. 111.	Trullian production of the second protein 2 (LRP2), mRNA	Training supports that density increase the great protein 2 (LRP2), mRNA	Hamper and Annual Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of 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Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Cont	111 H RM 1 and 104 0-101 ST NCI OGAP Sub7 Home sapiens cDNA clone IMAGE:3083839 3	A112352467 NIH MGC 39 Homo sapiens aDNA clane IMAGE:3689147 5'	ANTO 67378F1 NIH MGC 10 Homo sapiens cDNA clone IMAGE:3453834 5	Home easing high-mobility group (nonhistone chromosomal) protein 17 (HMG17), mRNA	rights express user the contribution of the chicken of the company of the contribution of the contribution of the contribution of the contribution of the contribution of the contribution of the contribution of the contribution of the contribution of the contribution of the contribution of the contribution of the contribution of the contribution of the contribution of the contribution of the contribution of the contribution of the contribution of the contribution of the contribution of the contribution of the contribution 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to TR:075208 075208	BASSICS, JS NIT_MICS_TO LISING SEPTION HYPOTHETICAL 35.5 KD PROTEIN.;	Homo sapiens similar to laminin receptor 1 (67/t0), ribosomal protein SA) (H. sapiens) (LOC83484), mRNA	" LOC63484), mRNA increases (LOC63484), mRNA	Homo explets single to enjoy of the HMBA1004795 5	AU118985 HEMBAT Home saplens of the HEMBA1004795 5	AUTIOSOUTIEMIENT FISHER PROPERTIES (WYHA), mRNA	Homo sapients myosin, ileavy purpopular il	Horno sapiens amylaid beta (A4) precursor protein (protease nexin-II, Alzheimer disease) (APP), mRNA	Homo sapiens chromosome 21 unknown mKNA	Homo saplens chromosome 21 unknown mRNA	Homo sapiens mRNA for T-box transcription factor (TBX20 gene), partial	Homo sapiens mRNA for T-box transcription factor (T3X20 gene), partial	
	Top Hit Datebase Source								14 A 44 H . T	Ţ	7	7	בייום ביים	Z	ŁZ	NAMI LI FAAN	_'l	N.	Z.	Ę.	Z	EST HUMAN	Ł		N	EST HUMAN	EST HUMAN	NT NT	LN	Į.	ΙŁΖ	LZ.	Į.	
, 	Top Hit Acession No.	100000	NIG160080	3806918			٦	6806918 NT	69 18	T	1	T	Ī	5031748 N I	2.0E-90 5031748 NT			2.0E-90 AB006627.1	1V 00802/C	11625901 NT	11525901 N	.0E-90 AW672686.1	TN 0257320		11427320 NT	2.0E-90 AU118985.1	AU1189	11024711 NT	4502166 NT	AF23102	4 of on A Francisco 4	1.0E-90 AF 231920.1	A 1227 503.1	1.0E-90 (AJZJ) J09.1
	Most Similar (Top) Hit BLAST E		4.0E-90	4.0E-90	4.0E-90 D87675.1	4.0E-90 AB033070.1	4.0E-90 M	4.0E-90	4.0E-90	3.0E-90 BF516168.1	3.0E-90 B	3.0E-90 B	2.0E-90 B	2.0E-90	2.0E-90		2.0E-90 F	2.0E-90 /	2.0E-90	2.0E-90	2.0E-90	2.0E-90	20 20 0	70.7	2.0E-90	2.0E-90		2.0E-90	1 08-90		1			╛
	Expression Signal		0.93	0.93	3.63	2.1	1.91	1.74	1.74	0.91	0.94	28.7	4.5	6.48	6.48		2.95	1.05	10.18		9.0	380		0.99	0.99		1.46		,					3 1.92
	ORF SEQ E		29281	29282	30900	31037	31047	29114	29115	34638	34639	38619	26473	27421	L		30103	30930	31135	L	32396			30023	36824				_				26932	
	Excn SEQ ID NO:		16264	16264	17914	18049	18069	16101	16101	21118	21119	24916	13442	14362	14362		17106	1	ì	1	19084	1		23032	23032	1_	١.	L	<u> </u>	- 1	5 16983	_ 1		3 13895
	SEQ ID 8		3088	3088	4779	4919	4939	12885	12885	8036	8036	11930	228	1200	1200		3948	4811	5029	2899	5896		200	8863	8	10185	10165	11758		287	ě	386	71;	71.

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000		Rxpression		Top Hit Acession	Top Hit	Top Hit Descriptor
SEQ ID ORF SEQ Expression (10p) Hit SEQ ID NO: Signal BLAST E Value		(Top) H BLAST Value		No.	Database	
00.57	62.5		100	OE OO A F 284750 1	IN LN	Homo sapiens ALR-like protein mRNA, partial cds
26971	387		3 8			Homo sapiens ALR-like protein mRNA, partial cds
26972 17.93	17.93	-],	200	07070		Homo saplens Kruppel-like factor 7 (ubiquitous) (KLF7), mKNA
2,25	2,25		3 8	10201014 1001010 TO		Homo capiens protein phosphatase 2A BR gamma subunit gene, exon 3
3.46	3.46		3 3	1		Homo saplens protein phosphatase 2A BR garnma subunit gene, exch.
	3.46		ਗ਼	T	T LI IMAN	601159563F2 NIH MGC 53 Homo saplens cDNA clone IMAGE:3511118 5
2.61			σT	BE379884.1	NO TONIOL 1	Homo sapiens similar to SALL1 (sal (Drosophila)-like (LOC57167), mRNA
28195 3.73	3.73		$\sim 1$			Homo sabiens chromosome 8 open reading frame 2 (C8ORF2), mRNA
	6.46	7	ĀΤ	07/0000		Homo sabiens mRNA for KIAA0903 protein, partial cds
30112 0.59 1	0.59					Homo sabiens mRNA for KIAA0903 protein, partial cds
30113 0.59 1	0.59			.0E-90 AB020710.1	Z	Homo saniens soluble interleukin 1 receptor accessory protein (IL1RAP) gene, exon 8, alternative exons 9
1.0E-90	1.68			.0E-90 AF167340.1		and complete cds, alternatively opliced
32286 2.08	2.08			.0E-90 AB014533.1		Homo sapiens minura lot norther (KIAA0623), mRNA
32460 0.9	0.9		$\sim$ 1	11426910 NT		Homo saprens runnout y gone runner management management of the complete cds
33500 0.73	0.73			1.0E-90 U91934.1	Z	Long sanions solute carrier family 1 (high affinity aspartate/glutamate transporter), member 6 (SLC1A6),
	2.31			11426758 NT		mRNA
35640	3		7	11422086 NT	NT	Homo sapiens dreferum A-militario grammo sapiente des, alternatively spliced
0.92	0.92		$\overline{}$	AF1638	Į.	Homo sapiens CGI-15 protein (LOC51006), mRNA
36148 1.4	1.4	4 1.0E-90			Z	United Supplies (G1-15 profein (LOC51006), mRNA
36149 1.4	1.4	4 1.0E-9		11422109 N I	- Z	Halifo September 1 iver HebG2 cell line. Homo septems cDNA clone s3813'
30444 8.29	8.29			012234	ESI HUMAIN	Homo saplens makorin, ring finger protein, 1 (MKRN1), mRNA
. 35118 1.14	1.14			11419Z34 N	NA TOT	CAL BT043-090299-075 BT043 Homo sapiens cDNA
37153 0.65	0.65		<u>ن</u> ا	7.0E-91 Al904151.1	EST HOMBIN	Annhot st Soares fetal liver spleen 1NFLS St Homo sapiens cDNA clone (MAGE:448013 3
29744 1.85	1.85		مادث	5.0E-91 AA702794.1	TOT TOWN	A1143539 Y79AA1 Homo saciens cDNA clone Y79AA1002087 5
30755 1.14	1.14		~ 1	5.0E-91 AU143539.1	ESI TOMAN	71.14.3539 V79AA1 Homo saplens cDNA clone Y79AA1002087 5
30756 1.14	1.14			AU14353	EST HUMAN	House scalens chromosome 22 open reading frame 5 (C22ORF5), mRNA
31042 0.67	0.67				LN	Home sapers champsome 22 open reading frame 5 (C22ORF5), mRNA
31043	79'0		t Con I	1 7110634 NT	LN.	
1.25	1.25		ု တု	5.0E-91/AI878995.1	EST_HUMAN	au49f09.x1 Schnelder fetal brein 00004 Homo sapiens cDNA clone IMAGE:2518121 3' smilar to SW-ASPG FLAME Q47898 N4 (BETA-N-ACETYLGLUCOSAMINYL)-L-ASPARAGINASE PRECURSOR SW-ASPG FLAME A Flore IMAGE:4130933 5'
35000	133		ነማ	5.0E-91 BF314682.1	EST_HUMAN	1801901624F1 NIH _MGC_18
1 47	1 47		13	5 0E-91 AV649878.1	EST HUMAN	AV64987B GLC Homo sapiens curve close of control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and c
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Top Hit Descriptor	AV649878 GLC Homo saplens cDNA clone GLCBYF08 3' AV649878 GLC Homo saplens cDNA clone IMAGE:1744365 3' similar to contains	de/0f14.X1 Soares tetal lung Industriew monte separate des constructions and separate separate separate separate separate separate separate separate separate separate separate separate separate separate separate separate separate separate separate separate separate separate separate separate separate separate separate separate separate separate separate separate separate separate separate separate separate separate separate separate separate separate separate separate separate separate separate separate separate separate separate separate separate separate separate separate separate separate separate separate separate separate separate separate separate separate separate separate separate separate separate separate separate separate separate separate separate separate separate separate separate separate separate separate separate separate separate separate separate separate separate separate separate separate separate separate separate separate separate separate separate separate separate separate separate separate separate separate separate separate separate separate separate separate separate separate separate separate separate separate separate separate separate separate separate separate separate separate separate separate separate separate separate separate separate separate separate separate separate separate separate separate separate separate separate separate separate separate separate separate separate separate separate separate separate separate separate separate separate separate separate separate separate separate separate separate separate separate separate separate separate separate separate separate separate separate separate separate separate separate separate separate separate separate separate separate separate separate separate separate separate separate separate separate separate separate separate separate separate separate separate separate separate separate separate separate separate separate separate separate separate separate separate separate separate separate separate separate separat	MIK.b2 Mith MIK tepeninye erement. Homo seniens tysophosphatidic acid acytransferaso-delta (LPAAT-delta) mRNA, complete cds	Turing separation of the activities and anythransferase delta (LPAAT-delta) mRNA, complete cds	Home supplies yespitations are an applications and the supplies of the supplies of the supplies of the supplies of the supplies of the supplies of the supplies of the supplies of the supplies of the supplies of the supplies of the supplies of the supplies of the supplies of the supplies of the supplies of the supplies of the supplies of the supplies of the supplies of the supplies of the supplies of the supplies of the supplies of the supplies of the supplies of the supplies of the supplies of the supplies of the supplies of the supplies of the supplies of the supplies of the supplies of the supplies of the supplies of the supplies of the supplies of the supplies of the supplies of the supplies of the supplies of the supplies of the supplies of the supplies of the supplies of the supplies of the supplies 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Himman I Anna calcium channel beta-1 subunit (CACNLB1) gene, exons 10 and 11	Luman Lype calcum channel beta-1 subunit (CACNLB1) gene, exons 10 and 11	Homo sanlens ankyrin-like with transmembrane domains 1 (ANKTM1), mRNA	Human mRNA for very low density lipoprotein receptor, complete ods	
Top Hit Database Source	EST_HUMAN		EST HUMAN		LN	LZ	EST_HUMAN	EST_HUMAN	EST HUMAN		EST HUMAN	L	1	I N	Z	Z		2	L L	LV	İ	Ę	Ę		Į.	z	Z	Z P	Z Z
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Most Similar (Top) Hit BLAST E Value	5.0E-91 AV		5.0E-91 AI193566.1	4.0E-91 AF	4.0E-91 AF156778.1	4.0E-91 AL163284.2	4.0E-91 M77994.1	4.0E-91 M	4 oE-91 M77894.1	201	4.0E-91 M	3.0E-91	3.0E-91	3.0E-01 A	3.0E-91 A	3.0E-91 A	3.0E-91 A	3.0E-91 A	3.0E-91.N	3.05-91	1				- 1	١	1		
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Page 415 of 550 Table 4 Single Exon Probes Expressed in Placenta

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Top Hit Descriptor	Home seniens mRNA for KIAA0594 protein, partial cds	The continue mBNA for KTA41080 protein, partial cds	Horito Sapietis Film Visit Str. 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	Homo Sapiens mirana lar Nicha Joseph Promitir Promitire and Carlotte expn 6	Homo septents beta-unetoproblemase (BCI 1) going, com 6	Homo sapiens baka-urekopropina isao (oor 1) yaara ja	Homo septens chromosome 21 segment rioz 1004 Francisco Control (1973) 2000 Substitution captens cDNA clone IMAGE:2735280 3	UI-H-BI3-axe-d-01-0-01.s1 NCCGACGB3 I WIND CAPAIN SEC.	Homo sapiens hypothetical process (1975) Anno sapiens cDNA clone IMAGE:4157804 5'	SOCIONAL INC. COMP. 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Most Similar (Top) Hit BLAST E		3.0E-91 A	3.0E-91 A	3.0E-91 A	3.0E-91 A	3.0E-91 A	1.0E-91 A	1.0E-91 A	1.0E-91	1.0E-91	1.0E-91	1.0E-91 /	1.0E-91 H15212.1	9.0E-92 /	9.0E-92	9.0E-92	9.0E-92	9.0E-92	9.0E-92	9.0E-92	9.0E-92	9.0E-92													1
Expression Signal		0.73	1.49	1.49	8.54	8.54	2.94	2.74	0.78	1.96	1.96	1.48	1.5	5.77	5.77	0.68	5.86	2.62	3.77	0.55							1.43	1.43	0.68						5.05
ORF SEQ ID NO:		36108	38207	38208	31430		L			33640	33641	38814		27496		L	31820	32210	33127	34644	34645					3 26547	28119					8 33225			35235
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Page 416 of 550 Table 4 Single Exon Probes Expressed in Placenta

Source   Human lens membrane protein (mp19) gene, exon 11   Human lens membrane protein (mp19) gene, exon 11   Human lens membrane protein (mp19) gene, exon 11   Human lens membrane protein (mp19) gene, exon 11   Human sapiens transcription tender, RNA polymerase II (TTF2), mRNA   Human sapiens mRNA for MBNL protein   Human sapiens mRNA for MBNL protein   Human sapiens declare president and protein partial dos   Human sapiens declare mRNA for MA0785 protein, partial dos   Human sapiens mRNA for MA0785 protein, partial dos   Human van Willebrand fector pseudogene corresponding to seons 23 though 34   Human van Willebrand fector pseudogene corresponding to seons 23 though 34   Human van Willebrand fector pseudogene corresponding to seons 23 though 34   Human van Willebrand fector pseudogene corresponding to seons 23 though 34   Human van Willebrand fector pseudogene corresponding to seons 23 though 34   Human van Willebrand fector pseudogene corresponding to seons 23 though 34   Human van Willebrand fector pseudogene corresponding to seons 23 though 34   Human van Willebrand fector pseudogene corresponding to seons 23 though 34   Human van Willebrand fector pseudogene corresponding to seons 23 though 34   Human van Willebrand fector pseudogene corresponding to seons 23 though 34   Human van Willebrand fector pseudogene corresponding to seons 24 (ACTR2), mRNA   Human van Willebrand fector pseudogene to the season (SIGTSD) mRNA   Human sapiens 34 (ACTR2), mRNA   Human van van declare protein corresponding to the season (ACTR2), mRNA   Human value and the season (SIGTSD) mRNA   Human value and the season (SIGTSD) mRNA   Human value and the season (SIGTSD) mRNA   Human value and the season (SIGTSD) mRNA   Human value and the season (SIGTSD) mRNA   Human value and the season (SIGTSD) mRNA   Human value and the season (SIGTSD) mRNA   Human value and 33 dutocorrebellar atexa 3, divopontocerebellar atexa 3, autocomal dominant, dashor 3) (MND). mRNA   Human mRNA for sigha-actitin   Human mRNA for sigha-actitin   Human m	ORF SEQ Expression	Most Similar Expression (Top) Hit	Most Similar (Top) Hit	를	Top Hit Ace	slon	Top Hit Database	Top Hit Descriptor
TT T T T T T T T T T T T T T T T T T T	ORF SEQ Expression (Top) Hit Signal BLASTE Value	Expression (Top) Hit Signal BLAST E Value	(Top) Hit BLAST E Value		Top Hit Ace No.	rolss		Top Hit Descriptor
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T HUMAN	32028 1.59 8.0	1.59 8.0E-92	1.59 8.0E-92	8.0E-92		704	NT	Jomo sapiens fragile X mental retardation, autosome intrinsipy 1 (73.1), illings
T HUMAN	26328 1.91 7.0	1.91	1.91	2.0	M60676.1		Į.	-luman von Willebrand lactor pseudogene controlleraine de controlleraine de controlleraine de controlleraine de controlleraine de controlleraine de controlleraine de controlleraine de controlleraine de controlleraine de controlleraine de controlleraine de controlleraine de controlleraine de controlleraine de controlleraine de controlleraine de controlleraine de controlleraine de controlleraine de controlleraine de controlleraine de controlleraine de controlleraine de controlleraine de controlleraine de controlleraine de controlleraine de controlleraine de controlleraine de controlleraine de controlleraine de controlleraine de controlleraine de controlleraine de controlleraine de controlleraine de controlleraine de controlleraine de controlleraine de controlleraine de controlleraine de controlleraine de controlleraine de controlleraine de controlleraine de controlleraine de controlleraine de controlleraine de controlleraine de controlleraine de controlleraine de controlleraine de controlleraine de controlleraine de controlleraine de controlleraine de controlleraine de controlleraine de controlleraine de controlleraine de controlleraine de controlleraine de controlleraine de controlleraine de controlleraine de controlleraine de controlleraine de controlleraine de controlleraine de controlleraine de controlleraine de controlleraine de controlleraine de controlleraine de controlleraine de controlleraine de controlleraine de controlleraine de controlleraine de controlleraine de controlleraine de controlleraine de controlleraine de controlleraine de controlleraine de controlleraine de controlleraine de controlleraine de controlleraine de controlleraine de controlleraine de controlleraine de controlleraine de controlleraine de controlleraine de controlleraine de controlleraine de controlleraine de controlleraine de controlleraine de controlleraine de controlleraine de controlleraine de controlleraine de controlleraine de controlleraine de controlleraine de controlleraine de controlleraine de controlleraine de controll
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T HUMAN	1.68 7.0E-92 AF00782	1.68 7.0E-92 AF00782	1.68 7.0E-92 AF00782	7.0E-92 AF00782	AF00782	- 1	Ę	Homo sapiens cyclopiasum copiuso (Inc. 1981) mRNA
T HUMAN	27533 1.94 7.0E-92	27533 1.94 7.0E-92	1.94 7.0E-92	7.0E-92		삙	LN.	Homo sapiens D-ceil OLL/19/Information 2 Veast) homolog (ACTR2), mRNA
T_HUMAN	28619 3.85 7.0E-92	28619 3.85 7.0E-92	3,85 7.0E-92	7.0E-92		띩	N	Holling Saprens AND (actin related protein 2 yeast) homolog (ACTR2), mRNA
T_HUMAN T_HUMAN	28520 3.85 7.0E-92	28520 3.85 7.0E-92	3.85 7.0E-92	7.0E-92		21	NI.	Homo sapiens An 2 (actual containing protein S52 precursor, mRNA, complete cds
T_HUMAN T_HUMAN	6.13 7.0E-92 AF16770	28868 6.13 7.0E-92 AF16770	6.13 7.0E-92 AF16770	7.0E-92 AF16770	AF16770	- 10	IN I	Homo saplens NRAS-related gene (D1S155E), mRNA
T_HUMAN	29010 5.84 /.UE-92	29010 5.84 /.UE-92	5.84 7.0E-⊌Z	7.0E-92		J 19	1	Homo sariens T-cell Imphoma Invasion and metastasis 1 (TIAM1) mRNA
T_HUMAN	7.0E-92	29609 0.7 7.0E-92	0.7 7.0E-92	7.0E-92		219	- L	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
T HUMAN	0.7 7.0E-92	29610 0.7 7.0E-92	0.7 7.0E-92	7.0E-92		51		N.CAM=145 kda neural cel adhesion molecule [human, small cell lung cancer cell line OS2-R, mRNA, 29
T HUMAN	17845 30828 1.19 7.0E-92 S71824.1	30828 1.19 7	1.19	7	2 S71824.1	1	LN	nt International Colline OS2-R, mRNA, 26
T HUMAN T HUMAN	30829 1.19 7.0E-92   S71824.1	30829 1.19 7.0E-92   S71824.1	1.19 7.0È-92 S71824.1	7.0È-92 S71824.1	2 571824.1		N	N-CAMET 40 Kdd freutal certading modern [mmm.]
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T_HUMAN	5.51	31446 5.51	5.51	<u>L</u> .	2 AA446206.1	- 1	EST HUMAN	ZWOODIZETI Soares Jesus, Mili Home Appendigue ataxia 3. olivoponiocerebellar ataxia 3. autosom
T HUMAN	16313 28441 0.96 3.0E-92	28441 0.96 3.0E-92	0.96 3.0E-92	3.0E-92	11434	ξ	4 NT	Homo septens Machaelo-Joseph usease (spilloco-coco.) dominant, ataxin 3) (MJD), mRNA
HUMAN	1 F3 13 28442 0.98 3.0E-92	28442 0.86 3.0E-92	0.96 3.0E-92	3.0E-92		<u> </u>		Homo saplens Machado-Joseph disease (sunocerolia) archive dominant, atada 3) (MJD), mRNA dominant, atada 3) (MJD), mRNA archive archive IMAGE 3902899 57
HUMAN	29048	2048 2.74	2.74		12 BE909714.1		EST_HUMAN	601501242F1 NIH MGC (0 notified september 2014) September 10 similar to ribosomal protein S13
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	24084 37716 3.26	37716 3.26	3.26		12 X15804.1		N	Human mkNA for alpha acumin
	37717	37717 3.26	3.26		12 X15804.1		뇐	Human mkina tot alpha-tautini

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	Top Hit Descriptor	RC1-GN0021-240800-012-e11 GN0021 Homo sapiens cDNA	Homo sapiens activin A receptor, type IIB (ACVR2B) mRNA	Homo sapiens hypothetical protein dJ462023.2 (DJ462023.2), mRNA	Homo sapiens hypothetical protein dJ462023.2 (DJ462023.2), mRNA	601118337F1 NIH MGC 17 Homo sapiens cDNA clone IMAGE:3028304.57	601118337F1 NIH MGC 17 Homo sapiens cDNA clone IMAGE:3028304 5	mrg=mas-related [human, Cenomic, 2416 nt]	WKZ7d07.x1 NCI_CGAP_Bm25 Homo sepiens cDNA cione IMAGE:2413549 3' similar to TR:Q12844 Q12844 BREAKPOINT CLUSTER REGION PROTEIN :	WAZ7d07.x1 NCI_CGAP_Bm28 Homo sepiens cDNA clone iMAGE:2413549 3' similar to TR:Q12844 G12844 BREAKPOINT CLUSTER REGION PROTEIN	Homo sepiens trensforming growth factor hera 3 (TGER3) mRNA	Homo sepiens transforming growth factor, beta 3 (TGFB3), mRNA	Homo saplens syndecan 4 (amphiglycan raidocan) (SDC4) mRNA	Homo sapiens calcineurin binding protein 1 (KIAA0330) mRNA	Homo sapiens chromosome 21 unknown mRNA	Homo saplens chromosome 21 unknown mRNA	Homo sapiens stress-induced-phosphoprotein 1 (Hsp70/Hsp00-programma protein (CTTIP1) mRNA	Human endogenous retrovital DNA (4-1), complete retroviral segment	DKFZp434C0414 r1 434 (synonym: htee3) Homo caplens oDNA clone DKFZp434Cn414 5	Homo sapiens P-glycoprotein (mdr1) mRNA, complete cds	Homo saplens Integrin, alpha L (antigen CD11A (p180), lymphocyte function-associated antigen 1; alpha	Homo saniens mRNA for KIAA 1068 protein partial cds	Human NPV Y1-like recentre oseudopene mRNA complete ode	Human NPY Y1-like receptor pseudogene mRNA, complete cds	hd02h02.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2908371 3' similar to TR:002711	002711 PRO-POL-DUTPASE POLYPROTEIN;	Homo sapiens thyroid stimulating hormone receptor (TSHR), mRNA	Homo sapiens zinc finger protein 198 (ZNF198), mRNA	CM4-LT0028-161299-062-g06 LT0026 Homo sapiens cDNA	CM4-LT0026-161299-062-g06 LT0026 Homo saplens cDNA	Homo sapiens mRNA for KIAA1093 protein, partial cds
	Top Hit Database Source	EST HUMAN	L	Ę	TN	T HUMAN		Г	EST HUMAN						LN	ħ			EST HUMAN	Π					П	HUMAN				T_HUMAN	TN T
	Top Hit Acession No.	BF367138.1	4501898 NT	11422948 NT	11422946 NT	2.0E-92 BE299190.1	2.0E-92 BE299190.1	2.0E-92 S78653.1	2.0E-92 AI818119.1	2.0E-92 AI818119.1	07464	4507464 NT	4506860 NT	6912457 NT	2.0E-92 AF231919.1	2.0E-92 AF231919.1	5803180 NT			2.0E-92 AF016535.1	450475B NT	2.0E-92 AB028991.1				2.0E-92 AW340174.1	11434900 NT	4759			2.0E-92 AB029016.1
	Most Similar (Top) Hit BLAST E Value	3.0E-92	2.0E-92	2.0E-92	2.0E-92	2.0E-92	2.0E-92	2.0E-92	20E-92	2.0E-92	2.0E-92	2.0E-92	2.0E-92	2.0E-92	2.0E-92	2.0E-92 /	2.0E-92	2.0E-82 M10976.1	2.0E-92	20E-92	2.05-92	20E-92/	2.0E-92 U67780.1	2.0E-92 U67780.1	200	2.05-92	2.0E-92	2.0E-92	2.0E-92 A	2.0E-92 A	2.0E-92
	Expression Signal	1.67	1.54	4.28	4.28	5.49	5.49	1.62	2.53	2.53	1.01	1.01	5.35	22.36	1.02	1.02	7.02	1.17	4.1	0.64	7 19	26	0.61	0.64	6	1.26	4.68	3.22	5.71	5.71	8.46
	ORF SEQ ID NO:					26897			28236	28237	28265	28266	28366	28954	29864	29865	29944	30530		32377		33297			05600	33080	37/09	37965	38134	38135	32035
	Exon SEQ ID NO:							14901	15132	15132	15161	15161	15245	15843	16862	16862	16938	17546	18236	19069	19599	19904	20697	20697		- 1	- }	24326	24470	24470	25502
	Probe SEQ ID NO:	12878	92	183	183	768	768	1752	. 1990	1990	2020	2020	2106	2725	3701	3701	3777	4403	5108	5879	6431	6748	7627	7657	9900	ocna Cona	/880L	1125/	1409	11409	12758

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	Top Hit Descriptor	Homo sapiens adenylosuccinate lyase gene, complete cds	Homo saplens calcineurin binding protein 1 (KIAA0330), mRNA	wane 08 r1 Source placenta Nb2HP Homo sapiens cDNA clone IMAGE: 143374 5	WROEGR 1 Scares placenta Nb2HP Homo saplens cDNA clone IMAGE:145574-5	Home saniens ribosomal protein, large, P1 (RPLP1) mRNA	HTM1-288F HTM1 Homo sapiens cDNA	houtboz x1 NCI CGAP CLL1 Homo saplens cDNA clone IMAGE:2107467 3 Similar to contains element	Q16825 PROTEIN-TYROSINE PHOSPHATASE D1 ;contains Alu repeutive delinous contains Alu repeutive delinous contains Alu repeutive delinous contains Alu repeutive delinous contains Alu repeutive delinous contains Alu repeutive delinous contains Alu repeutive delinous contains Alu repeutive delinous contains Alu repeutive delinous contains Alu repeutive delinous contains Alu repeutive delinous contains Alu repeutive delinous contains Alu repeutive delinous contains Alu repeutive delinous contains Alu repeutive delinous contains Alu repeutive delinous contains Alu repeutive delinous contains Alu repeutive delinous contains Alu repeutive delinous contains Alu repeutive delinous contains Alu repeutive delinous contains Alu repeutive delinous contains Alu repeutive delinous contains Alu repeutive delinous contains Alu repeutive contains Alu repeutive contains Alu repeutive contains Alu repeutive contains Alu repeutive contains Alu repeutive contains Alu repeutive contains Alu repeutive contains Alu repeutive contains Alu repeutive contains Alu repeutive contains Alu repeutive contains Alu repeutive contains Alu repeutive contains Alu repeutive contains Alu repeutive contains Alu repeutive contains Alu repeutive contains Alu repeutive contains Alu repeutive contains Alu repeutive contains Alu repeutive contains Alu repeutive contains Alu repeutive contains Alu repeutive contains Alu repeutive contains Alu repeutive contains Alu repeutive contains Alu repeutive contains Alu repeutive contains Alu repeutive contains Alu repeutive contains Alu repeutive contains Alu repeutive contains Alu repeutive contains Alu repeutive contains Alu repeutive contains Alu repeutive contains Alu repeutive contains Alu repeutive contains Alu repeutive contains Alu repeutive contains Alu repeutive contains Alu repeutive contains Alu repeutive contains Alu repeutive contains Alu repeutive contains Alu repeutive contains Alu repeutive contains Alu repeutive contains Alu repeutive contains Alu repeutive contains Alu repeutive contains Alu repeut	MEKT / repearate contents.  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MER17 repetitive element: AI 127881 MAMMA1 Homo sapiens cDNA clone MAMMA1000738 5'	FST188414 HCC cell line (matastasis to liver in mouse) il Homo sapiens cDNA 5' end similar to ribosomia.	protein L29	Home Aginal is vaccing.	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Single Exon Propes Express	Top Hit Database Source			MANN	TOT LINAN	NO PORTOR INC.	EST HIMAN	EST TIGINGS		EST HUMAN		EST HUMAN	ESI HUMAN	EST HUMAN	1	EST HUMAN	IN I	EST HUMAN	N <sub>T</sub>	TNIS	NT	LN LN	١ ١	EST_HUMAN	EST HUMAN	N N	TN	LN LN	N T		TN
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	Most Similar (Top) Hit BLAST E	ones	2.0E-92 AF	2.0E-92	1.0E-92 R78078.1	1.0E-92 R78078.	1.0E-92	1.0E-92 B		1.0E-92 A		1.0E-92 A	9.0E-93 /	9.0E-93		9.0E-93/	9.00-93	9.0E-93	7 0 1 03	00 00	8 OF 93	20 TO 8	5.0E-93	5.0E-93	5 0E-93	5 0F-93		1			
	Expression (		1.36	73.58	2.95	2.95	35.12	0.82		3.24		3.24	3.53	20.41		1.69	1.35	7.79	4.2.4	67.7	47.0	10.0	40.7	4.61	4 84	1			3.73		1.75
	ORF SEQ EX		32005	28954	28150	28151	28392	35051	-	35999		36000					29867			1						2 27007		1	79 29500		- 0
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	Probe E SEQ ID SI		12782	13086	1897	1807	2435	8441		9365		8960	2085	3	2700	2712	3703	11947	6723	256	3144	6819	7056	1412	1439	1439	1504	1860	3305	5920	6235
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	Top Hit Descriptor	Homo sapiens protein phosphatase-1 regulatory subunit 7 (PPP-1R7) gene, exxn 11, complete ods and alternatively spliced product	Homo seplens discs, large (Drosophila) homolog 2 (chapsyn-110) (DLGZ) mKNA	Homo saplens discs, large (Drosophila) homolog z (cnapayn-110) (u.e.s.) minno	Homo sapiens secretory pathway component Sec31B-1 mRNA, alternatively spliced, complete cds	Homo saplens TAR (HIV) RNA-binding protein 1 ( I AKBP 1) minna	Homo sapiens WSB1 protein (WSB1) mRNA, complete das	Homo saplens nucleobingin 2 (Nucez.), may have	Homo sapiens gamma-glutamywansierasa 1 (GOT1), miwwa Abab Mace-705688 3' similar to SW-CLPA RAT	zz60e09.s1 Soares, restis, INT I Harito Sapleris, CLIVA Chile Infance 100000 Climina	Homo sapiens interferon gamma receptor 1 (IFNGR1) mRNA	Homo saplens interferon gamma receptor 1 (IFNGR1) mIXNA	Homo sapiens pescadillo (zebrafish) homolog 1, contaming broot dunian (* Ed.), missy.	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2578	L	02	1.29		1.0E-93 AL137200.1	₽ <u>N</u>	NOVE INITIAL POLICIPATION OF CONTRACT OF CONTRACT SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERV
288	ı	80 27546	1.32		1.0E-93 BE297369.1	EST HUMAN	6011/7660F1 NIT MOC 17 TOTAL Services CDNA Clone IMAGE:3532965 5
0000	١		132		1_0E-93 BE297369.1	EST_HUMAN	6011/7686F1 NIH_MCC_II HOIRO SERVIS COLOR
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	Г	Γ	Т	Т	Т	T	T	Т		Т	Т	Γ	Т	T.	1-	Т	Γ	Т	Г	Г	Т	Π	Г	Г	T	7	Г	Г	Г	П		
Top Hit Descriptor	Homo saplens DNA for amyloid precursor protein, complete cds	Homo saplens long chain polyunsaturated fatty acid elongation enzyme (HELO1) mRNA, complete ads	Homo sapiens chromosome 21 segment HS21C084	Homo sapiens estrogen receptor alpha (ESR1) gene, exon 6	Homo sapiens estrogen receptor alpha (ESR1) gene, exon 6	Homo sapiens glucccorticoid receptor (GRL) gene, intron D, exon 5, and intron E	Homo sapiens glucocorticoid receptor (GRL) gene, intron D, exon 5, and intron E	Homo sapiens candidate taste receptor T2R14 gene, complete cds	Homo saplens neurofibromin 1 (neurofibromatosis, von Recklinghausen disease, Watson disease) (NF1) mRNA	Homo sapiens KIAA0672 gene product (KIAA0672), mRNA	Homo sapiens protein kinase C, beta 1 (PRKCB1), mRNA	Human mRNA for NF1 N-isoform-exon11, complete cds	Homo sapiens mRNA for KIAA1411 protein, partial cds	H.sapiens mRNA for MEMD protein	Homo sapiens protein kinase inhibitor gamma (PKIG) mRNA, complete cds	Homo sapiens mRNA for KIAA1485 protein, partial cds	Homo sapiens Trio isoform mRNA, complete cds	Human PreA4 gene for Alzheimer's disease A4 amyloid protein precursor (exon 9)	Human PreA4 gene for Alzhelmer's disease A4 amyloid protein precursor (excn 9)	Novel human gene mapping to chomosome 13, similar to rat RhoGAP	Homo sapiens ryanodine receptor 3 (RVR3), mRNA	Homo sapiens GGT1 gene, exon 1	Homo sapiens glutathione S-transferase theta 2 (GSTT2), mRNA	Homo sepiens calcineurin binding protein 1 (KIAA0330), mRNA	Homo saplens glutathione S-transferase theta 2 (GSTT2) and glutathlone S-transferase theta 1 (GSTT1)	genes, complete cds	Homo sapiens chromosome 21 segment HS210009	Homo sapiens transcription enhancer factor-5 mRNA, complete cds	Homo sapiens mRNA for KIAA0612 protein, partial cds	Homo sapiens mRNA for KIAA0612 protein, partial cds	zg87g06.s1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:4095943'	ot83d05.s1 Soares_total_feitus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:1623369 3*
Top Hit Database Source	LN	Ę	N L	NT	Z	Z.	N	N	LN	LN	LN.	LN	LN	LN	LN	LN LN	Ę	Z	TN	IN	Į.	NT	L	N		NT	NT	NT	NT	NT	EST_HUMAN	EST HUMAN
Top Hit Acession No.	)87675.1	1.0E-93 AF231981.1	1.0E-93 AL163284.2	1.0E-93 AF123498.1	1.0E-93 AF123498.1	178509.1	178509.1	1.0E-93 AF227138.1	4557792 NT	7862241 NT	11431590 NT	142072.1	1.0E-93 AB037832.1		1.0E-93 AF182032.1	1.0E-93 AB040918.1	1.0E-93 AF091395.1			1.0E-93 AL049801.1	11433646 NT	1.0E-93 AJ230125.1	11417856 NT	11417862 NT					5.0E-94 AB014512.1			5.0E-94 AI015800.1
Most Similar (Top) Hit BLAST E Value	1.0E-93 D87675.1	1.0E-93	1.0E-93 /	1.0E-93 /	1.0E-93 /	1.0E-93 U78509.1	1.0E-93 U78509.1	1.0E-93	1.0E-93	1.0E-93	1.0E-93	1.0E-93 D42072.1	1.0E-93 A	1.0E-93 Y10183.1	1.0E-93	1.0E-33 A	1.0E-93 A	1.0E-93 X13474.1	1.0E-93 X13474.1	1.0E-33 A	1.0E-93	1.0E-93	1.0E-93	1.0E-93		1.0E-93	8.0E-94 A	8.0E-94 A	5.0E-94 A	5.0E-94	5.0E-94 A	5.0E-94 A
	5.86	1.23	3.28	0.92	0.92	2.39	2.39	1.2	10.78	8.4	1.94	3.24	2.29	1.15	1.14	2.03	1.14	3.9	3.9	1.24	0.59	1.62	3.71	1.36	,	1.42	1.13	1.94	3.51	3.51	2.24	1.45
R <sub>O</sub> ⊕	29197		89906	31428	31427		32168	32383	32543	32855	33679	33946	35066	35353	35468	34608	34612	36403	36404	38555	36994			31941				30233	31698	31699	32696	33726
_ <u> </u>	16176	16461			18461		1	19074	19220	19498	20246	20478	21536	21819	21929	21094		22827	22827	22966	23384	25547	25608	25723		- (		_1	18682	18682	19349	20285
Probe SEQ ID NO:	3000	3287	4549	5348	5348	5684	5684	5885	2009	6326	1569	7400	8455	8740	0988	9651	9665	8787	9787	9265	10349	12820	12923	13108	30,00	13725	10819	4070	5483	5483	6173	7150

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Table 4
Single Exon Probes Expressed in Placenta

Single Exon Probes Expressed in Placenta	Top Hit Descriptor	601111696F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3352569 5'	601111696F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3352559 5'	Homo sapiens hypothetical protein (FLJ20746), mRNA	Escherichia coli K-12 MG1655 section 159 of 400 of the complete genome	DKFZp434G0314_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434G0314 5'	y/87f02.r1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:45053 5'	AV725992 HTC Homo sapiens cDNA clone HTCBEF05 5	Homo saplens chromosome 21 segment HS21C004	Homo sapiens chromosome 21 segment HS21C004	Homo sapiens paired box gene 5 (B-cell lineage specific activator protein) (PAX5), mRNA	601468748F1 NIH_MGC_67 Home sapiens cDNA clone IMAGE:3872099 5'	Homo sepiens II1 receptor antegontst II1Ra (II1RN) gene, afternatively spliced forms, complete ods	ap22e02.x1 Schiller digoderdroglioma Homo sepiens cDNA clone IMAGE:1956122 3' similar to TR.Q62845	GOZG45 NEOTAL CELL ALATESTON FINE DICE PRECURSUR.;	Homo saptens KIAA0164 gene product (KIAA0164), mRNA	601175762F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3531038 5'	601175762F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3531038 5'	Homo sapiens TNF-alpha stimulated ABC protein (ABC50) mRNA, complete cds	Homo sapiens KIAA0255 gene product (KIAA0255), mRNA	Homo saplens KIAA0255 gene product (KIAA0255), mRNA	Mmusculus glyT1 gene (exons 1c and 2)	M.musculus glyT1 gene (exons 1c and 2)	Homo sapiens progressive ankylosis-like protein (ANK) mRNA, complete cds	Homo sapiens carbamyl phosphate synthetase I mRNA, complete cds	we09e04.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2340606 3' similar to gb:K00558 TUBULIN ALPHA-1 CHAIN (HUMAN);	we09e04.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2340606 3' similar to gb:K00558	TUBULIN ALPHA-1 CHAIN (HUMAN);	Homo sapiens KIAA0183 gene product (KIAA0193), mRNA	Homo sapiens proteasome (prosome, macropain) 26S subunit, non-ATPase, 11 (PSMD11), mRNA	Homo sapiens proteasome (prosome, macropain) 26S subunit, non-ATPase, 11 (PSMD11), mRNA	Homo sapiens potassium channel subunit (HERG-3) mRNA, complete cds	Homo saplens KIAA0255 gene product (KIAA0255), mRNA
Exon Propes	Top Hit Database Source	EST_HUMAN 6	Г		NT					±N ±N		EST_HUMAN 6	IN TN	т	NAMOR 103	7		THUMAN	IN			NT IN	LN	TN	NT TN	EST HUMAN T	Г	T_HUMAN					
Single	Top Hit Acession No.	1.0E-94 BE263433.1	1.0E-94 BE253433.1	9506692 NT		(1		1.0E-94 AV725992.1		1.0E-94 AL163204.2	11428710 NT	1.0E-94 BE780478.1			1.0E-94 AIZ/ ZZ44.1	18871		1.0E-94 BE295714.1	9.0E-95 AF027302.1	7662027 NT	7662027 NT			9.0E-95 AF274753.1	8.0E-95 AF154830.1	8.0E-95 AI700998.1		8.0E-95 AI700998.1	11419376 NT	11426529 NT	11426529 NT	8.0E-95 AF032897.1	11420944 NT
	Most Similar (Top) Hit BLAST E Value	1.0E-94	1.0E-94	1.0E-94	1.0E-94	1.0E-94	1.0E-94 H08270.1	1.0E-94	1.0E-94	1.0E-94	1.0E-94	1.0E-94	1.0E-94 U65590.1	10,	1.05-94/	1.0E-94	1.0E-94	1.0E-94	9.0E-95	9.0E-95	9.0E-95	9.0E-95 X82569.1	9.0E-95 X82569.1	9.0E-95	8.0E-95	8.0E-95		8.0E-95	8.0E-95	8.0E-95	8.0E-95	8.0E-95/	8.0E-95
	Expression Signal	2.05	2.05	1.11	0.69	1.94	0.82	0.68	0.8	0.8	2.17	1.35	3.11	-	0.5	1.34	2.02	1.73	6.05	1.09	1.09	1.46	1.46	1.58	2.9	1.68		1.68	0.73	1.4	1.4	2.08	1.98
	ORF SEQ ID NO:	29342								34909	36138	36620	38028	70000	1000	١	١	28410						35054	26407	30778		Ì			33935	34998	36273
	Exen SEQ ID NO:	16333									22572	1	24384	04650	2000	_ [	ı						- 1	21527	13374	17794		- 1	20181		L	21472	22707
	Probe SEQ ID NO:	3158	3158	4478	6198	9396	6405	6648	8304	8304	9426	0666	11321	44507	100	12051	12639	12968	1506	3224	3224	5521	5521	8446	149	4658		4658	7087	7390	7390	8391	9565

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					, 		
Probe SEQ ID NO:	Exen SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Velue	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
9565		36274	1.98	8.0E-95	11420944 NT	LN	Homo saplens KIAA0255 gene product (KIAA0255), mRNA
10053	23091	26998	2,45	8.0E-95	5174644 NT	FN	Homo sapiens proline dehydrogenase (proline oxidase) (PRODH) mRNA
10083			2.92	8.0E-95	8.0E-95 AB037816.1	NT	Homo sapiens mRNA for KIAA1395 protein, partial cds
10440			0.81	8.0E-95	9845523 NT	TN	Homo sapiens early growth response 2 (Krox-20 (Drosophila) homolog) (EGR2), mRNA
10953		37670		8.0E-95	AF112152.1	NT	Homo saplens developmental arteries and neural crest EGF-like protein mRNA, complete cds
11773			1.72	8.0E-95	10864024 NT	N	Homo saplens HCF-binding transcription factor Zhangfel (ZF), mRNA
11982		38669	1.32	8.0E-95	7019572 NT	NT	Homo sapiens zinedin (ZIN), mRNA
11982	24967	38670		8.0E-95	7019572 NT	FN	Homo sapiens zinedin (ZIN), mRNA
10007			70 57	100			zu84b01.s1 Sogres_testis_NHT Homo sapiens cDNA clone IMAGE:744649 3' similar to contains L1.t1 L1
/007			17.71	8.05-90	8.0E-95 AA629056.1	ESI HUMAN	repenuve erement
286		26537	6.07	7.0E-95		۲	Homo sapiens DNA for amylold precursor protein, complete cds
286			6.07	7.0E-95	7.0E-95 D87675.1	INT	Hamo sapiens DNA for amyloid precursor protein, complete cds
2519	15645		1.37	7.0E-95		INT	Human hepatocyte growth factor gene, exon 8
2519	16645	28768	1.37	7.0E-95	7.0E-95 M75973.1	N	Human hepatocyte growth factor gene, exan 8
4486				7.0E-95		K	Homo sapiens Ly-6-like protein (CD59) mRNA, complete cds
4535			1.09	7.0E-95	7.0E-95 AL163246.2	NT.	Homo sapiens chromosome 21 segment HS21 C046
9418		89098		4.0E-95	4.0E-95 BE439625.1	EST_HUMAN	HTM1-288F HTM1 Homo sapiers cDNA
215	. :			3.0E-95	3.0E-95 AV648361.1	EST_HUMAN	AV648361 GLC Homo sapiens cDNA clone GLCBIF01 3'
9228	18756	31794	1.52	3.0E-95	3.0E-95 BF526041.1	EST HUMAN	602071146F1 NCI_CGAP_Brn64 Hamo sapiens cDNA clone IMAGE:4214147 5
5791		32285		3.0E-95	4503354 NT	LΝ	Homo sapiens dedicator of cyto-kinesis 1 (DOCK1) mRNA
7315	_		67.0	3.0E-95	3.0E-95 AA412321.1	EST_HUMAN	zi97d01.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:730273 5'
7315	20397	33860	67.0	3.0E-95	3.0E-95 AA412321.1	EST_HUMAN	ZI97d01.r1 Soares_testis_NHT Homo saplens cDNA clone IMAGE:730273 5'
7525				3.0E-95	3.0E-95 AW958121.1	EST_HUMAN	EST370191 MAGE resequences, MAGE Homo sapiens cDNA
7525	20598	34072	2.01	3.0E-95	3.0E-95 AW958121.1	EST_HUMAN	EST370191 MAGE resequences, MAGE Hamo sapiens cDNA
9556			1.62	3.0E-95	1062289 NT	N	Homo saplens KIAA0763 gene product (KIAA0763), mRNA
9555		36191	1.62	3.0E-95	10682289 NT	LN.	Homo saplens KIAA0763 gene product (KIAA0763), mRNA
9948	1		98.0	3.0E-95	3.0E-95 BF213446.1	EST_HUMAN	601845212F1 NIH_MGC_55 Homo saplens cDNA clone IMAGE:4070451 5'
1676	14828	27911	3.52	2.0E-95	TM 720207	F	Homo sapiens KIAA0255 gene product (KIAA0255), mRNA
1676	14828	27912		2.0E-95	7662027 NT	LN	Homo sapiens KIAA0255 gene product (KIAA0255), mRNA
2005	15136	CPCBC	76 87	2.05-95	TN:0157054	Į.	Homo sepions tissue inhibitor of metalloproteinase 3 (Sorsby fundus dystrophy, pseudoinflammatory) (TIMP3) mBNA
	1						1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
1998			3		BE39387	EST HUMAN	601312161F1 NIH_MGC_44 Homo septens CDNA clone IMAGE:3658862 5
2497						Ę	Homo sapiens G protein-coupled receptor 19 (GPR19) mRNA
2497	15624	28744	1.5	2.0E-95	5453665 NT	FN	Homo sapiens G protein-coupled receptor 19 (GPR19) mRNA

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Characteristics and the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second	Top Hit Descriptor	Homo sapiens glutathlone S-transferase theta 2 (GSTT2) and glutathlone S-transferase theta 1 (GSTT1)	Home society of this is	yadodn8 od Sonos Infort Lead Allih III	Home series (ferrels	Home canians incommendant	Homo sapiens unconveniend myosin-19 (LOC51168), mRNA	Homo sepiens mRNA for K/a4/328 section 21 12 12 12 12 12 12 12 12 12 12 12 12	qm01c02x1 Soares_NhHMPu_S1 Homo saptens cDNA clone IMAGE:1880546 3' similar to WP:T23G7.4	Home seniors hard - for	Source September (19532281A), mRNA	Honto Septens NAAU BY gene product (KIAA0187), mRNA Homo septens S164 gene, partial cds; PS1 and hypothetical protein genes, complete cds; and S171 gene.	Parital cos	The first septents cyst 48 protein (LOC31096), mRNA	Homo sapiens CGI-48 protein (LOC51096), mRNA	rrono sapiens angiotensin I converting enzyme (peptidy)-dipeptidase A) 2 (ACE2), mRNA	Homo sapiens anglotensin I converting enzyme (peptidyt-dipeptidase A) 2 (ACE2), mRNA	Homo saplens membrane protein, palmitovlated 3 (MAGLIK neft sulfamiliy membor e) //upp.o	Human muscle type phosphofructokinase (PFK-M) nene axxv 7	Homo sapiens transcription factor 2, hepatic: LF-83; variant henatic purchar factor (TCE2) mBNA	Homo sapiens transcription factor 2, hepatic; LF-B3; variant hepatic nuclear factor (TCF2) mRNA	Homo sapiens cillary dynein heavy chain 9 (DNAH9) mRNA, complete cds	Homo sapiens huntingtin (Huntington disease) (HD), mRNA	Homo sapiens ribophorin il (RPN2), mRNA	Homo sapiens KIAA 1065 protein (KIAA 1065), mRNA	Homo saplens bone morphogenetic protein receptor, type IA (BMPR1A) mRNA	Homo sapiens Ste20-related serina/threonine kinase (KIAAD20A) mRNA	Homo sapiens KIAA0763 gene product (KIAA0763) mRNA	Homo saplens KIAA0763 gene product (KIAA0763) mBNA	Homo sapiens HSPC302 mRNA, partial cds	Homo sapiens glutatrione S-transferase theta 2 (GSTT2) and glutatrione S-transferase theta 1 (GSTT1)	
ממין וומצין מ	Top Hit Database Source	TM	NT.	EST HIMAN		LN	Į.	LN.	FST HIMAN	FX	L	L L	12	17	12															LZ	E	
	Top Hit Acession No.	AF240788 1	4758423 NT	R16245.1	AF015452 1	TV0590017		AB03780	A1290264.1	7657185 NT	TREADZOINT	AF10aan7 1	15764	7705784 NT	1103Ferial	4400000	INISONOCZZI.I		A59724.1	11427182 NT	11427182	-257737.1		11421795N1	11434330 NT	4757853 NT	7661993 NT	7662289 NT	7662289 NT	F161420.1	-240786.1	
	Most Similar (Top) Hit BLAST E Value	2.0E-95	2.0E-95	2.0E-95	2.0E-95	2.0E-95	2.0E-95	2.0E-95	2.0E-95	2.0E-95	20F-95	2.0E-95	20E-95	2.0E-95	2.0F-95	200.00	Z:0E-30	2.05-35	2.0E-95.N	2.0E-95	2.0E-95	2.0E-95 A	2.05-93	2.0E-30	2.0E-95	2.0E-95	2.0E-95	2.0E-95	2.0E-95	2.0E-95/A	2.0E-95 A	
	Expression Signal	3.62	1.34	66.0	2.1	3.6	3.6	0.81	0.62	1.36	3.5	0.99	4.12	4.12	1.24	1 24		0.63	3.86	0.9	6.0	0.60	74.7	Q	96.0	98.	1.35	1.69	1.69	1.57	2.31	
	ORF SEQ ID NO:		28826					29870	30006	30602	31242	31321	31840	31841	32310	32311	0.00	70070	32793	33122	33123	33847	35073	07000	37270	0/0/0	37836	38691	38692		32047	
	SEQ ID NO:	15661		1	16400		- {	16867	17004		18273	18352		18792	19005	19005	1	2	1944	18/41	10858	2021R	22410	23627	24042	2 0	01747	74967	24987	26083	25407	
	Probe SEQ ID NO:	2536	2582	2862	3226	3655	3655	3706	3844	4481	5151	5230	5597	5597	5815	5815	RREK	3	278	8/20	6700	8003	9343	10502	10082	1,130	2 3	7007	12002	12103	12608	

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	Top Hit Descriptor	Loons canifers hypothetical protein (HS322B1A), mRNA	Homo sapiens adenylosuccinate lyase (ADSL), missis Homo sapiens cDNA clone IMAGE.714007 5' similar to Homo sapiens cDNA clone IMAGE.714007 5' similar to	723h04.r1 Soares over y comments.	TR:G106/054 Cross overy fumor NbHOT Homo sapiens cown comments over Sources overy fumor NbHOT Homo sapiens cown comments over the same sapiens cown comments over the same sapiens cown comments over the same sapiens cown comments over the same sapiens cown comments over the same sapiens country over the same sapiens country over the same sapiens country over the same sapiens country over the same sapiens country over the same sapiens country over the same sapiens country over the same sapiens country over the same sapiens country over the same sapiens country over the same sapiens country over the same sapiens country over the same sapiens country over the same sapiens country over the same sapiens country over the same sapiens country over the same sapiens country over the same sapiens country over the same sapiens country over the same sapiens country over the same sapiens country over the same sapiens country over the same sapiens country over the same sapiens country over the same sapiens country over the same sapiens country over the same sapiens country over the same sapiens country over the same sapiens country over the same sapiens country over the same sapiens country over the same sapiens country over the same sapiens country over the same sapiens country over the same sapiens country over the same sapiens country over the same sapiens country over the same sapiens country over the same sapiens country over the same sapiens country over the same sapiens country over the same sapiens country over the same sapiens country over the same sapiens country over the same same sapiens country over the same same same same sapiens country over the same same same same same same same sam	TR:G1067084 G1067084 F55H2.6;	RCS-FN0019-290600-011-011 11100-04 Homo sapiens cDNA	Indepto in Source Infant brain 1NIB Home sapieris com IMAGE:3922423 5	601437232F1 NIH MGC 72 Homo sapriens cDNA clone IMAGE:3899761 5	1601497608F1 NIH, MGC 70 Hours satisfies CDNA clone IMAGE:3899701 3	601497608F1 NIH MGC 70 Homo sapiens cDNA	1	П	_	П	Human grycus dene product (KIAAU 102), III.	Homo saplens Kildrot of Series product (KIAA0763), mRNA	Homo sapiens NIAAV to 3 - Seletal muscle, adult (missing most), heavy polypeptide 2, skeletal muscle, adult (missing most), heavy polypeptide 2, skeletal muscle, adult (missing most), heavy polypeptide 2, skeletal muscle, adult (missing most), heavy polypeptide 2, skeletal muscle, adult (missing most), heavy polypeptide 2, skeletal muscle, adult (missing most), heavy polypeptide 2, skeletal muscle, adult (missing most), heavy polypeptide 2, skeletal muscle, adult (missing most), heavy polypeptide 3, skeletal muscle, adult (missing most), heavy polypeptide 3, skeletal muscle, adult (missing most), heavy polypeptide 3, skeletal muscle, adult (missing most), heavy polypeptide 3, skeletal muscle, adult (missing most), heavy polypeptide 3, skeletal muscle, adult (missing most), heavy polypeptide 3, skeletal muscle, adult (missing most), heavy polypeptide 3, skeletal muscle, adult (missing most), heavy polypeptide 3, skeletal muscle, adult (missing most), heavy polypeptide 3, skeletal muscle, adult (missing most), heavy polypeptide 3, skeletal muscle, adult (missing most), heavy polypeptide 3, skeletal muscle, adult (missing most), heavy polypeptide 3, skeletal muscle, adult (missing most), heavy polypeptide 3, skeletal muscle, adult (missing most), heavy polypeptide 3, skeletal muscle, adult (missing most), heavy polypeptide 3, skeletal muscle, adult (missing most), heavy polypeptide 3, skeletal muscle, adult (missing most), heavy polypeptide 3, skeletal muscle, adult (missing most), heavy polypeptide 3, skeletal muscle, adult (missing most), heavy polypeptide 3, skeletal muscle, adult (missing most), heavy polypeptide 3, skeletal muscle, adult (missing most), heavy polypeptide 3, skeletal muscle, adult (missing most), heavy polypeptide 3, skeletal muscle, adult (missing most), heavy polypeptide 3, skeletal muscle, adult (missing most), heavy polypeptide 3, skeletal muscle, adult (missing most), heavy polypeptide 3, skeletal muscle, adult (missing most), heavy polypeptide 3, skeletal muscle, adult (missing most), he	Homo septem (KIAA0763 nene product (KIAA0705), min	Homo sepiens KIAA0763 gene product (KIAA0763), mHNA	Hours entiens mRNA for KIAA1172 protein, but and the sentiens mRNA for KIAA1172 protein, actial ods	Homo sapiens mRNA for KIAA1172 protein, Pourer	Homo sapiens mRNA for KIAA1172 protein. Proceedito, rod, alpha (PDE6A), mKNA	Homo saplens phosphodiesterase 0A, coming 5 (TRPC5), mRNA	Homo sapiens transfert receptor porential (7) (partial)	H. sapiens DNA for monoamine oxidase cypical dis	Homo saplens ALR-like protein minuth, Peres and 3	Home capiens NOD1 promin (NO 17) 3	mitochandrial 5(3)-deoxyribanucleotidase (alvi 2, 2007)	Homo sapiens dN 1-2 gain temper protein 1 (AKAP1), mxtvA	Homo sapiens A kinase (PRKA) anchor protein 1 (AKAP1), mKNA Homo saplens A kinase (PRKA) anchor protein 1	OHOLE		
Single Exon Flore		Database Source			EST_HUMAN	NAM.	EST HUMAN	EST HUMAN	EST HOMAN	EST HOWING	EST HIMAN	POT HIMAN	NT	EST HUMAN	LN	LN	TMIOSCOOL	7662289 NT	TNIOSOSOSO	7662289 NT	7662289 NT			1N	11416767 NT	6912735 NT			3.1 NT	<u> </u>	11424399 NT	11424399 NT		
Single		Top Hit Acession No.	11417860 NT	1141010	284651.1		284651.1	1.0E-93 BF370000.1	17806.1	9 0E-96 BE897259.1	8.0E-96 BE907607.1	E-96 BE907607.1	8.0E-96 AW836047.1	AF231920.1	6.0E-96 BE171984.1	6.0E-96 AL 10340	6.0E-96 M26873.1					AR03296	2.0E 90 AR032998.1	- oc oc AB032998.1	11		5 0E-96 X60812.1	R NE 96 AF264750.1	5.0E-96 AF149773.1	-	5.0E-96 AJ277557.1		5.0E-96	
	Most Similar		2.0E-95	2.0E-95	4 nF.95 AA284651.1		1.0E-95 AA284651.1	1.0E-43.0	1 0E-95 R17806.1	90E-30	8.0E-96	8.0E-96	8.0E-96	7.0E-96	6.0E-96	6.0E-90	6.0E-96	6.0E-96	6.0E-96	Ц		1	1	1			1	١	14		- 1	1	3.68 5.0	
	Mos	Expression (To Signal BL	13	7.4	-	8.08	8.06	4.11	12.4	2 9	38	88 0	2.8	125	2.48	0.71	10.25	2.41	2.41	1 94	1.32	1.32	3.55	3.4	3.4	1.72								
	-		+	94066	-	32219	32220	34229	34230	36197	34996	28687	2008	1	30183		232/2	29751	1	38518	38753	38754	26574	27104	27105		29284			33341	33413			١
	-	ORF SEQ	-		1_	18925		70748	20748	22625	21469	16012	16012	18822	17175	15405	16564	16736	24828	24828	248/2	25045	2000	44044	14041	ı	1	L	1_	19943	1	1	$\perp$	1 20236
	-	D SEQ ID		1	13067 25698	5732 189	١	- 1	200	L	L	L	$\sqcup$	5628 1	Ш	2334		1 1	11839	Ш	11891	12064	12884			202	2007	1000	5296	6788		6851	6921	6921
		Probe SEQ ID	<u></u>	127			1_	_		1	_ل	1		<u>_</u>	ــــــــــــــــــــــــــــــــــــــ	_	1	ا	_															

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באנון וסמסל באף מסססל ווון ממסוות	Top Hit Descriptor	Homo sapiens mRNA for KIAA0960 protein, partial cds	Homo sapiens mRNA for 14-3-3gamma, complete cds	Human type IV callagenase (CLG4B) gene, exan 5	Human type IV collagenase (CLG4B) gene, exon 6	Homo sapiens KIAA0175 gene product (KIAA0175), mRNA	y87h12.r1 Soares fetal liver spleen 1NFLS Homo saplens cDNA clone IMAGE:212327 5'	Homo sapiens chondroitin sulfate proteoglycan 4 (melanoma-associated) (CSPG4), mRNA	Homo sapiens chromosome 21 segment HS210048	Homo sapiens CGI-201 protein (LOC51340), mRNA	RC3-HT0230-040500-110-902 HT0230 Homo sapiens cDNA	QV4-GN0120-250900-427-512 GN0120 Homo sapiens cDNA	QV4-GN0120-250900-427-b12 GN0120 Homo sapiens cDNA	AV689461 GKC Homo sapiens cDNA clone GKCFMD07 5'	2819351.5prime NIH_MGC_7 Hamo sapiens aDNA clone IMAGE:2819351 5'	Homo sapiens neuronal cell adhesion molecule (NRCAM) mRNA	Homo sapiens neuronal cell adhesion molecule (NRCAM) mRNA	Human endogenous retrovirus type K (HERV-K), gag, pol and env genes	EST367124 MAGE resequences, MAGC Homo saplens cDNA	EST367124 MAGE resequences, WAGC Homo sapiens cDNA	Homo sapiens phospholipid transfer protein (PLTP) mRNA	Homo sapiens transient receptor potential channel 5 (TRPC5), mRNA	Нопо saptens guanine nucleotide exchange factor for Rap1 (KIAA0277), mRNA	Homo sapiens HSPC144 protein (HSPC144), mRNA	Homo sapiens HSPC144 protein (HSPC144), mRNA	Homo sapiens similar to ectonucleotide pyrophosphatese/phosphodiesterase 3 (H. sapiens) (LOC63214), mRNA	Homo sapiens secretory pathway component Sec31B-1 mRNA, alternatively spliced, complete cds	Homo sapiens mRNA for KIAA1290 protein, partial cds	Homo sapiens mRNA for KIAA1290 protein, partial cds	Homo sapiens neuronal cell adhesion molecule (NRCAM) mRNA	Homo sapiens neuronal cell adhesion molecule (NRCAM) mRNA	601863712F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4081202 5	L5-HT0117-011099-004-D07 HT0117 Homo sapiens cDNA
	Top Hit Database Source	TN.	N T	N	TN	IN	EST_HUMAN	NT	TN	TN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	LZ LZ	NT.	N	EST_HUMAN	EST_HUMAN	FZ	NT	NT	NT	NŦ	TN	LN LN	NT.	NT	N L	NT	EST_HUMAN	EST HUMAN
- A	Top Hit Acession No.	5.0E-96 AB023177.1	5.0E-96 AB024334.1	5.0E-96 M68347.1	5.0E-96 M68347.1	7661973 NT	H68656.1	4503098 NT	2.0E-96 AL163248.2	7706205 NT	2.0E-96 BE148074.1	2.0E-96 BF369731.1	2.0E-96 BF369731.1	2.0E-96 AV689461.1	2.0E-96 AW 249440.1	4826863 NT	4826863 NT		1.0E-96 AW955054.1	1.0E-96 AW955054.1	5453913 NT	6912735 NT	6912455 NT	7661803 NT	7661803 NT	11419429 NT	1.0E-96 AF274863.1		1.0E-96 AB033116.1	4826863 NT	4826863 NT	6.0E-97 BF245240.1	
	Most Similar (Top) Hit BLAST E Value	5.0E-96	5.0E-98	5.0E-96	5.0E-96	5.0E-96	3.0E-96 H68656.1	2.0E-96	2.0E-96	2.0E-96	2.0E-96	2.0E-96	2.0E-96	2.0E-96	2.0E-96	1.0E-96	1.0E-96	1.0E-96 Y18890.1	1.0E-96 /	1.0E-36 /	1.0E-96	1.0E-96	1.0E-96	1.0E-96	1.0E-96	1.0E-96	1.0E-96	1.0E-96	1.0E-96	1.0E-96	1.0E-96	6.0E-97	6.0E-97
	Expression Signal	0.91	0.76	1.87	1.87	1.33	15.95	5.76	1.1	1.03	1.56	0.59	0.59	4.9	2.54	0.86	0.86	3.08	9.97	16.6	1.59	1.19	0.71	6.0	6.0	21.44	2.22	99.0	0.68	3.29	3.29	0.72	3.4
	ORF SEQ ID NO:	33740	34231	34900		38769						34165	34166						28063	28064					35018	35531	35674	37007	37008			29290	
	Exon SEQ ID NO:	20296	20749	21379							18011	20690	20690						14971	14971			20059	21488	21488	21992	22130	_					
	Probe SEQ ID NO:	7163	7684	8297	8297	12083	4308	428	766	1834	4880	7620	7620	9181	12288	88	638	889	1822	1822	5331	7105	7194	8407	8407	8913	9051	10362	10362	12274	12274	3405	7730

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Top Hit Descriptor	601440317F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3925133 5'	601440317F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3925133 5'	EST22672 Adipose tissue, white II Homo sepiens cDNA 5' end	EST22872 Adipose tissue, white II Homo saplens cDNA 5' end	Human mRNA for alpha-ectinin	DKFZp434N0323_r1 434 (synonym: https://domo.sapiens.cDNA.clone.DKFZp434N0323 5	2x87e12.s1 Soares_NhHMPu_S1 Homo sepiens cDNA clone IMAGE:767758 3' similar to TR:G1304125	RC0-BT0812-250900-032-e09 BT0812 Homo sepiens cDNA	MR0-HT0241-150500-010-b02 HT0241 Homo sapiens cDNA	MRO-HT0241-150600-010-b02 HT0241 Homo sapiens cDNA	CMO-BN0106-170300-293-a06 BN0106 Homo saplens cDNA	Homo sapisns brefeldin A-inhibited guanine nucleotide-exchange protein 2 (BIG2), mRNA	Homo sapiens apolipoprotein H (beta-2-glycoprotein I) (APOH) mRNA	Homo sapiens mRNA for GalNAc alpha-2, 6-sialytransferase I, long form	Homo saplens mRNA for GalNAc alpha-2, 6-statyltransferase I, long form	Homo sapiens ligase III, DNA, ATP-dependent (LIG3), transcript variant alpha, mRNA	Homo sepiens cystic fibrosis transmembrane conductance regulator, ATP-binding cassette (sub-family C, member 7) (CFTR), mRNA	Homo sapiens laminin, alpha 2 (merosin, congenital muscular dystrophy) (LAMA2) mRNA	Homo sapiens v-src avian sarcoma (Schmidt-Ruppin A-2) viral encegene hemdeg (SRC), mRNA	Homo sapiens N-myc (and STAT) Interactor (NMI), mRNA	Homo sapiens cytochrome P450, subfamily IVB, polypeptide 1 (CYP4B1), mRNA	Homo sapiens mRNA for KIAA0594 protein, partial cds	Homo sapiens mRNA for KIAA0594 protein, partial cds	Homo saplens N-myc (and STAT) interactor (NMI), mRNA	Homo saplens AXL receptor tyrosine kinase (AXL), transcript variant 1, mRNA	Homo sapiens AXL receptor tyrosine kinase (AXL), transcript variant 1, mRNA	Homo saplens mRNA, similar to rat myomegalin, complete cds	Homo sapiens G-2 and S-phase expressed 1 (GTSE1), mRNA	Homo sapiens mRNA for KIAA1172 protein, partial ods	Homo sapiens amyloid beta (A4) precursor protein (protease nexin-il, Alzheimer disease) (APP), mRNA
Top Hit Database Source	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	N-	EST_HUMAN	ECT LIMAN	EST HUMAN	Т-	Г	EST_HUMAN	Ę	M	F	¥		Į,	N	N	TN	NT	NT	M	NT	NT	NT	ΙN	LN	NT	LN
Top Hit Acessian No.	6.0E-97 BE898012.1	6.0E-97 BE898012.1	6.0E-97 AA320332.1	6.0E-97 AA320332.1	6.0E-97 X15804.1	.0E-97 AL043314.2	R OF D7 44418026 1			.0E-97 BE148597.1	4.0E-97 BE004436.1	5463672 NT	4557326 NT	1.0E-97 Y11339.2	1.0E-97 Y11339.2	7710125 NT	11422155 NT	4557708 NT	· 11421793 NT	11431060 NT	11423233 NT	.0E-97 AB011168.1	4.0E-97 AB011166.1	11431060 NT	11863122 NT	11863122 NT	1.0E-97 AB042557.1	11418318 NT	.0E-97 AB032998.1	4502166 NT
Most Similar (Top) Hit BLAST E Value	6.0E-97	6.0E-97	6.0E-97	6.0E-97	6.0E-97	5.0E-97	A 0E.07	5.0E-97	5.0E-97	5.0E-97	4.0E-97	4:0E-97	4.0E-97	4.0E-97	4.0E-97	4.0E-97	4.0E-97	4.0E-97	4.0E-97	4.0E-97	4.0E-97	4.0E-97	4.0E-97	4.0E-97	4.0E-97	4.0E-97	4.0E-97	4.0E-97	3.0E-97	3.0E-97
Expression Signal	0.75	0.75	0.65	0.65	2.42	1.73	11 21	3.12	1.68	1.68	2.13	1.41	0.82	6.47	6.47	1.09	0.92	1.06	1.43	0.51			1.06		1.89	1.99	4.51	5.26	1.58	7.16
ORF SEQ ID NO:		35758	37475	37478	38381	34809	34943	36502	38519	38520	27196	28202	32166	.33615	33616	33737		34937	35171								37528		26504	27138
Exan SEQ ID NO:	22213		23854	23854		21286	21417		24829					20190	20190	20294	20079										23905	25325	13473	14073
Probe SEQ ID NO:	9134	9134	10821	10821	11692	8204	8336	9877	11840	11840	362	1959	5683	6962	6962	7161	7214	8329	8553	8779	8820	9449	9449	10652	11435	11435	11719	12472	253	897

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	Top Hit Descriptor	Homo sapiens amyfold beta (A4) precursor protein (profease nextn-ll, Alzheimer disease) (APP), mRNA	Homo sapiens N-myc (and STAT) interactor (NMI), mRNA	Human beta-prime-adaptin (BAM22) gene, exon 7	Homo saplens pericentrin (PCNT) mRNA	Homo sapiens eukaryotic translation elongation factor 1 alpha 1 (EEF1A1) mRNA	601339520F1 NIH_MGC_63 Homo sapiens cDNA clone IMAGE;3681821 5	Homo sapiens phosphorylase kinase, gamma 1 (muscle) (PHKG1) mRNA	yf38c08.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:129134.3'	Homo sapiens KIAA0649 gene product (KIAA0649), mRNA	Homo sapiens KIAA0649 gene product (KIAA0649), mRNA	nk29g02.s1 NCI_CGAP_Co11 Homo sapiens cDNA clone IMAGE:1014962.3'	Homo sapiens ribosomal protein S15 (RPS15), mRNA	Homo sapiens ribosomal protein S15 (RPS15), mRNA	PM4-BT0724-010400-008-a12 BT0724 Homo saplens cDNA	Homo sapiens cat eye syndrome critical region gene 1 (CECR1), mRNA	Homo sapiens CLDN12 gene for daudin-12	Homo sapiens mRNA for KIAA 1636 protein, partial cds	Homo sapiens mRNA for KIAA1636 protein, partial cds	Homo sapiens death-associated protein (DAP), mRNA	Homo saplens death-associated protein (DAP), mRNA	Human mRNA for amyloid A4(751) protein	Homo sapiens succinate-CoA ligase, GDP-forming, alpha subunit (SUCLG1), mRNA	Homo sapiens mRNA for KIAA 1365 protein, partial cds	Homo saplens 17-beta-hydroxysteroid dehydrogenase IV (HSD17B4) gene, exon 8	Homo septens SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 3 (SMARCA3) mRNA	Homo sapiens SWISNF related, matrix associated, actin dependent regulator of chromatin, subfamily a,	member 3 (SMARCA3) mRNA	Home capions inecitol polyphosphate 1-phosphatece (INPP1) gene, complete ods	Homo saplens protease-activated receptor 3 (PAR3), mRNA	Homo sapiens mRNA for KIAA1005 protein, partial cds	Homo saplens mRNA for KIAA1005 protein, partial cds	PM4-BT0724-010400-008-a12 BT0724 Homo saplens cDNA
	Top Hit Database Source	뒫	Ę	٦	NT	NŢ	EST_HUMAN	LΝ	EST_HUMAN	LΝ	LΝ	EST_HUMAN	N	TN	EST HUMAN	IN	LN	ΙN	LN	LN	NT	LN	LN	NT	NT	L Z		FN	ĹΝ	۲N	LΝ	LN	EST_HUMAN
	Top Hit Acession No.	4502166 NT	4758813 NT	U36255.1	5174478 NT	4503470 NT	1.0E-97 BE566486.1	5453881 NT	1.0E-97 R10887.1	11427757 NT	11427757 NT	1.0E-97 AA553761.1	11426272 NT	11426272 NT	9.0E-98 BE090973.1	8393092 NT	9.0E-98 AJ250713.1	9.0E-98 AB046856.1	9.0E-98 AB046856.1	4758119 NT	4758119 NT		11321580 NT		9.0E-98 AF057726.1	TN 0202024	0101001	4507070 NT	9.0E-98 AF141325.2	11431544 NT	9.0E-98 AB023222.1		9.0E-98 BE090973.1
	Most Similar (Top) Hit BLAST E Value	3.0E-97	3.0E-97	3.0E-97	3.0E-97	1.0E-97	1.0E-97	1.0E-97	1.0E-97	1.0E-97	1.0E-97	1.0E-97	1.0E-97	1.0E-97	9.0E-98	9.0E-98			9.0E-98	9.0E-98	9.0E-98	9.0E-98 X06989.	9.0E-98	9.0E-98	9.0E-98	90-70 p	20.0	9.0E-98	9.0E-98	9.0E-98	9.0E-98	9.0≅-98	9.0E-98
	Expression Signal	7.16	<u>\$</u>	2.4	0.96	22.23	2.72	0.69	1.02	2.84	2.84	1.38	8.3	8.3	2.34	1.32	62.0	4.13	4.13	29:5	5.62	1.78	1.12	1.6	0.81	1 28	3	1.28	29'0	0.5	2.62	2.62	4.97
	ORF SEQ ID NO:	27139	27712	28755								38324		37569		27528			34584	34711		35943	36064	36112		36976				37215	37962	37963	
	Exan SEQ ID NO:	14073	16039	15998						24027	Ш	24642	23942	23942	14099		19600	1		21191	21191	22392	22499	22549	22605	99709	2	22709	23502	23610	24322	24322	14099
	Probe SEQ ID NO:	897	1473	2508	3333	4902	6557	7039	9966	10945	10945	11589	11756	11756	924	1305	6432	8020	8020	8109	8109	9316	9425	9492	9540	2950		9567	10467	10575	11253	11253	12487

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Top Hit Descriptor	Homo sapiens hPAD-colony10 mRNA for peptidylarginine deiminase type I, complete cds	Homo sapiens IL 2-inducible T-cell kinase (ITK), mRNA	Homo sapiens IL2-inducible T-cell kinase (ITK), mRNA	Homo sapiens PMS2L16 mRNA, partial cds	Homo sapiens PMS2L16 mRNA, partial cds	Human mitochondrial creatine kinase (CKMT) gene, complete cds	601507503F1 NIH_MGC_71 Homo sepiens cDNA clone IMAGE:3909097 57	AJ403124 3.4 (downregulated in larymx carcinoma) Homo sapiens cDNA clone I8	Homo sapiens mRNA for KIAA0707 protein, partial cds	7B18H01 Chromosome 7 Fetal Brain cDNA Library Homo sapiens cDNA clone 7B18H01	Homo sapiens activator of S phase kinase (ASK), mRNA	Homo saplens activator of S phase kinase (ASK), mRNA	yo17g09.r1 Soares adult brain N2b5HB55Y Homo sapiens cDNA clone IMAGE:178240 5'	Homo sapiens uncharacterized bone marrow protein BM039 (BM039), mRNA	AJ403124 3.4 (downregulated in larynx carcinoma) Homo sapiens cDNA clone 18	AJ403124 3.4 (downregulated in larymx carcinoma) Homo sapiens cDNA clone is	601673686F1 NIH_MGC_21 Homo sapiens cDNA done IMAGE:3956517 51	Human fumarase precursor (FH) mRNA, nuclear gene encoding mitochondrial protein, complete ods	qb80h02.x1 Soares_feta_heart_NbHH19W Homo sapiens cDNA clone IMAGE:1706451 3'	Homo saplens Ran GTPase activating protein 1 (RANGAP1), mRNA	601149486F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3502245 5'	601172658F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3528134 57	Homo sapiens chromosome 21 segment HS21C002	Homo sapiens potassium channel subunit (HERG-3) mRNA, complete cds	Homo sapiens fatty-acid-Coenzyme A ligase, long-chain 4 (FACL4) mRNA	Homo sepiens attractin precursor (ATRN) gene, exon 16	Homo saplens attractin precursor (ATRN) gene, exon 16	Homo saplens PDZ domain-containing guanine nucleotide exchange factor I (LOCS1735), mRNA	Homo sapiens phosphatidy/inositol 3-kinase, class 2, alpha polypeptide (PIK3C2A) mRNA	Homo sapiens hypothetical protein FLJ10488 (FLJ10488), mRNA	Homo sapiens hypothetical protein FLJ10488 (FLJ1048B), mRNA	Homo sapiens SH3-domain GRB2-like 2 (SH3GL2), mRNA	Homo sepiens SH3-domain GRB2-like 2 (SH3GL2), mRNA
Top Hit Database Source	Į.	F	NT	NT	NT NT	LN	EST_HUMAN	EST_HUMAN	LNT	EST_HUMAN	۲	۲	EST_HUMAN	۲	EST_HUMAN	EST_HUMAN	EST_HUMAN	LΝ	EST HUMAN	L	EST_HUMAN	EST_HUMAN	NT ·	NT	NT	LN	NT	LN	TN	NT	NT	NT	NT.
Top Hit Acession No.	3.0E-98 AB033768.1	5031810 NT	5031810 NT	3.0E-98 AB017007.1	3.0E-98 AB017007.1		5.0E-98 BE885873.1	3.0E-98 AJ403124.1	3.0E-98 AB014507.1	3.0E-98 AA077498.1	11419210 NT	11419210 NT		8922096 NT	3.0E-98 AJ403124.1		3.0E-98 BE900454.1		3.0E-98 AI159975.1	11418177 NT	2.0E-98 BE261694.1		2.0E-98 AL163202.2	2.0E-98 AF032897.1	4758331 NT	2.0E-98 AF218902.1	2.0E-98 AF218902.1	7706512 NT	4505798 NT	11431271 NT	11431271 NT	11428813 NT	11428813 NT
Most Similar (Top) Hit BLAST E Value	8.0E-98	80-30'8	8.0E-98	8.0E-98	8.0E-98	8.0E-98 J04469.1	5.0E-98	3.0E-98	3.0E-98	3.0E-98	3.0E-98	3.0E-98	3.0E-98 H46698.1	3.0E-98	3.0E-98	3.0E-98	3.0E-98 E	3.0E-98 U59309.1	3.0E-98	3.0E-98	2.0E-98	2.0E-98 E	2.0E-98 /	2.0E-98 /	2.0E-98	2.0E-98	2.0E-98	2.0E-98	2.0E-98	2.0E-98	2.0E-98	2.0E-98	2.0E-98
Expression Signal	0.93	1.1	1.1	2.79	2.79	6.45	960	1.35	2.1	5.04	1.99	1.99	4.07	0.54	1.82	1.82	0.89	2.56	222	3.01	29.0	4.06	2.21	0.82	4.23	1.39	1.39	4.76	1.7	1.25	1.25	4.44	4.44
ORF SEQ ID NO:	27631	27825	27826	28009	28010	30055	32732	28508	28910		33602		35571	36116			37330	37899	38504		28980	28399	28578	30538	30577	31052	31053	31708	33347	34348			35427
Exon SEQ ID NO:	14557	14743	14743	14914	14914	17055	19382	15380	15793	15921	20179	20179	22030	22553	23125	23125	23724	24264	24808	25739	13935	15277	15443	17553	17599	18078	18078	18691	19948	20857	20857	21886	21886
Probe SEQ ID NO:	1403	1591	1591	1765	1765	3896	6207	2247	2673	2807	7085	7085	8951	9497	10087	10087	10691	11195	11819	13138	754	2141	2311	4411	4459	4948	4948	5492	6793	7801	7801	8807	8807

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Top Hit Descriptor	Homo sapiens NKAT4b mRNA, complete cds	Homo sapiens NKAT4b mRNA, complete cds	H.sapiens arginase gene exon 3 (EC 3.5.3.1)	Homo capiens AIM-1 protein (LOC51151), mRNA	Homo saplens mRNA for KIAA1593 protein, partial cds	Homo saplens chromosome 12 open reading frame 3 (C12ORF3), mRNA	w36b04.x1 NC _CGAP_Ut1 Homo sapiens cDNA clone IMAGE:2281743 3' similar to SW:RI_2B_HUMAN P28316 60S RIBOSOMAL PROTEIN L23A.;	PM0-BN0065-100300-001-c06 BN0065 Home sapiens cDNA	y/23/05.r1 Scares fetal liver spleen 1NFLS Home sapiens cDNA clone IMAGE:243585 5' similar to PR:S54204 S54204 ribosomal protein 1:29 - human	zp88c09.r1 Stratagene muscle 937209 Homo sapiens cDNA clone IMAGE:628240 5' similar to TR:G806562	G806562 NEBULIN.;	601284986F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3606692 5'	601284986F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3606692 5'	Homo saplens beta-tubulin mRNA, complete cds	Homo sapiens beta-tubulin mRNA, complete cds	QV-BT073-191298-012 BT073 Homo saplens cDNA	QV-BT073-191298-012 BT073 Homo saplens cDNA	EST380711 MAGE resequences, MAGJ Homo sapiens cDNA	tm69h07.x1 NCI_CGAP_Bm25 Home sapiens cDNA clone IMAGE:2163421 3' similar to SW:BID_HUMAN 's P56957 BH3 INTERACTING DOMAIN DEATH AGONIST;	m69h07x1 NCL_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2163421 3' similar to SW:BID_HUMAN P55957 BH3 INTERACTING DOMAIN DEATH AGONIST:	zn90d02.r1 Stratagene lung carcinoma 837218 Homo sapiens cDNA clone IMAGE: 565443 5' similar to	TR. G662994 G62994 GPI-ANCHORED PROTEIN P137.;	Human endogenous retrovirus, complete genome	Homo sapiens oscillin (hl.n) gene, exon 5	Homo sapiens NK-receptor (KIR-G2) gene, linker region exon	Human G2 protein mRNA, partial cds	Homo sapiens cysteine-rich repeat-containing protein S52 precursor, (LOC51232), mRNA	Homo sapiens cystelne-rich repeat-containing protein S52 precursor, (LOC51232), mRNA	EST388473 MAGE resecuences, MAGN Homo sapiens cDNA	Homo sapiens CD34 antigen (CD34) mRNA
Top Hit Database Source	Į.		Ł		LZ		EST HUMAN	П	EST HUMAN	Т	EST_HUMAN C	EST_HUMAN 6	EST_HUMAN	Г	- LN	EST_HUMAN	EST_HUMAN C	EST_HUMAN E	EST_HUMAN F	EST HUMAN	Г	EST_HUMAN T		1 L	TN TN	INT.			T_HUMAN	
Top Hit Acession No.			2.0E-98 X12664.1	7705868 NT	2.0E-98 AB046813.1	11435947 NT	1.0E-98 AI862007.1	-	1 0E-98 N49818 1		1.0E-98 AA195854.1	1.0E-98 BE390627.1	1.0E-98 BE390627.1	1.0E-98 AF141349.1	1.0E-98 AF141349.1	9.0E-99 A1905004.1	9.0E-99 A1905004.1	9.0E-99 AW968635.1	9.0E-99 A1479829.1	9.0E-99 AI479829.1		9.0E-99 AA134604.1	9635487 NT		7.0E-99 AF001886.1	3.0E-99 U10991.1	11430555 NT	11430555 NT	6.0E-99 AW976364.1	4502660 NT
Most Similar (Top) Hit BLAST E Value	2.0E-98 L76665.1	2.0E-98 L76666.1	2.0E-98	2.0E-98	2.0E-98	2.0E-98	1.0E-98	1.0E-98	1.05-98		1.0E-98	1.0E-98	1.0E-98	1.0E-98 /	1.0E-98	9.0E-99	9.0E-39	9.0E-39	9.0E-39	9.0E-99		9.0E-99	8.0E-99	7.0E-99	7.0E-99	6.0E-99	6.0E-99	6.0E-99	6.0E-99	6.0E-99
Expression Signal	0.8	0.8	1.56	1.65	1.61	2.23	27.52	3.27	26.16		3.3	0.97	76'0	0.59	0.59	1.05	1.05	4.01	1.85	1.85		1.72	1.19	9.25	1.91	0.72	6.2	6.2	2.8	1.42
ORF SEQ ID NO:	35503		36376			32062	26653	26698	28086		31610	32172	32173	35815	35816	32438	32439	32688	38105	38106		38389	35542	32458	38599	26713	28456	28457	30160	30986
SEQ ID	21968		20822	89982	25116	25340	13613	13662	14986	1	18632	18881	18881	72277	22277		19125	19341	24445	24445		24697	22003	19142	24896	13678		15331		18003
Probe SEQ ID NO:	8888	8889	9737	10624	12136	12492	418	467	1840		5432	5687	2687	9199	9189	5939	5939	6165	11384	11384		11700	8924	5956	11909	484	2196	2196	3995	4870

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Oligie Exoli Probes Expressed in Placenta	Top Hit Descriptor	Homo sapiens GAP-like protein (LOC5/1306), mRNA	Homo sapiens polyovstic kidney disease (PKD1) gene exces 27-30	Homo saplens polycystic kidney disease (PKD1) gene, expns 27-30	H. sapiens mRNA for estrogen receptor	Homo sapiens ankyrin-like with transmembrane domeins 1 (ANKTM1), mRNA	Homo sapiens NDST4 mRNA for N-deacetylase/N-sulfotransferase 4, complete cds	Hamo sapiens lodester protein mRNA, complete cds	Homo sapiens todestar protein mRNA, complete cds	Homo sapiens inositol 14,5-triphosphate receptor, type 1 (ITPR1), mRNA	Homo sapiens inositol 1,4,5-triphosphate receptor, type 1 (ITPR1), mRNA	Homo saplens BH3 Interacting domain death agonist (BID). mRNA	Homo sapiens UDP-glucose; glycoprotein glucosyftanisfense 1 (HUGT1), mRNA	Homo sapiens UDP-glucose:glycoprotein glucosyltransferase 1 (HUGT1), mRNA	H sapiens IMPA gene, excn 8	Homo sapiens T cell receptor beta locus, TCRBV7S3A2 to TCRBV12S2 region	601513157F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3914391 5'	Human E2A/HLA fusion protein (E2A/HLF) mRNA, complete cds	xp09e06.x1 NCI_CGAP_HN9 Home sapiens cDNA clone IMAGE:2739874 3' similar to gb:M31212 MYOSIN	Human Ku (070/080) subunit mRNA, complete cds	Homo sapiens short chain L-3-hydroxyacyl-CoA dehydrogenase precursor (HADHSC) gene, nuclear gene	encoding mitochondrial protein, complete cds	Homo saplens ciliary dynein heavy chath 9 (DNAH9) mRNA, complete cds	2b48d06.r1 Soares, fetal Jung, NbHL19W Homo sapiens CDNA clone IMAGE:306635 5' similar to qb:M45182 BETA-GLUCURONIDASE PRECURSOR (HUMAN).	yi81b09.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:145625 51	Homo sapiens myosin X (MYO10) mRNA, complete cds	Homo sapiens potassium channel, subfamily K, member 10 (KCNK10), mRNA	Homo sapiens intersectin long Isoform (ITSN) mRNA, complete cds	Homo sapiens GA-binding protein transcription factor, eighe subunit (60kD) (GABPA), mRNA	Human Ku (p70/p80) subunit mRNA, complete cds	Homo sapiens truncated Niemann-Pick C3 protein (NPC3) mRNA, complete cds	Homo saplens truncated Niemann-Pick C3 protein (NPC3) mRNA, complete cds	Homo sapiens FK608-binding protein 6 (36kD) (FKBP6) mRNA, and translated products
EXOLI PIO	Top Hit Database Source	TN	K	۲	Ν	NT	N	N	FN	FZ	NT L	Ę	NT	NT	μN	ΙN	EST_HUMAN	Z.	MAN H	LN		뉟	L L	EST HUMAN	EST HUMAN	F	¥	N	Ę	Į.	L	NT	FZ
Illino	Top Hit Acession No.	7706138 NT	6.0E-99 L43610.1	6.0E-99 L43610.1	6.0E-99 X99101.1	6601589 NT			6.0E-99 AF080255.1	11431994 NT	11431994 NT	11526299 NT	9910279 NT	9910279 NT	5.0E-99 Y11365.1	5.0E-99 AF009660.1	5.0E-99 BE890177.1	3.0E-99 M95586.1	2 0F-99 AW274792 1	T			2.0E-99 AF257737.1	2.0E-99 W23507.1	2.0E-99 R78254.1	2.0E-99 AF247457.2	10863960 NT	1.0E-99 AF114487.1	26150	1.0E-99 M30938.1		.0E-99 AF192523.1	4503730 NT
<u> </u>	Most Similar (Top) Hit BLAST E Value	6.0E-99	6.0E-99	6.0E-99	6.0E-99	6.0E-99	6.0E-99	6.0E-99	6.0E-99	6.0E-99	6-30.9	6.0E-99	6.0E-99	6.0E-99	5.0E-99	5.0E-99	5.0E-99	3.0E-99	2 OF-99	2.0E-99		2.0E-99	2.0E-99	2.0E-99	2.0E-99	2.0E-99	2.0E-99	1.0E-99	1.0E-99	1.0E-99	1.0E-99	1.0E-99	1.0E-99
	Expression Signal	0.94	0.74	0.74	1.85	0.59	2.67	7.6	7.6	0.59	0.59	3.15	2.02	2.02	1	1.81	2.49	4.95	36.2	4.		1.82	0.76	10.79	0.75	3.16	1.64	1.49	1.75	3.61	1.16	1.16	1.21
	ORF SEQ ID NO:	33280	33376	33377	34899	34921			35689		35745	37674	37553	37554	28268	60808				29522		30787	34410	35523	35986	38085	38767	26571	26632	27684	27819	27820	28224
	Exon SEQ ID NO:	19888	19969	19969	21378			22143	- 1			24039	23928	23928	15163	17821	25346	21597	14426	16504		1/800	20906	21983	22428	24428	25061	13539	13596	14605	14739	14739	15123
	Probe SEQ ID NO:	6732	6816	6816	8296	8314	8964	9064	9064	9123	9123	10958	11742	11742	2022	4686	12502	8516	1268	3331		4 665	7851	8904	9353	11367	12081	325	390	1452	1587	1587	1980

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					<u>,                                    </u>		
Probe SEQ ID NO:	Exan SEQ ID NO:	<u>R</u> □	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
1980		28225		1.0E-99	4503730 NT	NT	Homo sapiens FK506-binding protein 6 (36kD) (FKBP6) mRNA, and translated products
3154			26°C	1.0E-99	1.0E-99 J03171.1	N.	Human interferon-alpha receptor (HulFN-alpha-Rec) mRNA, complete cds
4499				,	1.0E-99 AF098018.1	M	Homo sapiens fatty acid emide hydrolase (FAAH) gene, exon 14
4499	_				1.0E-99 AF098018.1	NT	Homo saplens fatty acid amide hydrolase (FAAH) gene, exon 14
6943				1.0E-99	11421007 NT	N	Homo sapiens glycine receptor, alpha 2 (GLRA2), mRNA
6943				1.0E-99	11421007 NT	N	Homo sapiens glycine receptor, alpha 2 (GLRA2), mRNA
7289		33827	18.0	1.0E-99	.0E-99 X98022.1	님	H.sepiens E6-AP gene exon 2
9400	22474		92'0	1.0E-99	11419721 NT	<u>F</u> N	Homo sapiens ALEX1 protein (LOC51309), mRNA
0620	20700	92696		100	77270767110	TOL	hd02h02.xt Soares_NFL_T_GBC_S1 Hamo sapiens cDNA clone IMAGE:2908371 3' similar to TR:002711
11403			7 83.0	1.05-99	HW 340	ESI HUMAIN	UOZ/11 FRO-POL-DO I PASE POL (PRO IEIN )
2	107/6		00.4	88-30.		1	norto seprets nuturgun merecing protein 1 (TIP-1), mKNA
11403	$\perp$		5.56	1.05-99		L	Homo sapiens huntingtin interacting protein 1 (HIP1), mRNA
11462				1.0E-99	5901979 NT	LN	Homo sapiens heat shock transcription factor 2 binding protein (HSF2BP), mRNA
11659	1	38429	2.83	1.0E-99	.0E-99 AB023222.1	NT	Homo saplens mRNA for KIAA1005 protein, partfal cds
11998	24981	38687		1.0E-99	11417191 NT	TN	Homo sapiens leucy//cystiny/ aminopeptidase (LNPEP), mRNA
			į	. !		ļ	Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1)
12257	┙		4.52	1.0E-99	.0E-99 AF240786.1	Ł	genes, complete cds
	13241	26241	1.7	1.0E-100	E-100 AL163247.2	LN	Homo sapiens chromosome 21 segment HS21C047
2		26241	2.91	1.0E-100	E-100 AL163247.2	TN	Homo saplens chromosome 21 segment HS210047
20		26329	1.62	1.0E-100	11418230(NT	ĮN.	Homo sapiens Testis-specific XK-related protein on Y (XKRY), mRNA
70	13307	26330	1.62	1.0E-100	11418230 NT	ĮN.	Homo sapiens Testis-specific XK-related protein on Y (XKRY), mRNA
88		26353		1.0E-100	E-100 AW275237.1	T_HUMAN	xv78b11.x1 NCI_CGAP_Bm53. Home sapiens cDNA clone IMAGE:2824605 3'
173		26425	0.89	1.0E-100	E-100 AL163206.2		Homo sapiens chromosome 21 segment HS210006
327	_]	26573	1.84	1.0E-100	7.7	LN	Homo saplens chromosome 21 segment HS21 C049
353	13564	26592	1.87	1.0E-100	E-100 T05087.1	EST_HUMAN	EST02975 Fetal brain, Stratagene (cat#936206) Homo sapiens cDNA clone HFBCR32
į			٠				Homo sapiens X-linked anhidroitic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat
450	┙		2.24	1.0E-100	3.1		regions
502			5.88	1.0E-100	E-100 X89631.1		G.gorilla DNA for ZNF80 gene homolog
522			121	1.0E-100	DE-100 BE180609.1	EST_HUMAN	RC3-HT0625-040500-022-509 HT0625 Homo sapiens cDNA
1044		27266	4.57	1.0E-100	7661685 NT	NT	Homo sapiens DKFZP586M0122 protein (DKFZP586M0122), mRNA
10 4		27267	4.57	1.0E-100	TN 681685 NT		Homo saplens DKFZP586M0122 protein (DKFZP586M0122), mRNA
1577	14730		1.3	1.0E-100	E-100 AW 207555.1	EST_HUMAN	U.H-Bi1-afk-c-07-0-UI.s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2722164 3'
1581	14733	27814	1.66	1.0E-100	E-100 A1200857.1	EST HUMAN	of62f09.x1 Soares_bastis_NHT Homo sapiens cDNA clone IMAGE:1754633 3' similar to SW:CYT_COTJA P81061 CYSTATIN:
	J					7	

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Top Hit Descriptor	Rat mRNA for short type PB-cadherin, complete cds	H.saplens mRNA for IFN-gamma (pKC-0)	Homo sapiens KIAA0957 protein (KIAA0957), mRNA	Homo sapiens RGH2 gene, retrovirus-like element	Homo sapiens myotubularin-related protein 1a mRNA, partial cds	Homo saplens follicle sumulating hormone receptor (FSHR) mRNA	Homo saplens small optic idbes (Drosophila) homolog (SOLH) mRNA	Homo sapiens small optic idoes (Drosophila) homolog (SOLH) mRNA	801863164F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4080999 5	xa82f01 x1 NCI, CGAP_CML1 Homo sapiens cDNA clone IMAGE:2573305 3' similar to gb:X12433 PROTEIN PHPS1-2 (HUMAN):	AU118182 HEMBA1 Homo sapiens cDNA clone HEMBA1003046 5	Homo sapiens NF-E2-related factor 3 gene, complete cds	Human mRNA for plasma inter-alpha-trypsin Inhibitor heavy chain H(3)	Homo sapiens ER to nucleus signalling 1 (ERN1) mRNA	Homo sapiens ER to nucleus signalling 1 (ERN1) mRNA	AU140214 PLACE2 Homo sapiens cDNA clone PLACE2000137 5'	yf38c08.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:129134 3'	Homo sapiens Rho GTPase activating protein 6 (ARHGAP6), transcript variant 4, mRNA	ae33b06.r1 Gessler Withis tumor Homo saplens cDNA clone IMAGE:897587 5' similar to TR:0487418 C487418 ACTIN FILAMENT ASSOCIATED PROTEIN	ae33b06.r1 Gessler Wilms fumor Homo sapiens cDNA clone IMAGE:897587 5' similar to TR:G487418	G487418 ACTIN FILAMENT-ASSOCIATED PROTEIN.;	MR1-TN0046-060900-004-b05 TN0046 Home saptens cDNA	MR1-TN0046-060900-004-b05 TN0046 Homo saplens cDNA	Human mRNA for kidney epidermal growth factor (EGF) precursor	601647357F1 NIH_MGC_61 Homo sapiens cDNA clone IMAGE:3931310 5	Homo sapiens chromosome 21 segment HS21C003	AU118951 HEMBA1 Homo sepiens cDNA clone HEMBA1000343 5'	AU116951 HEMBA1 Homo sapiens cDNA clone HEMBA1000343 5	Homo saplens mRNA for KIAA1485 protein, partial cds	wr37g09.x1 NCI_CGAP_Pr28 Homo septens cDNA clone IMAGE:2489920 3' similær to contains element	inent;	PM0-BN0065-100300-001-c06 BN0065 Homo saplens cDNA
	Rat mRNA for sho	H.saplens mRNA	Homo sapiens KIA	Homo sapiens RG	Homo sapiens my	Homo saplens foll	Homo sapiens sm	Homo sapiens sm	601863164F1 NIF	xa82f01.x1 NCI_CGAP_CML1   PROTEIN PHPS1-2 (HUMAN);	AU118182 HEMB	Homo sepiens NF	Human mRNA for	Homo sapiens ER	Homo sapiens ER	AU140214 PLACE	yf38c08.s1 Soares	Homo sapiens Rh	ae33b06.r1 Gessli G487418 ACTIN	ae33b06.r1 Gessl	G487418 ACTIN F	MR1-TN0046-060	MR1-TN0046-060	Human mRNA for	601647357F1 NIF	Homo sapiens chr	AU118951 HEMB	AU118951 HEMB	Homo saplens mR	wr37g09.x1 NCI_C	MER22 repetitive element;	PMo-BN0065-100
Top Hit Database Source	NT L	IN	Į.	IN	N L	Į,	Į.	۲	EST_HUMAN	EST HUMAN	EST HUMAN	Z	NT	LN	IN	EST_HUMAN	EST_HUMAN	IN	EST HUMAN		EST_HUMAN	EST_HUMAN	EST_HUMAN	IN	EST HUMAN	IN	EST_HUMAN	EST HUMAN	NT		EST_HUMAN	EST_HUMAN
Top Hit Acession No.	383349.1	(62468.1	11418976 NT	J11078.1	.0E-100 AF057354.1	4503792 NT	5032104 NT	5032104 NT	.0E-100 BF244218.1	.0E-100 AW075983.1	.0E-100 AU118182.1	1.0E-100 AF135116.1	(14690.1	4557568 NT	4557568 NT	.0E-100 AU140214.1	210887.1	7382479 NT	.0E-100 AA496841.1		.0E-100 AA496841.1	.0E-100 BF376478.1	.0E-100 BF37647B.1	04571.1	1.0E-100 BF103853.1	.0E-100 AL163203.2	.0E-100 AU116951.1	.0E-100 AU116951.1	.0E-100 AB040918.1		.0E-100 AI972388.1	1.0E-100 AW998611.1
Most Similar (Top) Hit BLAST E Value	1.0E-100 D83349.1	1.0E-100 X62468.1	1.0E-100	1.0E-100 D11078.1	1.0E-100	1.0E-100	1.0E-100	1.0E-100	1.0E-100	1.0E-100	1.0E-100	1.0E-100 /	1.0E-100 X14690.1	1.0E-100	1.0E-100	1.0E-100	1.0E-100 R10887.1	1.0E-100	1.0E-100/		1.0E-100	1.0E-100	1.0E-100	1.0E-100 X04571.1	1.0E-100	1.0E-100	1.0E-100	1.0E-100	1.0E-100	To	1.0E-100/	1.0E-100/
Expression Signal	1.14	1.41	2.5	6.55	1.67	2.28	3.01	3.01	1.74	0.76	1.45	1.78	0.85	6.0	6.0	5.62	1.36	1.77	1.02		1.02	1.18	1.18	6.2	3.53	5.59	0.47	. 0.47	3.88	10,	1.65	2.28
ORF SEQ ID NO:		28754	28896		30456		31291		31578	31893			32461		32818	33174		33653	33638						35345			35838				34588
Exon SEQ ID NO:	15447	15634					18323		18606	18819	1				19465	19786	1	20223	20210	i			20162					22294				21076
Probe SEQ ID NO:	2315	2507	2771	3083	4326	4351	5202	5202	5404	5625	5818	5864	9999	6292	6292	9299	6824	8069	2869		6982	7026	7026	7033	8729	8766	9216	9216	9433	9	9510	9633

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Top Hit Descriptor  Top Hit Descriptor  Top Home sapiens cDNA clone NT2RP2001918 5'	AU12/1/20 IN LANT 2 Train September 2000.	Aomo sapiens in the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and th	Homo saplens mRNA for KIAA 1620 protein, per use LAAA 1626 File	hR82c11.yl NCI_CGAP_GU1 Homo capiens curva durie invo Crosecope File	heact1.y1 NCI_CGAP_GU1 Home sapiens cDNA clone IMAGE. 2909090 5	602020554F1 NCI_CGAP_Brn67 Homo sapiens cDNA cione IMAGE: 4130103 3	Human endogenous retrovirus HERV-K, pol gene	MRO-BN0070-270300-008-h11 BN0070 Homo sapiens cDNA	H. sapiens CD97 gene exon 4	H.sapiens CD97 gene exon 4	Homo sapiens 14q32 Jagged2 gene, complete cds; and univioun gene	Homo sapiens 14q32 Jagged2 gene, complete cds; and unknown gene	Homo sapiens chromosome 21 segment HS21C047	Homo sapiens golgin-like protein (GLP) gene, complete ods	Homo sapiens clase gene, exon 12	Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transita as a upor	genes, complete cds Tanabana vi Nici CGAP 1.124 Homo saplens cDNA clone IMAGE: 3' similar to TR:Q21997 Q21997	COSMID R161. [2] TR:Q9UAD8;	Homo saplens SH3-domain binding protein 1 (2) (3) (1) (1) (1) (1) (1) (1) (1) (1) (1) (1	Homo sapiens KIAAutoo gelis procus (***)	Hono septens unisconducturante de la SEC14.2), mRNA	Home sapiens SEC14 (S. cerevisiae) like 2 (SEC14L2), mRNA	Home sapiens and for KIAA0448 protein, partial cds	Ligens capital arliarior homeobox 2 (VAX2), mRNA	Homo saplens ventral anterior homeobox 2 (VAX2), mRNA	Homo sapiens pescadillo (zebrafish) homolog 1, containing BRCT domain (PES1), ministra	Home sapiens phosphoribosyglycinamide formytransferase, phosphoribosyglycinamide synutomos	phosphoribosylaminoimidazole synthetase (GART) mKNA i se sentene of certiles abble myosin heavy chain gene	Ronal Red 14F1 NIH MGC 83 Homo sapiens cDNA clone IMAGE:42972915	Indige 09 x1 Scares NFL T GBC S1 Homo sapiens cDNA clone IMAGE: 1843330 3	Homo sapiens butyrophilin, subfamily 2, member A1 (BTN2A1), mKNA	
Top Hit Database Source	EST HUMAN	LZ	E	FST HUMAN	EST HUMAN	EST HIMAN	LV	EST HIMAN	- PI	Į.	LZ.	12	FZ	- FZ	Z IZ		LZ LX	EST_HUMAN	NT	NT NT	4 NT	4 NT	LN 4	z	N 4	1 t	Z	TN 4	LZ I	FOI HOMAN	TIME TO TO THE TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOT	11100
sslon				T	T			,	E-100 BF3Z/29Z.1	94033.1	7444470	DE-100 AF1111 / 0.3	DE-100 AF111170.3	0E-100 ALT03247.2	1.206269.1	0E-100/AJ131034.1	.0E-100 AF240786.1	OE-100 BF446549.1	11545732 NT	11418123 NT	11417974 NT	7110714 NT	.0E-101 7110714 NT	AB007915.2 NI			765/454 N	4503914 NT	1.0E-101 Z20656.1	1.0E-101 BF681218.1	AI221878	
Most Similar (Top) Hit BLAST E Value	1.0E-100 AU127720.1	1 0F-100 AF	1 0E 100 AB048846.1	1.05-100 001-001	1.0E-100 AWGS0467.1	1.0E-100 A	1.0E-100 Br34/318.	1.0E-100 110391.1	1.0E-100 B	1.0E-100 X94033.1			1.0E-100 A	1.0E-100	1.0E-100 AF-206289.1	1.0E-100/	1.0E-100	1 OF-100	1.0E-100	1.0E-100	1.0E-100	Ĺ		L			1.0E-101	_				4. 1.0E-101
Expression Signal	0.84	217	17.0	71.7	1.81	1.81	0.64	1.35	6.64	1.56	1.55	3.91	3.91	3.07	2.21	1.93	7.59		4 97					1.4	5 6.12	6.12	3 1.37	7 1.35	2 0.85			1.44
ORF SEQ ID NO:		1	36400	36401	36687	36688	37327					38405		26241		38812	38832		22062			1	L		4 26945	_	L	27117		L		
Exon SEQ ID NO:	207726	25/37	- 1		23086	23086	23721	23815	24075	24619	24619	L	24715	13241	24962	L		1	ı	25341	1	22//8	- 1	1_	L	1	792 13971	14052	048 14121	١.	L	l
Probe SEO ID NO:		200	9782	9782	10048	10048	10688	10782	10996	11564	11564	11635	11635	11665	11977	12128	4 24 7.7	3	12312	12493	12/34	13195	2 2	25,	3   2		۲		o là	1009	2	۴

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Table 4
Single Exon Probes Expressed in Placenta

	Top Hit Acession Database Top Hit Descriptor Source	5921460 NT Homo sepiens butyrophilin, subfamily 2, member A1 (BTN2A1), mRNA	7662183 NT Hamo sepiens KIAA0569 gene product (KIAA0569), mRNA	7662183 NT Homo sepiens KIAA0569 gene product (KIAA0569), mRNA	4502996 NT Homo sepiens carboxypeptidass A1 (pancreatio) (CPA1) mRNA	0E-101 BE843070.1 EST_HUMAN RC3-ST0281-160600-016-109 ST0281 Homo sapiens cDNA	5729992 NT Homo septens A kinase (PRKA) anchor protein 6 (AKAP6), mRNA	0E-101 X72993.1 NT H-sapiens EWS gene, exon 5	.0E-101 A\237744.1   NT   Homo sepiens RIBIIR gene (partial), exon 12	0E-101 AJ237744.1 NT Homo septens RIBIIR gene (perfal), exon 12	0E-101 AJ252312.1 NT Homo sepiens genomic downstream Rhesus box	4885270 NT Homo sepiens gamma-glutamyltransferase 1 (GGT1) mRNA	OE-101 BF035327.1   EST_HUMAN   601458531F1 NIH_MGC_66 Home sapiens cDNA clone IMAGE:3862086 5'		N	.0E-101 AJ237744.1 NT Homo sapiens RIBIIR gene (partial), exon 12	0E-101 AB022785.1 NT Homo sepiens ASH2L gene, complete cds, similar to Drosophila ash2 gene		5921460 NT Homo sapiens butyrophilin, subfamily 2, member A1 (BTN2A1), mRNA	EST_HUMAN	EST_HUMAN	OE-101 AW 965139.1   EST HUMAN   EST377212 MAGE resequences, MAGI Homo sapiens cDNA	7512 NT	7427512 NT	11430734 NT	11545780 NT	NT	0E-101 AF208970.1 NT Homo septiens Kruppel-type zinc finger protein (PEG3) mRNA, atternative splice form 4, partial cds	OE-101 AW008475.1   EST_HUMAN   wv55f12.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2533487.3'	.0E-101 BE257384.1   EST_HUMAN   601109217F1 NIH_MGC_16 Homo sepiens cDNA clone IMAGE:3349901 5'	0E-101 BF330759.1 EST_HUMAN RC1-BT0313-220700-018-f12 BT0313 Homo septems cDNA	EST_HUMAN	<b>EST_HUMAN</b>	0E-101 BF02974.1   FST HUMAN   601764686F1 NIH MGC 53 Homo sepiens cDNA clone IMAGE:3996837 5
,[	Top Hit Acession No.	5921460	7662183	7662183	4502996	BE843070.1	5729892	X72993.1	4J237744.1	4,1237744.1	4J252312.1	4885270	3F035327.1	AW965556.1	4J237744.1	4J237744.1	4B022785.1	5921460	5921460	3E612554.1	BE612554.1	4W965139.1	7427512	7427512	11430734	11545780	AF208970.1	AF208970.1	AW008475.1	BE257384.1	BF330759.1	BE275821.1	3E275821.1	3F020174 1
	Most Similar (Top) Hit BLAST E Value	1.0E-101	1.0E-101	1.0E-101	1.0E-101	1.0E-101	1.0E-101	1.0E-101	1.0E-101	1.0E-101	1.0E-101	1.0E-101	1.0E-101	1.0E-101	1.0E-101	1.0E-101	1.0E-101	1.0E-101	1.0E-101	1.0E-101	1.0E-101	1.0E-101	1.0E-101	1.0E-101	1.0E-101	1.0E-101	1.0E-101	1.0E-101	1.0E-101	1.0E-101	1.0E-101	1.0E-101	1.0E-101	1 0E-101
	Expression Signal	1.44	1.57	1.57	2.07	2.70	1.2	4.62	9.27	9.27	20.15	2.97	23	1.82	3.59	3.59	3.81	1.14	1.14	9.0	9.0	1.94	4.07	4.07	0.96	1.26	4.22	4.22	7.65	1.99	6.54	0.74	0.74	1.6
	ORF SEQ ID NO:	27850	28028	28029	28247	28373			23052			29467				29026	١.		31240						33396			34020						34843
	Exen SEQ ID NO:	14767	14934	14934		15254					16196					15916					- 1				- 1	1		1	20714	20809		$\perp$		21327
	Probe SEQ ID NO:	1614	1785	1785	1999	2116	2425	2680	2802	2802	3020	3273	3313	3468	3487	3487	3981	5147	5147	5248	5248	5433	6126	6126	6834	7423	7473	7473	7645	7749	7900	8097	8097	8245

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Top Hit Descriptor	hh74g10.y1 NCL_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2988578 6' similar to gb:J03143 INTERFERON-GAMMA RECEPTOR ALPHA CHAIN PRECURSOR (HUMAN);	hh74g10.y1 NCI_CGAP_GU1 Homo sepiens cDNA clone IMAGE:2868578 5' similar to gb:J03143 INTERFERON-GAMMA RECEPTOR ALPHA CHAIN PRECURSOR (HUMAN);	zk29g08.r1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA cione IMAGE:471998 6' similar to PIR:S54640 S54640 YD9335.03c protein - yeast;	Homo sapiens mRNA for KIAA1351 protein, pertial cds	Homo sapiens mRNA for KIAA1351 protein, partial cds	Human mRNA for pancreatic gamma-glutamytransferase	Human mRNA for pancreatic gamme-glutamytransforase	Homo saplens gamma-glutamyltransferase 1 (GGT1), transcript variant 3, mRNA	601472808T1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3875953 3'	601472808T1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3875953 3'	Homo sapiens potassium channel, subfamily K, member 10 (KCNK10), mRNA	Homo sapiens Janus kinase 2 (a protein tyrosine kinase) (JAK2), mRNA	b77411.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2184309 3' similar to gb:M26326 KERATIN, TYPE I CYTOSKELETAL 18 (HUMAN);	b77d11.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2184309 3' similar to gb:M26326	KERATIN, TYPE I CYTOSKELETAL 18 (HUMAN);	601680825F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:3950887 5'	601680825F1 NIH_MGC_83 Homo saplens cDNA clone IMAGE:3950887 5'	Homo sapiens mRNA for KIAA0819 protein, partial cds	RC-BT163-290499-085 BT163 Homo sapiens cDNA	RC-BT163-290499-085 BT163 Homo sapiens cDNA	QV3-HT0460-230200-101-d03 HT0460 Homo sapiens cDNA	QV1-DT0068-240200-085-a01 DT0068 Homo saplens cDNA	Homo sepiens phosphatidylinositol 4-kinase 230 (p4K230) mRNA, complete cds	Homo sapiens chromosome 21 segment HS21C103	601108292F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3344326 5'	Homo sapiens down-regulated in adenoma (DRA) mRNA	Human endogenous retroviral DNA (4-1), complete retroviral segment	Homo sapiens solute carrier family 2 (facilitated glucose transporter), member 9 (SLC2A9), mRNA	Homo saplens solute carrier family 2 (facilitated glucose transporter), member 9 (SLC2A9), mRNA	601299982F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3829901 5'
Top Hit Database Source	EST_HUMAN	EST_HUMAN	EST_HUMAN	L	LN	L	ΙΝ	NT	EST_HUMAN	EST_HUMAN	N-	N	EST HUMAN		EST_HUMAN	EST_HUMAN	EST_HUMAN	NT	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	L'N	NT	EST_HUMAN	NT	LΝ	FN		EST_HUMAN
Top Hit Acession No.	.0E-101 AW630070.1	.0E-101 AW630070.1	.0E-101 AA036800.1	1.0E-101 AB037772.1	I.0E-101 AB037772.1	(60069.1	(60069.1	8845492 NT	.0E-101 BE619667.1	.0E-101 BE619667.1 EST_	10863960	11429127 NT	.0E-101 AI570293.1		.0E-101 AI570293.1	.0E-101 BE973648.1	.0E-101 BE973648.1	.0E-101 AB020626.1	.0E-101 A1908168.1	.0E-101 AI908168.1	.0E-101 BE163587.1	.0E-101 AW939051.1	.0E-102/AF012872.1	.0E-102 AL163303.2	.0E-102 BE252470.1	4657534 NT	A10976.1	11437146 NT	11437146 NT	.0E-102 BE408447.1
Most Similar (Top) Hit BLAST E Value	1.0E-101	1.0E-101	1.0E-101	1.0E-101	1.0E-101	1.0E-101 X60069.1	1.0E-101 X60069.1	1.0E-101	1.0E-101	1.0E-101	1.0E-101	1.0E-101	1.0E-101		1.0E-101	1.0E-101	1.0E-101	1.0E-101	1.0E-101	1.0E-101	1.0E-101	1.0E-101	1.0E-102/	1.0E-102	1.0E-102	1.0E-102	1.0E-102 M10976.1	1.0E-102	1.0E-102	1.0E-102
Expression Signal	0.71	0.71	1.1	0.99	0.99	17.36	17.38	19.41	3.36	3.38	99.0	1.94	4.37		4.37	0.83	0.83	1.31	1.85	1.85	2.24	12.79	0.81	4.57	19.0	1.06	1.9	2.05	2.05	355.9
ORF SEQ ID NO:	35132	35133	35832	36167	36168	34619	34620	36209	36593	36594	36737	37264	37299		37300	37426	37427	38089	38748	38749			26284	26589	26844	27028	27362	27518	27519	27681
Exan SEQ ID NO:	21598	21598		22596	22596	21103	21103				23136	23654	23690		23690	23804	23804	24432	25040	25040	25489	25529	13278	13562	13820	13975	14306	14453	14453	14603
Probe SEQ ID NO:	8517	8517	9212	9531	9531	9661	9861	9676	9959	6966	10098	10620	10656		10656	10771	10771	11371	12059	12029	12738	12793	40	351	989	796	1141	1297	1297	1450

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Table 4 · · Single Exon Probes Expressed In Placenta

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Top Hit Descriptor	am80c10.x1 Johnston frontal cortex Homo seplens cDNA done IMAGE:1539954 3' similar to SW:GG95_HUMAN Q08379 GOLGIN-95.;	am60c10.x1 Johnston frontal cortex Homo sapiens cDNA done IMAGE:1539954 3' similar to SW:GG05 HUMAN Q08379 GOLGIN-96. ;	Homo sepiens PRKY exon 7	Homo sapiens KIAA0187 gene product (KIAA0187), mRNA	AU141005 PLACE4 Homo sapiens cDNA clone PLACE4000650 5'	AU141005 PLACE4 Homo sapiens cDNA clone PLACE4000650 5'	Hono sapiens chromosome 21 segment HS21C007	601107843F1 NIH_MGC_16 Homo sepiens cDNA clone IMAGE:3343882 5'	yi32e04.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:140934 67	Homo saplens protein phosphatase-1 regulatory subunit 7 (PPP1R7) gene, exon 7	Homo sapiens HSC54 mRNA for heat shock cognate protein 54, complete cds	Homo seplens histone deacet/lase 7 (HDAC7), mRNA	Homo sapiens histone deacetylase 7 (HDAC7), mRNA	Homo sapiens hect domain and RLD 2 (HERC2), mRNA	ar82109.x1 Barshad colon HPLRB7 Homo sapiens cDNA clone IMAGE:2151785 3' similar to TR.Q13137	C. 13197 NDT-52., [1]-H-RiSali-d-40A-11 st NCI CGAP SubS Homo saniens cDNA done IMAGE 2736835.3	601561505F1 NIH MGC 20 Homo sapiens cDNA clone IMAGE:3831241 5'	601277215F1 NIH_MGC_20 Homo sapiens cDNA done IMACE:3618243 5'	Homo sapiens mRNA for KIAA0960 protein, partial cds	Homo sapiens mRNA for Centaurin-alpha2 protein	AV710738 Cu Homo sapiens cDNA clone CuAAKD03 5	QV3-NT0025-210600-236-h08 NT0025 Homo sapiens cDNA	AV694817 GKC Homo saplens cDNA clone GKCEEE11 5'	AV694817 GKC Homo sapiens cDNA clone GKCEEE11 5'	Homo sapiens mRNA for KIAA0454 protein, partial cds	601283770F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3605536 5'	601283770F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3605536 5'	AV755842 BM Homo sepiens cDNA clone BMFAUD06 5'	yd13d07,r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:67021 5'	yd13d07.r1 Soares fetal liver spleen 1NFLS Homo saplens cDNA clone IMAGE:67021 5'	AU124629 NT2RM4 Homo septens cDNA clone NT2RM4000309 5'
Top Hit Database Source	EST_HUMAN	EST HUMAN	Г		EST_HUMAN		Г	EST_HUMAN	T	T	NT				FO	T	Т	Т	Ϊ́		EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	NT.	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN		EST HUMAN
Top Hit Acession No.	0E-102 A1124669.1	0E-102 A1124669.1	0E-102 Y13932.1	TN 621979	0E-102 AU141005.1	0E-102 AU141005.1	0E-102 AL163207.2	0E-102 BE251310.1	0E-102 R66488.1	0E-102 AF067133.1	0E-102 AB034951.1	TN63398 NT	TN05398 NT	11433046 NT	05 400 8 1450005 4	0E-102 AIN453625.1	0E-102 BE729323.1	.0E-102 BE386106.1	0E-102 AB023177.1		.0E-102 AV710738.1	.0E-102 BE763051.1	.0E-102 AV694817.1	.0E-102 AV694817.1	.0E-102 AB007923.1	.0E-102 BE388063.1	.0E-102 BE388063.1	.0E-102 AV755842.1	.0E-102 T70393.1	T70393.1	.0E-102 AU124629.1
Most Similar (Top) Hit BLAST E Value	1.0E-102	1.0E-102	1.0E-102	1.0E-102	1.0E-102	1.0E-102	1.0E-102	1.0E-102	1.0E-102	1.0E-102	1.0E-102	1.0E-102	1.0E-102	1.0E-102	1 0 1	1 0F-102	1.0E-102	1.0E-102	1.0E-102	1.0E-102	1.0E-102	1.0E-102	1.0E-102	1.0E-102	1.0E-102	1.0E-102		1.0E-102	1.0E-102	1.0E-102	1.0E-102
Expression Signal	1.91	1.91	0.74	1.47	3.73	3.73	1.74	2.57	1.28	1.6	6.87	3.25	3.25	0.81	2 04	107	0.91	1.02	1.5	8.03	261	3.85	1.71	1.71	0.81	1.2	1.2	0.84	2		3.11
ORF SEQ ID NO:	28642	28643			29387		30472					32408		32414	93000			<u> </u>	33977	34057										36156	
Exen SEQ ID NO:	15514	16514	16266		16378		17490		1		19057			19100	10504	1	1		l		1										
Probe SEQ ID NO:	2383	2383	3090	3133	3203	3203	4347	4533	5224	5487	5867	5905	5905	5912	8400	7227	7286	7314	7429	7510	7802	8418	8691	8691	8802	9131	9131	9481	9522	9522	9611

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Top Hit Descriptor	Hamo saptens phosphalipid scramblase 1 gene, exon 1 and 5' flanking region	Hamo sapiens myamesin (M-protein) 2 (165kD) (MYOM2), mRNA	Hamo sapiens myamesin (M-protein) 2 (165kD) (MYOM2), mRNA	RC-BT074-260499-014 BT074 Homo sapiens cDNA	RC-BT074-260499-014 BT074 Homo sapiens cDNA	on57h04.s1 Soares, NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1560823 3' similar to SW:CAV2 HUMAN P51686 CAVEOLIN-2: 111:	601439392F1 NIH MGC 72 Homo sapiens cDNA clone IMAGE:3924168 57	Homo sapiens UDP glycosyltransferase 2 family, polypeptide B11 (LIGT2B11) mRNA	Homo sapiens UDP glycosytransferase 2 family polypeptide B11 (UGT2B11) mRNA	ak49h10.s1 Soares_testls_NHT Homo sapiens cDNA clone IMAGE:1409347 3'	RC6-ET0072-150600-011-F01 ET0072 Homo sapiens cDNA	Human chromosome 16 creatine transporter (SLC8A8) and (CDM) parapools genes, complete cris	Homo sepiens chromosome 21 segment HS21C080	M07c12.x1 NCI_CGAP_Co20 Homo sepiens cDNA clone IMAGE:2666038 31	Homo sepiens myeloid/lymphoid or mixed-lineage leukemia (trithorax (Drosophila) honolog); translocated to, 4 (MLL14), mRNA	601500405F1 NIH MGC 70 Homo satiens cDNA clone IMAGE:3902305 5	601500405F1 NIH MGC 70 Hamo sapiens cDNA clone IMAGE:3902305 5	Homo sapiens mRNA for KIAA0235 protein, partial cds	Homo sapiens nucleolar protein (KKE/D repeat) (NOP56) mRNA	Homo sapiens mRNA for pregnancy-associated plasma protein-E (PAPPE gene)	801485388F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3887876 5'	Homo sapiens phosphatidylinositol 4-kinase 230 (pi4K230) mRNA, complete cds	Homo saplens ang GDS-ASSOCIATED PROTEIN (SMAP), mRNA	Homo sapiens bone morphogenetic protein 8 (osteogenic protein 2) (BMP8) mRNA	Homo saplens bone morphogenetic protein 8 (osteogenic protein 2) (BMP8) mRNA	AU134991 PLACE1 Hamo sapiens cDNA clone PLACE1000965 5'	Homo sapiens promyelocytic leukemia zinc finger protein (PLZF) gene, complete cds	weld08s1 Soares placenta Bto9weeks 2NhHP8th9W Homo senians cDNA clone MAGE-255509 2	601573113F1 NIH MGC 9 Homo sepiens cDNA clone IMAGE:3834315 51	UI-H-BW0-ajt-h-11-0-UI.s1 NG_CGAP_Sub6 Homo sepiens cDNA clone IMAGE:2733165 3'
Top Hit Database Source	NT	NT	TN	EST_HUMAN	EST_HUMAN	EST HUMAN	EST HUMAN	FZ	ΙΝ	EST_HUMAN	EST HUMAN	IN	Į.	EST HUMAN	L L	EST HUMAN	EST HUMAN	LN	N	LN	EST_HUMAN	IN	NT	L'N	Į.	EST_HUMAN	۲	EST HUMAN	EST HUMAN	EST_HUMAN
Top Hit Acession Na	.0E-102 AF153715.1	11425430 NT	11425430 NT	.0E-102 AI905037.1	.0E-102 A1905037.1	.0E-102 AA970786.1	.0E-102 BE897468.1	4507822 NT	4507822 NT	.0E-102 AA868675.1	.0E-102 BF359243.1	.0E-102 U41302.1	0E-102 AL163280.2	0E-102 AW300862.1	11419159 NT	0E-103 BE908158.1	0E-103 BE908158.1	0E-103 D87078.2	5453793 NT			0E-103 AF012872.1	7657592 NT	4502428 NT	4502428 NT	0E-103 AU134991.1	DE-103 AF060568.1	0E-103 N32770,1	0E-103 BE744722.1	
Most Similer (Top) Hit BLAST E Value	1.0E-102	1.0E-102	1.0E-102	1.0E-102	1.0E-102	1.0E-102	1.0E-102	1.0E-102	1.0E-102	1.0E-102	1.0E-102	1.0E-102	1.0E-102	1.0E-102	1.0E-102	1.0E-103	1.0E-103	1.0E-103	1.0E-103	1.0E-103	1.0E-103	1.0E-103	1.0E-103	1.0E-103	1.0E-103	1.0E-103	1.0E-103 /	1.0E-103	1.0E-103	1.0E-103
Expression Signal	0.64	0.67	29.0	3.26	3.26	1.5	1.37	2.44	2.44	1.47	2.47	2.83	5.69	5.67	1.25	0.85	0.85	8.24	0.84	74.34	7.08	3.51	1.02	0.95	0.95	1.95	1.84	+	2.76	5.33
ORF SEQ ID NO:			37292		37326	37394	38030				38378	38699		32000	32015	26331	26332	26365	26466	27234	27500	27863	28207	28280	28281	28638	28772	28921		29853
SEQ ID NO:	23628	23681	23681	23720	2372D	23781					24688		25142	25517	25553	13308	13308	13338	13436	14175	14429	14778	15107	15172	15172	15510	15548	15805	16313	
Probe SEQ (D NO:	10593	10647	10647	10687	10687	10748	11323	11327	11327	11600	11690	12009	12182	12775	12831	71	74	102	213	1004	1272	1626	1964	2031	2031	2379	2523	2685	3137	3467

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	Top Hit Descriptor	Harmon m RNA for K (AA1459 protein, partial cds	Macaca mulatta cyclophilin A mRNA, complete cds	Abrilda Strategene lung (#937210) Homo saplens cDNA clone IMAGE:840407 3' similar to contains	olement LTR10 repetitive alement ;	Homo sepiens neuropilin 1 (INRP1), mKNA	seq340 b4HB3MA-Cot109+10-Bio Homo sapiens contact an incommendation of the light seq 10 seq 10 seq 10 seq 10 seq 10 seq 10 seq 10 seq 10 seq 10 seq 10 seq 10 seq 10 seq 10 seq 10 seq 10 seq 10 seq 10 seq 10 seq 10 seq 10 seq 10 seq 10 seq 10 seq 10 seq 10 seq 10 seq 10 seq 10 seq 10 seq 10 seq 10 seq 10 seq 10 seq 10 seq 10 seq 10 seq 10 seq 10 seq 10 seq 10 seq 10 seq 10 seq 10 seq 10 seq 10 seq 10 seq 10 seq 10 seq 10 seq 10 seq 10 seq 10 seq 10 seq 10 seq 10 seq 10 seq 10 seq 10 seq 10 seq 10 seq 10 seq 10 seq 10 seq 10 seq 10 seq 10 seq 10 seq 10 seq 10 seq 10 seq 10 seq 10 seq 10 seq 10 seq 10 seq 10 seq 10 seq 10 seq 10 seq 10 seq 10 seq 10 seq 10 seq 10 seq 10 seq 10 seq 10 seq 10 seq 10 seq 10 seq 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MAGC Homo sapiens cDNA	ESTSCOSS WASE resequences, MAGC Homo sapiens cDNA	For 1 Source, facility NHT Homo saplens cDNA clone 1391452 3'	dazecusa I scares, control alpha 2 subunit (GLRA2) gene, excn 4	Thomas Saprens 97 Similar to TR:013769	umbabusa Norgon.	Im58b05.x1 NCI_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2162289 3 similar to 15.2153	Q13769 ANONYMOUS.; Lame series distroblin (muscular dystrophy, Duchenne and Becker types), includes DXS142, DXS164,	DXS206, DXS230, DXS239, DXS268, DXS269, DXS270, DXS272 (DMD), transcript variant DP421111,	mRNA	Homo septetts Vysory III. (DMS 268, DXS 269, DXS 270, DXS 272 (DMD), transoript variant UP42 / III.) DXS 206, DXS 239, DXS 239, DXS 268, DXS 209, DXS 200, DXS 200, DXS 200, DXS 200, DXS 200, DXS 200, DXS 200, DXS 200, DXS 200, DXS 200, DXS 200, DXS 200, DXS 200, DXS 200, DXS 200, DXS 200, DXS 200, DXS 200, DXS 200, DXS 200, DXS 200, DXS 200, DXS 200, DXS 200, DXS 200, DXS 200, DXS 200, DXS 200, DXS 200, DXS 200, DXS 200, DXS 200, DXS 200, DXS 200, DXS 200, DXS 200, DXS 200, DXS 200, DXS 200, DXS 200, DXS 200, DXS 200, DXS 200, DXS 200, DXS 200, DXS 200, DXS 200, DXS 200, DXS 200, DXS 200, DXS 200, DXS 200, DXS 200, DXS 200, DXS 200, DXS 200, DXS 200, DXS 200, DXS 200, DXS 200, DXS 200, DXS 200, DXS 200, DXS 200, DXS 200, DXS 200, DXS 200, DXS 200, DXS 200, DXS 200, DXS 200, DXS 200, DXS 200, DXS 200, DXS 200, DXS 200, DXS 200, DXS 200, DXS 200, DXS 200, DXS 200, DXS 200, DXS 200, DXS 200, DXS 200, DXS 200, DXS 200, DXS 200, DXS 200, DXS 200, DXS 200, DXS 200, DXS 200, DXS 200, DXS 200, DXS 200, DXS 200, DXS 200, DXS 200, DXS 200, DXS 200, DXS 200, DXS 200, DXS 200, DXS 200, DXS 200, DXS 200, DXS 200, DXS 200, DXS 200, DXS 200, DXS 200, DXS 200, DXS 200, DXS 200, DXS 200, DXS 200, DXS 200, DXS 200, DXS 200, DXS 200, DXS 200, DXS 200, DXS 200, DXS 200, DXS 200, DXS 200, DXS 200, DXS 200, DXS 200, DXS 200, DXS 200, DXS 200, DXS 200, DXS 200, DXS 200, DXS 200, DXS 200, DXS 200, DXS 200, DXS 200, DXS 200, DXS 200, DXS 200, DXS 200, DXS 200, DXS 200, DXS 200, DXS 200, DXS 200, DXS 200, DXS 200, DXS 200, DXS 200, DXS 200, DXS 200, DXS 200, DXS 200, DXS 200, DXS 200, DXS 200, DXS 200, DXS 200, DXS 200, DXS 200, DXS 200, DXS 200, DXS 200, DXS 200, DXS 200, DXS 200, DXS 200, DXS 200, DXS 200, DXS 200, DXS 200, DXS 200, DXS 200, DXS 200, DXS 200, DXS 200, DXS 200, DXS 200, DXS 200, DXS 200, DXS 200, DXS 200, DXS 200, DXS 200, DXS 200, DXS 200, DXS 200, DXS 200, DXS 200, DXS 200, DXS 200, DXS 200, DXS 200, DXS 200, DXS 200, DXS 200, DXS 200, DXS 200, DXS 200, DXS 200, DXS 200, DXS 200, DXS 200, DXS 200, DXS 200, DXS 200, D	mRNA " I like (BDI 31 ) mRNA	Homo saptens ribosomal protein Lo-ino (v. 2017)	Homo sapients Nizhvozi gene (rem.)	7	1	$\neg \tau$	
	Top Hit Database Source		Į.	Z	EST_HUMAN	E	EST_HUMAN		EST HUMAN	HIST TOWNS	Z !		7	EST HUMAN	EST HUMAN	EST HUMAN	12	NAME IN POS	NGIOL COL	EST_HUMAN		FN.		N	NT	LN LN	EST HUMAN	ESI HOMAN	EST_HUMAN	EST_HUMAN
66.00	Top Hit Acession No.			-103 AF023861.1	-103 AA485683.1  E	30878					179995.1	11435053 NT	83		1				1.1700861	1590071.1		5032282 NT		5032282 NT	11431100 NT	1.0E-103 AJ289880.1	1.0E-103 AW965776.1	0E-103 BE748158.1	0E-103 AI590071.1	.0E-103 AI590071.1
	<u>т</u> т п	value	1.0E-103 AB(	1.0E-103 AF	1 0F-103 AA	4 OF-403	1 0F-103 T23683.1		1.0E-103 AA451618.1	1.0E-103 BF569527.1	1.0E-103 AF179995.1	1.0E-103	1.0E-103	1.0E-103 AW 954586.1	1.0E-103 AW954566.1	1.0E-103 AA781442.1	1.0E-103 AF053490.1		1.0E-103 Albs0071.1	1.0E-103 AI590071.1		1.0E-103		1.0E-103	1.0E-103	1.0E-103	1.0E-103	1.0E-103	1.0E-103	
	Expression (Signal B		0.95	5.46	- 0	4 54	1.04	3	0.63	0.0	1.67	0.8	8.0	0.84	28.0	1.15	0.91		1.66	1.86		1.77		1,77				3.6	4	2
	ORF SEQ ID NO:		29700		1000	30053	30080	30204		32563	32571	32926	32927	33130					33422	33423		31521			31022	L	1_	١		
	SEQ ID	j	16691	17010		17053	17092	17264	18438	19238	19245	19568	19596	19748	10748	25831	19924		20011	20011		18506			18305		Ţ	1	1	١
	Probe E SEQ ID SI		3526	3850		3894	3933	4110	5325	8056	8083	2059	202	6587	6507	6725	89/9	3	6828	6859		GOR7			280	100	7375	748	7951	7951

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יסטס בילונים	. Top Hit Descriptor	EST27193 Human Brain Homo sapiens cDNA 5' end similar to None	AU140344 PLACE2 Homo saplens cDNA clone PLACE2000374 5	AU140344 PLACE2 Homo saplens cDNA clone PLACE2000374 5'	7780e03.x1 Sogres_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:3525964.3' similar to SW PTNF HUMAN 0.16825 PROTEIN.TYROSINF PHOSPHATASE D1	Homo sapiens trible functional domain (PTPRF interaction) (TRIO) mRNA	Homo sapiens triple functional domain (PTPRF interacting) (TRIO), mRNA	nd13c02.s1 NCJ CGAP_Ov1 Homo sapiens cDNA clone IMAGE:800162 3' similar to gb:L02426 26S PROTEASE SUBUNIT 4 (HUMAN):	H. sapiens mRNA for latent transforming growth factor-beta hinding contein (1 TBP-2)	EST375749 MAGE resequences, MAGH Homo saplens cDNA	au51g04.y1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2518326 5' similar to TR:015046 015046 KIAA0338	7b41f03.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3230813 3' similar to gb:M69043 MAJOR HISTOCOMPATIBILITY COMPLEX ENHANGER-BINDING PROTEIN (HIMAN):	002d06.y6 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1522283 5' similar to TR:Q62084 Q62084 PHOSPHOLIPASE CNEIGHBORING:	Homo sapiens AXL receptor tyrosine kinase (AXL) mRNA	Homo saplens AXL receptor tyrosine kinase (AXL), mRNA	Homo sapiens NOD1 protein (NOD1) gene, exons 1, 2, and 3	Homo sapiens NOD1 protein (NOD1) gene, exons 1, 2, and 3	AU136283 PLACE1 Homo sapiens cDNA clone PLACE1003923 5'	Homo sapiens polycystic kidney disease (PKD1) gene, exons 27-30	Homo sapiens TSA305 gene, exon 16	7e68a10.x1 Scares_NSF_F8_9W_OT_PA_P_S1 Homo saplens cDNA clone IMAGE:3287610.3' similar to contains MER29.t3 MER29 repetitive element:	Homo sapiens mannosidase, beta A, Iysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D3) genes, complete cds	Homo saplens hypothetical protein FLJ20454 (FLJ20454) mRNA	Homo sapiens gene for AF-6, complete cds	DKFZp564H1072_r1 564 (synonym: hfbr2) Homo sapiens cDNA clone DKFZp564H1072 5	DKFZp564H1072_r1 564 (synonym: hfbr2) Homo saplens cDNA clone DKFZp564H1072 5	Homo sapiens bone morphogenetic protein 8 (osteogenic protein 2) (BMP8) mRNA
	Top Hit Database Source	EST HUMAN	EST HUMAN	EST_HUMAN	EST HUMAN	TN	LN LN	EST HUMAN	N <sub>T</sub>	EST_HUMAN	EST_HUMAN	EST HUMAN	EST HUMAN	IN	F	LN	LN	EST_HUMAN	NT	LN	EST HUMAN	NT	F	\ L	EST_HUMAN		Г
2	Top Hit Acession No.	.0E-103 T31080.1	.0E-103 AU140344.1	.0E-103 AU140344.1	.0E-103 BF109244.1	6005921 NT	6005921 NT	.0E-103 AA581086.1	237976.1	.0E-103 AW963676.1	.0E-103 AI878966.1	.0E-103 BE549706.1	.0E-103 AI792759.1	24061	11424061 NT	.0E-103 AF149773.1	.0E-103 AF149773.1	3.1		.0E-103 AB024759.1	.0E-103 BE644611.1	0E-103 AF224669.1	26291	.0E-103 AB011399.1	0E-104 AL037549.3	0E-104 AL037549.3	4502428
	Most Similar (Top) Hit BLAST E Vatue	1.0E-103	1.0E-103	1.0E-103	1.0E-103	1.0E-103	1.0E-103	1.0E-103	1.0E-103 Z37976.1	1.0E-103	1.0E-103	1.0E-103	1.0E-103	1.0E-103	1.0E-103	1.0E-103	1.0E-103	1.0E-103 /	1.0E-103 L43610.1	1.0E-103 /	1.0E-103	1.0E-103 A	1.0E-103	1.0E-103	1.0E-104	1.0E-104 A	1.0E-104
	Expression Signal	0.59	1.05	1.05	1.34	3.18	3.18	0.97	2.04	2.07	10.79	1.52	9.5	2.45	2.45	2.4	2.4	2.67	4.1	1.71	2.28	3.4	1.22	1.71	2.46	2.46	1.92
	ORF SEQ ID NO:		35440	35441		35934	35935	35980	36896	36944	37083	37591	37684	37785	. 37786	37794	37795	38426	37542		38730			32083	26494	26495	28182
	Exon SEQ ID NO:	21565	21901	21901	21979	22383	22383	- 1	23298	23339	23478	23963	24051	24147	24147	24157	24157	24735	23917	24953	25025	25138	25162	26293	13465	13465	15080
	Probe SEQ ID NO:	8484	8822	8822	8900	9307	9307	9349	10263	10304	10443	10878	10971	11072	11072	11083	11083	11856	11731	11968	12044	12178	12209	12414	243	243	1937

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
2267	15400	28528	33,29	1.0E-104	.0E-104 AA132975.1	EST_HUMAN	zo22c06.s1 Stratagene colon (#897204) Homo sapiens cDNA clone IMAGE:587626 3' similar to gb:Z14116_ma1 CD59 GLYCOPROTEIN PRECURSOR (HUMAN);
2277	15409	28540		1.0E-104	.0E-104 BE744628.1	EST_HUMAN	601577460F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3926438 5'
2442	15570			1.0E-104	.0E-104 BF334221.1	EST_HUMAN	RC1-CT0249-110900-214-f12 CT0249 Homo sepiens cDNA
2442	15570		9.73	1.0E-104	.0E-104 BF334221.1	EST_HUMAN	RC1-CT0249-110900-214-f12 CT0249 Homo sapiens cDNA
2506	15633	28753	2	1.0E-104	5031570 NT	N	Homo sapiens ARP2 (actin-related protein 2, yeast) homolog (ACTR2), mRNA
2934	16111	29125	17.99	1	.0E-104 M34671.1	TN	Human lymphocytic antigen CD59/MEM43 mRNA, complete ods
2983	16159		2.15	1.0E-104	.0E-104 Y11151.1	TN	H.saplens gene encoding phenylpyruvate tautomerase il
3337	16510	29526	0.99	1.0E-104	.0E-104 AU133926.1	EST_HUMAN	AU133926 OVARC1 Homo sapiens cDNA clone OVARC1000936 5'
3478	16645		2.33	1.0E-104	.0E-104 AA319436.1	EST_HUMAN	EST21658 Adrenal gland tumor Homo sapiens cDNA 5' end
3690	16852	29860	0.65	1.0E-104		N⊤	Homo sapiens mRNA for KIAA1276 protein, partial cds
3690	16852		0.65	1.0E-104	.0E-104 AB033102.1	IN	Homo sapiens mRNA for KIAA1276 protein, partial cds
4053	17209		0.71	1.0E-104	.0E-104 AB032998.1	N	Homo sapiens mRNA for KIAA1172 protein, partial cds
4248	17394		0.71	1.0E-104	.0E-104 F11745.1	EST_HUMAN	HSC31A071 normalized infant brain cDNA Homo sapiens cDNA clone c-31a07
4496	17636		33.95	1	.0E-104 X02761.1	LN	Human mRNA for fibronectin (FN precursor)
4732	17867	30849	1.2	1.0E-104	.0E-104 AF231920.1	TN	Homo sapiens chromosome 21 unknown mRNA
4732	17867	30850	1.2	1.0E-104	.0E-104 AF231920.1	NT	Homo sapiens chromosome 21 unknown mRNA
6061	19243	32567	1.05	1.0E-104	.0E-104 U43379.1	NT	Human Down Syndrome region of chromosome 21 DNA
6061			1.05	1.0E-104	.0E-104 U43379.1	LN	Human Down Syndrome region of chromosome 21 DNA
6108	19288	32623	0.93	1.0E-104	.0E-104 AB017332.1	TN	Homo sapiens alk3 mRNA for Aurora/Ip/1-related kinase 3, complete cds
6596	19756	33142	8.5	-	.0E-104 AI768797.1	EST_HUMAN	wj03b12.x1 NCJ_CGAP_Kid12 Homo sapiens.cDNA cione IMAGE:2401727 3' similar to TR:Q14145 Q14145 KIAA0132 PROTEIN ; contains element LTR7 repetitive element;
9629			8.5	١	.0E-104 A1768797.1	EST HUMAN	wj03b12.x1 NCI_CGAP_Kid12 Homo sapiens cDNA done IMAGE:2401727 3' similar to TR:Q14145 Q14145 KIAA0132 PROTEIN ; contains element LTR7 repetitive element;
6786	19941	3333	0.74	1.0€-104	7706512	7706512 NT	Homo sapiens PDZ domain-containing guanine nucleotide exchange factor I (LOC51735), mRNA
6942			3.39	l I	.0E-104 BE314182.1	EST_HUMAN	501150451F1 NIH_MGC_19 Homo sapiene cDNA clone IMAGE:3503220 5
6942				ι	.0E-104 BE314182.1	EST_HUMAN	501150451F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3503220 5'
7373			2.01	1.0E-104	11425572 NT	FA	Homo sapiens adaptor-related protein complex 2, beta 1 subunit (AP2B1), mRNA
8796	21875			1.0E-104	.0E-104 BF509244.1	EST_HUMAN	UI-H-BI4-aow-b-09-0-UI.s1 NCI_CGAP_Sub8 Homo saplens cDNA clone IMAGE:30861763
8986	_ 1			-	.0E-104 BF448230.1	EST_HUMAN	nad16g11 x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3365948 3'
9463	1	36082		١	.0E-104 AA682308.1	EST_HUMAN	zj98b06.s1 Soares_fetal_liver_sploen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:462897 3'
9484	- 1		1.03		.0E-104 T74219.1	EST_HUMAN	yc83f02.r1 Scares infant brain 1NIB Homo sapiens cDNA clone IMAGE:22440 5'
9515		36146			.0E-104 AF091395.1	· L	Homo sapiens Trio isoform mRNA, complete cds
9515	22580		5		.0E-104 AF091395.1	۲	Homo sapiens Trio isoform mRNA, complete cds

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Exan ORF SEQ Expressic Signal NO: Signal NO: Signal NO: 21084 34597 4 221894 36589 0 22393 36838 37890 37408 0 23489 37408 0 23790 37408 0 23820 37408 0 23820 37408 0 23820 37408 0 23820 38310 4 24853 38310 4 24853 38350 25502 25062 38788 4 25502 25062 38788 26541 15981 26511 28118 115091 28524 15529 15529 15509 16547 15509 16547 15509 16547 15509 16547 15509 16547 15509 16547 15509 16547 15509 16547 15509 16547 15509 16547 15509 16547 15509 16547 15509 16547 15509 16547 15549 16547 15549 16547 15549 16547 15549 16547 15549 16547 15549 16547 15549 16547 15549 16547 15549 16547 15549 16547 15549 16547 15549 16547 15549 16547 15549 16547 15549 16547 15549 16547 15549 16547 15549 16547 15549 16547 15549 16547 15549 16547 15549 16547 15549 16547 15549 16547 15549 16547 15549 16547 15549 16547 15549 16547 15549 16547 15549 16547 15549 16547 15549 16547 15547 15547 15547 15547 15547 15547 15547 15547 15547 15547 15547 15547 15547 15547 15547 15547 15547 15547 15547 15547 15547 15547 15547 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	Top Hit Database Source		Т	Т	Т	EST HUMAN	EST HUMAN	ST HUMAN	Į.		EST HOWAIN	EST TOWAR	EST HUMAN	NT	EST_HUMAN	EST HUMAN	N	LZ	EST HUMAN	EST HUMAN	EST HUMAN	NT FOR	ESI TIONING	EST_HUMAN	1407	NAMOR IN	DOT HIMAN	TA	- LV	2 12	Z
	Top Hit Acession No.				٦	1	l							E-107 L49141.1		0E-107 BES40550.1	11419701 NT	11419701 NT	0E-107 AA001415.1		-	18000.1	0E-108 BF020/28.1	0E-108 A1686040.1		.0E-108 AIG86040.1	4 4 0000	OE-108 BEZUGGGG I	180000	.0E-108 AF032897.1	.0E-108 AF032897.1
}	Most Similar (Top) Hit To BLAST E		1.0E-107 AF020671.1	1.0E-107 AV	1.0E-107 BE	1.0E-107 AW503913.1	1.0E-107 AW503913.1	1.0E-107 AI765078.1	1.0E-107 AJ404468.1	1.0E-107 AJ404468.1	1.0E-107 AU122469.1	1.0E-107 BE168726.1	1 0E-107 A	1.0E-107	1.0E-107 B	1.0E-107 B	1.0E-107	1.0E-107	1.0E-107	1.0E-107	1.0E-108	1.0E-108 Y18000.1	1.0E-108	1.0E-108/		1.0E-108	,				
	Expression Signal		4.89	0.64	2.71	1.33	1.33	1.36	0.59	0.59	0.99	1.92	900	1.58	2.3	3.91			7.14		1.72		1,02	12 14		1211					5 0.64
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Page 449 of 550 Table 4 Single Exon Probes Expressed in Placerta

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Top Hit Descriptor	hi12a11x1 NCI_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2972080 3' similar to SW:3BP1_MOUSE P55194 SH3-BINDING PROTEIN 3RP-1	Human heoatocyte nuclear factor 4-alpha gene expn 2	Human hebatocyte nuclear factor 4 Jahns dens sown 2	Homo sapiens KIAA0187 gene product (KIAA0187) mRNA	UI-HF-BNO-alr-e-04-0-UI,71 NIH MGC 50 Home saplens child close IMA CE 2006/456 51	Homo saplens PSN1 gene, alternative transcript	RC0-HT0372-241199-031-d03 HT0372 Homo caniane cDNA	601444922F1 NIH MGC 65 Home septems cDNA clone IMA CE-38A8080 F1	601444922F1 NIH MGC 65 Home sanians PINA Alone MACE-2848080 C	Homo saplens familial mental retardation protein 2 (FMR2) was 200	PM4-CT0403-240700-001-c10 CT0403 Homo seniens cin\u00e4	Homo sapiens FYVE domain-containing dual specificity protein phosphatase FYVE-DSP2 mRNA, complete cds	Homo saplens FYVE domain-containing dual specificity protein phosphatase FYVE-DSP2 mRNA, complete eds	Homo saplens caveolin-1/-2 locus, Contig1, D7S522, genes CAV2 (exons 1, 2a, and 2b), CAV1 (exons 1 and 2)	PW4-CT0403-240700-001-010 CT0403 Home confere APNA	Homo saplens E6.4D uhlatuijin-protein linese / IBE2A/ pop.	Homo sapiens E6-AP ubiquitin-protein linese (1 IDE 34) gene, excit 4	Homo saplens G protein-counsed recents family C croins 5 moments D (CDB CED)	Homo sapiens delta-6 fatty acid desaturase (FADSD8) mRNA	601113471F1 NIH MGC 16 Homo sapiens cDNA clone IMAGE:33540R4 F	602043384F1 NCI_CGAP_Bm67 Homo sapiens cDNA clone IMAGF-4181037 5/	602043384F1 NCI CGAP Bm67 Homo septems cDNA clone IMAGE:4484697 F	Hamo sapiens connective tissue growth factor-like practing mRNA commissionals	UHHF-BMO-gds-6-12-0-Ulf1 NIH MGC 38 Home services cDNA Acres NAA CESSOSSE	UFHF-BM0-ads-9-12-0-ULT NIH MGC 38 Home senions -DNA -clara MAA CE 300-257 21	Homo sabjens ETS-family transcription factor FHIE/FIHIS MENA company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the compa	yy35h10.r1 Soares mekmocyte 2NhHM Homo sapiens cDNA done IMAGE:273283 5' similar to PIR:A46773 4 A45773 tech protein long form - finit fly.	Homo saplens similar to high-mobility group (nonhistone chromosomal) protein 4 (H. saplens) (LOC63446), Henron RNA
Top Hit Database Source	EST HUMAN	Z	LN	LΝ	EST HUMAN	NT NT	EST HUMAN	EST HUMAN	EST HUMAN	LN	EST HUMAN	Ę	Į.		EST HUMAN	L	Z	F	LN.	EST_HUMAN	EST_HUMAN	EST_HUMAN	L	EST HUMAN	EST HUMAN	¥	EST HUMAN	5
	AW664438.1	U72961.1	U72961.1	7661979	AW504789.1	AJ008005.1	AW384094.1	BE869016.1	BE869016.1	AF012623.1	BF334851.1	AF264717.1	AF264717.1			Γ	Π	31857	4758333									11428155 NT
Most Similar (Top) Hit BLAST E Value	1.0E-108	1.0E-108	1.0E-108	1.0E-108	1.0E-108	1.0E-108	1.0E-108	1.0E-108	1.0E-108	1.0E-108	1.0E-108	1.0E-108	1.0E-108	1.0E-108	1.0E-108	1.0E-108	1.0E-108	1.0E-108	1.0E-108	1.0E-108	1.0E-108	1.0E-108	1.0E-108	1.0E-108	1.0E-108	1.0E-108	1.0E-108	1.0E-108
Expression Signal	1.57	2.62	2.62	3.37	0.63	3.18	1.24	2.56	2.56	99.0	0.74	6.14	6.14	1.22	1.09	0.64	0.64	4.52	2.12	1.32	0.73	0.73	1.72	0.61	0.61	0.77	0.46	1.08
ORF SEQ ID NO:						31166					32644	32789	32790	32921	32644	33302	33303	33850	34143	34193	34218	34219		34910	34911	35869	35912	37500
						- 1		- 1	_ ]	19232	19304	19441	19441	19561	19304	19909	19909	20390	20667	20715	20739	20739	21336	21388	21388	22324	22363	23880
Probe SEQ ID NO:	4273	4647	4647	4927	5037	5083	2296	5644	5644	6049	6125	6267	6267	6392	6489	6753	6753	7308	7597	7846	7674	7674	8254	8306	8306	9247	9287	10847
	Expn ORF SEQ Expression (Top) Hit Top Hit Acession NO: Signal BLASTE No. Source	Expn SEQ ID NO:         ORF SEQ Signal.         Expression Signal.         Most Similar (Top) Hit Signal.         Top Hit Signal.         Top Hit Signal.         Top Hit Signal.         Top Hit Signal.         Top Hit Signal.         Top Hit Signal.         Top Hit Signal.         Signal.         Signal.         Signal.         Signal.         Signal.         Signal.         Signal.         Signal.         Signal.         Signal.         Signal.         Signal.         Signal.         Signal.         Signal.         Signal.         Signal.         Signal.         Signal.         Signal.         Signal.         Signal.         Signal.         Signal.         Signal.         Signal.         Signal.         Signal.         Signal.         Signal.         Signal.         Signal.         Signal.         Signal.         Signal.         Signal.         Signal.         Signal.         Signal.         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Expn NO:         ORF SEQ ID NO:         Expression Signal         (Top) Hit RLASTE Value         Top Hit No.         Top Hit Source Source           177418         30406         1.57         1.0E-108         AW664438.1         EST_HUMAN           17783         30766         2.62         1.0E-108         U72861.1         NT	Exon NO:         ORF SEQ ID NO:         Expression Signal         (Top) Hit BLASTE Value         Top Hit No.         Top Hit Source Source           17418         30406         1.57         1.0E-108         AW664438.1         EST_HUMAN           17783         30766         2.62         1.0E-108         U72861.1         NT           17783         30766         2.62         1.0E-108         U72861.1         NT	Exon NO: ID NO: ID NO: ID NO: ID NO: ID NO: ID NO: Signal. Signal. Signal. Signal. Signal. Signal. ID NO: Signal. Signal. ID NO: Signal. Signal. ID NO: Signal. ID NO: Signal. ID NO: Signal. 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Most Similar (Top) Hit Signal.         (Top) Hit BLASTE         Top Hit No.         Top Hit Source           17418         30406         1.57         1.0E-108         AW664438.1         EST_HUMAN           17783         30766         2.62         1.0E-108         U72861.1         NT           18057         31040         3.37         1.0E-108         7661979 NT           18165         31141         0.63         1.0E-108 AW5604799.1         EST HUMAN	Exon NO:         ORF SEQ SIGNal:         Expression Signal:         (Top) Hit FLASTE Value         Top Hit Acession No.         Top Hit Acession Source         Top Hit Acession Source           17418         30406         1.57         1.0E-108         AW664438.1         EST_HUMAN           17783         30766         2.62         1.0E-108         U72861.1         NT           18057         31040         3.37         1.0E-108         URS04769.1         NT           18158         31141         0.63         1.0E-108         AW5604789.1         EST_HUMAN           18191         3.1166         3.18         1.0E-108         AW5604789.1         EST_HUMAN	Exon NO:         ORF SEQ ID NO:         Expression Signal.         (Top) Hit ICAP)         Top Hit Acession No.         Top Hit Acession No.         Top Hit Acession Source           177418         30406         1.57         1.0E-108         AW664438.1         EST_HUMAN           17783         30766         2.62         1.0E-108         U72961.1         NT           18057         31040         3.37         1.0E-108         U72961.1         NT           18165         31141         0.63         1.0E-108         AW504799.1         EST_HUMAN           18791         31839         1.2E-108         AW384994.1         EST_HUMAN	Exon NO:         ORF SEQ ID NO:         Expression Signal.         Most Similar (Top) Hit Value         Top Hit Acession No.         Top Hit Acession Source         Top Hit Acession Source           17418         30406         1.57         1.0E-108         AW664438.1         EST_HUMAN           17783         30766         2.62         1.0E-108         U72961.1         NT           18057         31141         0.63         1.0E-108         AW504798.1         EST_HUMAN           18191         31166         3.18         1.0E-108         AW504798.1         EST_HUMAN           18791         31899         1.24         1.0E-108         AW384094.1         EST_HUMAN           18838         31916         2.56         1.0E-108         AW384094.1         EST_HUMAN           18838         31916         2.56         1.0E-108         AW384094.1         EST_HUMAN	Expn NO:         ORF SEQ ID NO:         Expression Signal.         (Top) Hit ILAST E Value         Top Hit Acession No.         Top Hit Acession Source         Top Hit Acession Source           17418         30406         1.57         1.0E-108         AW664438.1         EST_HUMAN           17783         30766         2.62         1.0E-108         U72961.1         NT           18057         31040         3.37         1.0E-108         U72961.1         NT           18161         31141         0.63         1.0E-108         AW504799.1         EST_HUMAN           18781         31410         0.63         1.0E-108         AW304004.1         EST_HUMAN           18838         31916         2.56         1.0E-108         BE869016.1         EST_HUMAN           18838         31917         2.56         1.0E-108         BE869016.1         EST_HUMAN           18838         31917         2.56         1.0E-108         BE869016.1         EST_HUMAN	Expn NO:         ORF SEQ ID NO:         Expression Signal.         (Top) Hit ILAST E Value         Top Hit Acession No.         Top Hit Acession Source           17418         30406         1.57         1.0E-108         AW664438.1         EST_HUMAN           17783         30766         2.62         1.0E-108         U72961.1         NT           18057         31040         3.37         1.0E-108         U72961.1         NT           18191         3166         2.62         1.0E-108         AW504789.1         EST_HUMAN           18791         3166         3.37         1.0E-108         AW364789.1         EST_HUMAN           18838         31916         2.56         1.0E-108         AW384094.1         EST_HUMAN           18838         31917         2.56         1.0E-108         BE869016.1         EST_HUMAN           19232         1.0E-108         BE869016.1         EST_HUMAN	Expn NO:         ORF SEQ ID NO:         Expression Signal.         Most Similar (Top) Hit Signal.         Top Hit Acession ILAST E No.         Top Hit Acession Source         Top Hit Acession Source           17418         30406         1.57         1.0E-108         AW664438.1         EST_HUMAN           17783         30766         2.62         1.0E-108         U72961.1         NT           18057         31040         3.37         1.0E-108         U72961.1         NT           18191         31140         0.63         1.0E-108         AW504799.1         EST_HUMAN           18838         31916         2.56         1.0E-108         AW304094.1         EST_HUMAN           18838         31917         2.56         1.0E-108         BE869016.1         EST_HUMAN           19232         0.66         1.0E-108         BE869016.1         EST_HUMAN           19232         0.66         1.0E-108         BE869016.1         EST_HUMAN           19232         0.66         1.0E-108         BE869016.1         EST_HUMAN           19234         0.66         1.0E-108         BE869016.1         EST_HUMAN           19234         0.66         1.0E-108         BE8689016.1         EST_HUMAN           19234	Exon NO:         ORF SEQ Signal:         Expression Signal:         (Top) Hit FIASE         Top Hit Acession No:         Top Hit Acession Source         Top Hit Acession No:         Top Hit Acession Source           17418         30406         1.57         1.0E-108         AW664438.1         EST_HUMAN           17783         30766         2.62         1.0E-108         U72861.1         NT           18057         31040         3.37         1.0E-108         AW564789.1         EST_HUMAN           18191         3.166         3.18         1.0E-108         AW560789.1         EST_HUMAN           18791         31839         1.24         1.0E-108         AW3604094.1         EST_HUMAN           18838         31916         2.56         1.0E-108         AW3604094.1         EST_HUMAN           19232         0.66         1.0E-108         BE869016.1         EST_HUMAN           19232         0.66         1.0E-108         BE869016.1         EST_HUMAN           19304         3264         0.74         1.0E-108         BF344951.1         EST_HUMAN	Exon NO:         ORF SEQ ID NO:         Expression Signal.         (Top) Hit LASTE Value         Top Hit Acession No.         Top Hit Acession Source         Top Hit Source           17743         30406         1.57         1.0E-108         AW664438.1         EST_HUMAN           17783         30766         2.62         1.0E-108         U72861.1         NT           18057         31040         3.37         1.0E-108         U72861.1         NT           18191         3141         0.63         1.0E-108         U72861.1         NT           18791         3141         0.63         1.0E-108         UAV504789.1         EST_HUMAN           18791         31916         3.18         1.0E-108         AW0504789.1         EST_HUMAN           18838         31916         2.56         1.0E-108         AW0504789.1         EST_HUMAN           19232         0.66         1.0E-108         BE869016.1         EST_HUMAN           19232         0.66         1.0E-108         BE869016.1         EST_HUMAN           19344         32789         0.16         1.0E-108         BF34861.1         INT           19441         32789         0.14         1.0E-108         AF264717.1         NT	Expn NO: ID NO: ID NO: ID NO: ID NO: ID NO: ID NO: ID NO: ID NO: ID NO: ID NO: ID NO: ID NO: ID NO: ID NO: ID NO: ID NO: ID NO: ID NO: ID NO: ID NO: ID NO: ID NO: ID NO: ID NO: ID NO: ID NO: ID NO: ID NO: ID NO: ID NO: ID NO: ID NO: ID NO: ID NO: ID NO: ID NO: ID NO: ID NO: ID NO: ID NO: ID NO: ID NO: ID NO: ID NO: ID NO: ID NO: ID NO: ID NO: ID NO: ID NO: ID NO: ID NO: ID NO: ID NO: ID NO: ID NO: ID NO: ID NO: ID NO: ID NO: ID NO: ID NO: ID NO: ID NO: ID NO: ID NO: ID NO: ID NO: ID NO: ID NO: ID NO: ID NO: ID NO: ID NO: ID NO: ID NO: ID NO: ID NO: ID NO: ID NO: ID NO: ID NO: ID NO: ID NO: ID NO: ID NO: ID NO: ID NO: ID NO: ID NO: ID NO: ID NO: ID NO: ID NO: ID NO: ID NO: ID NO: ID NO: ID NO: ID NO: ID NO: ID NO: ID NO: ID NO: ID NO: ID NO: ID NO: ID NO: ID NO: ID NO: ID NO: ID NO: ID NO: ID NO: ID NO: ID NO: ID NO: ID NO: ID NO: ID NO: ID NO: ID NO: ID NO: ID NO: ID NO: ID 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NO: ID NO: ID NO: ID NO: ID NO: ID NO: ID NO: ID NO: ID NO: ID NO: ID NO: ID NO: ID NO: ID NO: ID NO: ID NO: ID NO: ID NO: ID NO: ID NO	Expn NO:         ORF SEQ Signal         Expression Signal         Most Similar (Top) Hit Alue         Top Hit Acession No.         Top Hit Acession Source           17418         30406         1.57         1.0E-108         AW664438.1         EST_HUMAN           17783         30766         2.62         1.0E-108         U72861.1         NT           18057         31040         3.37         1.0E-108         AW664438.1         EST_HUMAN           18191         31040         3.37         1.0E-108         AW66478.1         NT           18191         31640         3.37         1.0E-108         AW664789.1         EST_HUMAN           18791         31896         1.24         1.0E-108         AW660789.1         EST_HUMAN           18838         31916         2.66         1.0E-108         BE889016.1         EST_HUMAN           19232         0.66         1.0E-108         BE889016.1         EST_HUMAN           19304         32644         0.74         1.0E-108         BF264717.1         NT           19561         32821         1.0E-108         AV133269.1         NT           19304         32644         1.0B-108         AV1332469.1         EST_HUMAN	Expn NO:         ORF SEQ Signal         Expression Signal         Most Similar (Top) Hit Alue         Top Hit Acession No.         Top Hit Acession Source           17418         30406         1.57         1.0E-108         AW664438.1         EST_HUMAN           17783         30766         2.62         1.0E-108         U72861.1         NT           18057         31040         3.37         1.0E-108         WW664438.1         EST_HUMAN           18191         3166         2.62         1.0E-108         WW664438.1         EST_HUMAN           18191         3166         3.37         1.0E-108         AW664789.1         EST_HUMAN           18791         31896         1.24         1.0E-108         AW664789.1         EST_HUMAN           18838         31917         2.56         1.0E-108         BE889016.1         EST_HUMAN           19232         0.66         1.0E-108         BE889016.1         EST_HUMAN           19441         32789         6.14         1.0E-108         AF264717.1         NT           19561         32824         0.66         1.0E-108         AF264717.1         NT           19804         32644         1.09         1.0E-108         AF264717.1         NT	Exon         ORF SEQ         Expression Signal         Most Similar (Top) Hit Acession Source Source Signal         Top Hit Acession Signal         Top Hit Acession Source Source Source Source Source Source Source Source Source 1.57 1.0E-108 AW664438.1         EST HUMAN           17783         30766         2.62         1.0E-108 AW664438.1         EST HUMAN Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source	Exon         ORF SEQ         Expression         Most Similar (Top) Hit Acession         Top Hit Acession         Top Hit Acession         Top Hit Acession         Top Hit Acession         Top Hit Acession         Top Hit Acession         Top Hit Acession         Top Hit Acession         Top Hit Acession         Top Hit Acession         Top Hit Acession         Top Hit Acession         Top Hit Acession         Top Hit Acession         Top Hit Acession         Top Hit Acession         Top Hit Acession         Top Hit Acession         Top Hit Acession         Top Hit Acession         Top Hit Acession         Top Hit Acession         Top Hit Acession         Source         Source         Source         Source         Ace In Ace In Acession         Source         Source         Source         Source         Ace In Ace In Aces In Aces In Aces In Aces In Aces In Aces In Aces In Aces In Aces In Aces In Aces In Aces In Aces In Aces In Aces In Aces In Aces In Aces In Aces In Aces In Aces In Aces In Aces In Aces In Aces In Aces In Aces In Aces In Aces In Aces In Aces In Aces In Aces In Aces In Aces In Aces In Aces In Aces In Aces In Aces In Aces In Aces In Aces In Aces In Aces In Aces In Aces In Aces In Aces In Aces In Aces In Aces In Aces In Aces In Aces In Aces In Aces In Aces In Aces In Aces In Aces In Aces In Aces In Aces In Aces In Aces In Aces In Aces In Aces In Aces In Aces In Aces In Aces In Aces In Aces In Aces In Aces In Aces In Aces In Aces In Aces In Aces In Aces In Aces In Aces In Aces In Aces In Aces In Aces In Aces In Aces In Aces In Aces In Aces In Aces In Aces In Aces In Aces In Aces In Aces In Aces In Aces In Aces In Aces In Aces In Aces In Aces In Aces In Aces In	Exon NO:         ORF SEQ Signal         Expression Signal         Most Similar (Top) Hit Aubter         Top Hit Acession No.         Top Hit Acession Source         Top Hit Acession Source           17783         30406         1.57         1.0E-108         AW664438.1         EST_HUMAN           17783         30766         2.62         1.0E-108         AW664789.1         NT           18057         31040         3.75         1.0E-108         AW664789.1         EST_HUMAN           18191         31040         3.71         1.0E-108         AW664789.1         NT           18057         31040         3.71         1.0E-108         AW664789.1         NT           18791         31141         0.63         1.0E-108         AW86005.1         NT           18791         31839         1.24         1.0E-108         AW384094.1         EST_HUMAN           19232         0.66         1.0E-108         BE869016.1         EST_HUMAN           19241         32789         6.14         1.0E-108         AF264717.1         NT           19304         32789         6.14         1.0E-108         AF264717.1         NT           19804         33303         0.64         1.0E-108         AF204777.1         NT	Exon NO:         ORF SEQ Signal         Expression Signal         Most Similar (Top) Hit Aubte         Top Hit Acession No.         Top Hit Acession Source         Top Hit Acession Source           17783         30406         1.57         1.0E-108         AW664438.1         EST_HUMAN           17783         30766         2.62         1.0E-108         LV2861.1         NT           18057         31040         3.37         1.0E-108         LV2861.1         NT           18165         31441         0.63         1.0E-108         LV2801.8         NT           18791         31839         1.24         1.0E-108         LV3809.1         EST_HUMAN           18781         31839         1.24         1.0E-108         RE859016.1         EST_HUMAN           19838         31917         2.56         1.0E-108         RE859016.1         EST_HUMAN           19232         0.66         1.0E-108         RE859016.1         EST_HUMAN           19304         32789         6.14         1.0E-108         RF264717.1         NT           19441         32789         6.14         1.0E-108         RF264717.1         NT           19809         33302         0.64         1.0E-108         RF264717.1         NT	Exon NO:         ORF SEQ Signal         Expression Signal         Most Similar (Top) Hit Auban         Top Hit Acession No.         Top Hit Acession Source         Top Hit Acession Source           17748         30406         1.57         1.0E-108         AW664438.1         EST_HUMAN           17783         30766         2.62         1.0E-108         U72861.1         NT           18057         31040         3.37         1.0E-108         LV2861.1         NT           18193         31441         0.63         1.0E-108         LV2801.1         NT           18239         1.24         1.0E-108         AW384094.1         EST_HUMAN           18239         1.24         1.0E-108         AW384094.1         EST_HUMAN           19232         0.66         1.0E-108         BE899016.1         EST_HUMAN           19241         32789         6.14         1.0E-108         BE899016.1         EST_HUMAN           19304         32789         6.14         1.0E-108         BF8934851.1         IST_HUMAN           19304         32789         6.14         1.0E-108         BF834851.1         IST_HUMAN           19304         33264         0.74         1.0E-108         AF264717.1         NT <td< td=""><td>Exon NO: 100: 100: 100: 100: 100: 100: 100: 10</td><td>Exon NO: 17418         ORF SEQ Signal         Expression Signal         Most Similar (Top) Hit Aubue         Top Hit Acession Cap Hit Acession         Top Hit Acession Source         Top Hit Acession Source           17718         30406         1.57         1.0E-108         AW664438.1         EST_HUMAN           17783         30766         2.62         1.0E-108         AW664438.1         EST_HUMAN           18057         31040         2.62         1.0E-108         AW664438.1         EST_HUMAN           18161         31040         2.62         1.0E-108         AW664789.1         EST_HUMAN           18163         31141         0.63         1.0E-108         AW664789.1         EST_HUMAN           18791         31839         1.24         1.0E-108         AW664789.1         EST_HUMAN           18838         31916         2.56         1.0E-108         BE869016.1         EST_HUMAN           19341         32789         6.14         1.0E-108         AF264717.1         NT           19341         32789         6.14         1.0E-108         AF264717.1         NT           19809         33302         0.64         1.0E-108         AF264717.1         NT           19809         33303         0.64         <td< td=""><td>Exon NO:         ORF SEQ Signal         Expression Signal         Most Similar (Top) Hit Aubt         Top Hit Acession Top Hit Acession         Top Hit Acession Source           17418         30406         1.57         1.0E-108         AW664438.1         EST_HUMAN           17783         30766         2.62         1.0E-108         AW664438.1         EST_HUMAN           18057         31040         3.37         1.0E-108         AW664438.1         EST_HUMAN           18057         31040         3.37         1.0E-108         AW664789.1         EST_HUMAN           18165         31141         0.63         1.0E-108         AW664789.1         EST_HUMAN           18791         31829         1.24         1.0E-108         AW664789.1         EST_HUMAN           18838         31916         2.56         1.0E-108         BE889016.1         EST_HUMAN           19304         32644         0.74         1.0E-108         AF264717.1         NT           19304         32292         4.22         1.0E-108         AF264717.1         NT           19809         33302         0.64         1.0E-108         AF264717.1         NT           19809         33302         0.64         1.0E-108         AF264717.1</td><td>Exon         ORF SEQ         Expression Signal         Most Similar (Top) Hit Acession No.         Top Hit Acession Source Source No.         Top Hit Acession Source Source No.         Top Hit Acession Source Source Source Source No.         Top Hit Acession Source Source Source Source Source Source No.         Top Hit Acession Source Source Source Source Source Source Source Source Source No.         Top Hit Acession No.         Top Hit Acession Source Source Source Source Source Source Source Source Source Source Source Source Source Source No.         Top Hit Acession No.         Top Hit Acession No.         Top Hit Acession Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Sou</td><td>Exon         ORF SEQ         Expression Signal         Most Similar (Top) Hit Acession Signal         Top Hit Acession Signal         Top Hit Acession Signal         Top Hit Acession Signal         Top Hit Acession Source Source Source Source Source Source Survey           17783         30766         1.57         1.0E-108 AW664438.1         EST HUMAN           17783         30766         2.62         1.0E-108 AW664438.1         EST HUMAN           18057         31040         3.37         1.0E-108 AW664438.1         EST HUMAN           18165         3141         0.63         1.0E-108 AW664438.1         EST HUMAN           18167         31404         3.37         1.0E-108 AW664438.1         EST HUMAN           18168         3141         0.63         1.0E-108 BE869016.1         EST HUMAN           18232         0.66         1.0E-108 BE868016.1         EST HUMAN           19334         32644         0.74         1.0E-108 BE834851.1         INT           19561         32521         1.0E-108 BE34851.1         INT           19661         32544         0.74         1.0E-108 BE34851.1         INT           19661         32543         1.0E-108 BE34851.1         INT           19809         33302         0.64         1.0E-108 BE34851.1</td><td>Exan         ORF SEQ         Expression of Tray Hit Acession of Tray Hit Acession of Signal         Most Similar of Tray Hit Acession of Source of Signal         Top Hit Acession of Source of Augus         Top Hit Acession of Source of Augus         Top Hit Acession of Source of Augus         Top Hit Acession of Source of Augus         Top Hit Acession of Source of Augus         Top Hit Acession of Source of Augus         Top Hit Acession of Source of Augus         Top Hit Acession of Augus         Top Hit Acession of Augus         Top Hit Acession of Augus         Top Hit Acession of Augus         Top Hit Acession of Augus         Top Hit Acession of Augus         Top Hit Acession of Augus    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      ORF SEQ Signal         Expression Signal         Most Similar (Top) Hit Aubue         Top Hit Acession Cap Hit Acession         Top Hit Acession Source         Top Hit Acession Source           17718         30406         1.57         1.0E-108         AW664438.1         EST_HUMAN           17783         30766         2.62         1.0E-108         AW664438.1         EST_HUMAN           18057         31040         2.62         1.0E-108         AW664438.1         EST_HUMAN           18161         31040         2.62         1.0E-108         AW664789.1         EST_HUMAN           18163         31141         0.63         1.0E-108         AW664789.1         EST_HUMAN           18791         31839         1.24         1.0E-108         AW664789.1         EST_HUMAN           18838         31916         2.56         1.0E-108         BE869016.1         EST_HUMAN           19341         32789         6.14         1.0E-108         AF264717.1         NT           19341         32789         6.14         1.0E-108         AF264717.1         NT           19809         33302         0.64         1.0E-108         AF264717.1         NT           19809         33303         0.64 <td< td=""><td>Exon NO:         ORF SEQ Signal         Expression Signal         Most Similar (Top) Hit Aubt         Top Hit Acession Top Hit Acession         Top Hit Acession Source           17418         30406         1.57         1.0E-108         AW664438.1         EST_HUMAN           17783         30766         2.62         1.0E-108         AW664438.1         EST_HUMAN           18057         31040         3.37         1.0E-108         AW664438.1         EST_HUMAN           18057         31040         3.37         1.0E-108         AW664789.1         EST_HUMAN           18165         31141         0.63         1.0E-108         AW664789.1         EST_HUMAN           18791         31829         1.24         1.0E-108         AW664789.1         EST_HUMAN           18838         31916         2.56         1.0E-108         BE889016.1         EST_HUMAN           19304         32644         0.74         1.0E-108         AF264717.1         NT           19304         32292         4.22         1.0E-108         AF264717.1         NT           19809         33302         0.64         1.0E-108         AF264717.1         NT           19809         33302         0.64         1.0E-108         AF264717.1</td><td>Exon         ORF SEQ         Expression Signal         Most Similar (Top) Hit Acession No.         Top Hit Acession Source Source No.         Top Hit Acession Source Source No.         Top Hit Acession Source Source Source Source No.         Top Hit Acession Source Source Source Source Source Source No.         Top Hit Acession Source Source Source Source Source Source Source Source Source No.         Top Hit Acession No.         Top Hit Acession Source Source Source Source Source Source Source Source Source Source Source Source Source Source No.         Top Hit Acession No.         Top Hit Acession No.         Top Hit Acession Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Sou</td><td>Exon         ORF SEQ         Expression Signal         Most Similar (Top) Hit Acession Signal         Top Hit Acession Signal         Top Hit Acession Signal         Top Hit Acession Signal         Top Hit Acession Source Source Source Source Source Source Survey           17783         30766         1.57         1.0E-108 AW664438.1         EST HUMAN           17783         30766         2.62         1.0E-108 AW664438.1         EST HUMAN           18057         31040         3.37         1.0E-108 AW664438.1         EST HUMAN           18165         3141         0.63         1.0E-108 AW664438.1         EST HUMAN           18167         31404         3.37         1.0E-108 AW664438.1         EST HUMAN           18168         3141         0.63         1.0E-108 BE869016.1         EST HUMAN           18232         0.66         1.0E-108 BE868016.1         EST HUMAN           19334         32644         0.74         1.0E-108 BE834851.1         INT           19561         32521         1.0E-108 BE34851.1         INT           19661         32544         0.74         1.0E-108 BE34851.1         INT           19661         32543         1.0E-108 BE34851.1         INT           19809         33302         0.64         1.0E-108 BE34851.1</td><td>Exan         ORF SEQ         Expression of Tray Hit Acession of Tray Hit Acession of Signal         Most Similar of Tray Hit Acession of Source of Signal         Top Hit Acession of Source of Augus         Top Hit Acession of Source of Augus         Top Hit Acession of Source of Augus         Top Hit Acession of Source of Augus         Top Hit Acession of Source of Augus         Top Hit Acession of Source of Augus         Top Hit Acession of Source of Augus         Top Hit Acession of Augus         Top Hit Acession of Augus         Top Hit Acession of Augus         Top Hit Acession of Augus         Top Hit Acession of Augus         Top Hit Acession of Augus         Top Hit Acession of Augus         Top Hit Acession of Augus         Top Hit Acession of Augus         Top Hit Acession of Augus         Top Hit Acession of Augus         Top Hit Acession of Augus         Top Hit Acession of Augus         Top Hit Acession of Augus         Top Hit Acession of Augus         Top Hit Acession of Augus         Top Hit Acession of Augus         Top Hit Acession of Augus         Top Hit Acession of Augus         Top Hit Acession of Augus         Top Hit Acession of Augus         Top Hit Acession of Augus         Top Hit Acession of Augus         Top Hit Acession of Augus         Top Hit Acession of Augus         Top Hit Acession of Augus         Top Hit Acession of Augus         Top Hit Acession of Augus         Top Hit Acession of Augus         Top Hit Acession of Augus         Top Hit Acession of Augus         Top Hit Acession of Augus         Top Hit Acession of Augus         Top Hit Acession of Augus</td></td<>	Exon NO:         ORF SEQ Signal         Expression Signal         Most Similar (Top) Hit Aubt         Top Hit Acession Top Hit Acession         Top Hit Acession Source           17418         30406         1.57         1.0E-108         AW664438.1         EST_HUMAN           17783         30766         2.62         1.0E-108         AW664438.1         EST_HUMAN           18057         31040         3.37         1.0E-108         AW664438.1         EST_HUMAN           18057         31040         3.37         1.0E-108         AW664789.1         EST_HUMAN           18165         31141         0.63         1.0E-108         AW664789.1         EST_HUMAN           18791         31829         1.24         1.0E-108         AW664789.1         EST_HUMAN           18838         31916         2.56         1.0E-108         BE889016.1         EST_HUMAN           19304         32644         0.74         1.0E-108         AF264717.1         NT           19304         32292         4.22         1.0E-108         AF264717.1         NT           19809         33302         0.64         1.0E-108         AF264717.1         NT           19809         33302         0.64         1.0E-108         AF264717.1	Exon         ORF SEQ         Expression Signal         Most Similar (Top) Hit Acession No.         Top Hit Acession Source Source No.         Top Hit Acession Source Source No.         Top Hit Acession Source Source Source Source No.         Top Hit Acession Source Source Source Source Source Source No.         Top Hit Acession Source Source Source Source Source Source Source Source Source No.         Top Hit Acession No.         Top Hit Acession Source Source Source Source Source Source Source Source Source Source Source Source Source Source No.         Top Hit Acession No.         Top Hit Acession No.         Top Hit Acession Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Source Sou	Exon         ORF SEQ         Expression Signal         Most Similar (Top) Hit Acession Signal         Top Hit Acession Signal         Top Hit Acession Signal         Top Hit Acession Signal         Top Hit Acession Source Source Source Source Source Source Survey           17783         30766         1.57         1.0E-108 AW664438.1         EST HUMAN           17783         30766         2.62         1.0E-108 AW664438.1         EST HUMAN           18057         31040         3.37         1.0E-108 AW664438.1         EST HUMAN           18165         3141         0.63         1.0E-108 AW664438.1         EST HUMAN           18167         31404         3.37         1.0E-108 AW664438.1         EST HUMAN           18168         3141         0.63         1.0E-108 BE869016.1         EST HUMAN           18232         0.66         1.0E-108 BE868016.1         EST HUMAN           19334         32644         0.74         1.0E-108 BE834851.1         INT           19561         32521         1.0E-108 BE34851.1         INT           19661         32544         0.74         1.0E-108 BE34851.1         INT           19661         32543         1.0E-108 BE34851.1         INT           19809         33302         0.64         1.0E-108 BE34851.1	Exan         ORF SEQ         Expression of Tray Hit Acession of Tray Hit Acession of Signal         Most Similar of Tray Hit Acession of Source of Signal         Top Hit Acession of Source of Augus         Top Hit Acession of Source of Augus         Top Hit Acession of Source of Augus         Top Hit Acession of Source of Augus         Top Hit Acession of Source of Augus         Top Hit Acession of Source of Augus         Top Hit 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Acession of Augus         Top Hit Acession of Augus         Top Hit Acession of Augus         Top Hit Acession of Augus         Top Hit Acession of Augus         Top Hit Acession of Augus

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Table 4
Single Exon Probes Expressed in Placenta

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	Top Hit Descriptor	601058769F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3445361 51	Homo sapiens mRNA for Golgi-associated microtubule-binding protein (GMAP-210)	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, econs 7-49, and partial cds, alternatively splined	FST378258 MAGE recentiences MAGI Home series conta	AV708790 ADC Homo saplens cDNA clone ADCAEE03 5:	AV708790 ADC Hamo sapiens cDNA clone ADCAEE03 5	Homo sapiens G protein-coupled receptor 48 (GPR48), mRNA	tt91e10.x1 NCI_CGAP_Pr28 Home sapiens cDNA clone IMAGE:2248938 3' similar to gb:M14219 BONE PROTEOGLYCAN II PRECURSOR (HUMAN);	trans10.x1 NCL_CGAP_Pr28 Homo expiens cDNA clone IMAGE;2248938 3' similar to gb:M14219 BONE PROTEOGLYGAN II PRECURSOR (HUMAN):	Homo sapiens COL4A6 gene for a6(IV) collagen, exch 23	Homo saplens mRNA for FL00037 protein, partial cds	602018571F1 NCI_CGAP_Bm67 Homo saplens cDNA done IMAGE:4154297 5	IL2-UM0077-260400-079-D06 UM0077 Homo sapiens cDNA	Human mRNA for KIAA0220 gene, partial cds	Homo sapiens hypothetical protein FLJ11316 (FLJ11316), mRNA	Homo sapiens reticulocalbin 1, EF-hand calcium binding domain (RCN1), mRNA	Homo sapiens tetratricopeptide repeat domain 2 (TTC2) mRNA	Homo sapiens mRNA for KIAA0999 protein, partial cds	Homo sapiens mRNA for KIAA0999 protein, partial cds	Homo sapiens chromosome 21 segment HS21C049	Homo saplens nucleolar phosphoprotein B23 (NPM1) mRNA, complete cds	Homo saplens nucledar phosphoprotein B23 (NPM1) mRNA, complete cds	601186922F2 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:2959636 5'	601186922F2 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:2959636 5	Homo sapiens mRNA for KIAA0018 protein, partial cds	Homo saplens chromosome 21 segment HS21C084	Homo sapiens SNF5/INI1 gene, excn 6	ow95a01 x1 Soares_fetal_liver_spleen_INFLS_S1 Homo saplens cDNA clone IMAGE:1654536 3' similar to TR:002197 C02197 CIRCULATING CATHODIC ANTIGEN.;	ow95a01.x1 Scares_fetal_liver_spleen_1NPLS_S1 Homo sapiens cDNA clone IMAGE:1654536 3' similar to TR:002197 002197 CIRCULATING CATHODIC ANTIGEN :
ביים ו	Top Hit Database Source	EST HUMAN	ΙN	FZ	EST HIMAN	EST HUMAN	EST HUMAN	11441465 NT	EST_HUMAN	EST HUMAN	Į.	뉟	EST HUMAN	EST HUMAN	F	- LN	Ē	۲N	TN	TN	LN	IN	. LN	EST_HUMAN	EST_HUMAN	NT	IN	ĹΝ	EST_HUMAN	EST_HUMAN
5	Top Hit Acesslon No.	.0E-108 BE53527.1	.0E-108 Y12490.1	0E-108 AF223391 1	0E-108 AW966185 1	.0E-108 AV708790.1	.0E-108 AV708790.1	11441465	.0E-108 AI686040.1	.0E-108 Al686040.1	.0E-108 D63539.1	.0E-108 AK02447.1	.0E-108 BF346356.1	.0E-109 AW803116.1	.0E-109 D86974.1	11422486 NT	11438391 NT	4507712 NT	.0E-109 AB023216.1	.0E-109 AB023216.1	.0E-109 AL163249.2	.0E-109 M28699.1	.0E-109 M28699.1	.0E-109 BE293673.1	.0E-109 BE293673.1	.0E-109 D13643.2	.0E-109 AL163284.2	0E-109 Y17123.1	.0E-109 AI022328.1	.0E-109 AI022328.1
	Most Similar (Top) Hit BLAST E Value	1.0E-108	1.0E-108	1.0F-108	1.0E-108	1.0E-108	1.0E-108	1.0E-108	1.0E-108	1.0E-108	1.0E-108	1.0E-108	1.0E-108	1.0E-109	1.0E-109		1	1.0E-109	1	1.0E-109	1.0E-109	1.0E-109	1.0E-109	1.0E-109	1.0E-109	1.0E-109	1.0E-109	1.0E-109	1.0E-109	1.0E-109
	Expression Signal	2.09	2.67	1.35	3.46	1.71	1.71	2.77	2.99	2.99	1.72	4.15	5.09	1.9	1.17	3.34	2.77	2.28	14.77	14.77	1.62	8.5	6.38	0.99	0.99	2.3	5.46	3.65	19.35	19.35
	ORF SEQ ID NO:	34549	31537	38027	38283		38344		28665	28666	38446	32064		26287			•	26705			27262				27807			28589	28923	28924
	Exon SEQ ID NO:		18501	24382	Ι.	1_	24658	24731	15538	15538	24752	25344	25618	13281	13303	13447	13456	13674	13800	13800	14205	14389	14389	14726	14726	1		15457	15807	15807
	Probe SEQ ID NO:	10904	11066	11319	11549	11605	11605	11652	11688	11688	11712	12499	12940	43	8	225	235	479	611	611	1037	1229	1230	1573	1573	1923	2314	2325	2687	2687

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Top Hit Descriptor	Homo sapiens guanylate cyclase activator 1A (retina) (GUCA1A) mRNA	J2816F Human fetal heart, Lambde ZAP Express Homo capiens cDNA clone J2816 6' similar to ZINC FINGER PROTEIN ZNF43	CM3-NN0009-190400-150-f10 NN0009 Homo sapiens cDNA	CM3-NN0009-190400-150-f10 NN0009 Homo sapiens cDNA	Homo sapiens retinol dehydrogenase homolog isoform-1 (RDH) mRNA, complete cds	MR0-HT0209-110400-108-a04 HT0209 Homo saplens cDNA	ts98e06.x1 NCI_CGAP_GC9 Homo saplens cDNA clone IMAGE:2239330 3' similar to WP:F53A2.8 CE16100;	Homo sapiens guanylate cyclase activator 1A (retina) (GUCA1A) mRNA	Homo saplens KIAA0377 gene product (KIAA0377), mRNA	601186922F2 NIH_MGC_15 Homo saplens cDNA clone IMAGE:2959636 5	601186922F2 NIH MGC 15 Homo sapiens cDNA clone IMAGE:2959636 6'	AU137282 PLACE1 Homo saplens cDNA clone PLACE1006159 5	602136446F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4272922 5	Homo sapiens placental protein 11 (serine proteinase) (P11) mRNA	RC1-HT0615-200400-022-d04 HT0615 Homo sapiens aDNA	CM1-UT0038-060900-399-h07 UT0038 Homo saplens cDNA	RC1-HT0615-200400-022-d04 HT0615 Homo saplens cDNA	19986108.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:18421113'	Homo sapiens myosin, heavy polypeptide 4, skeletal muscle (MYH4), mRNA	Homo sapiens myosin, heavy polypeptide 4, skeletal muscle (MYH4), mRNA	Homo sapiens mRNA for KIAA1591 protein, partial cds	Homo sapiens AT-binding transcription factor 1 (ATBF1), mRNA	601809495F1 NIH_MGC_18 Homo sapiens cDNA clone IMAGE:4040279 5'	601809495F1 NIH_MGC_18 Homo sapiens cDNA clone IMAGE:4040279 5'	Novel human gene mapping to chomosome 13	PM0-BT0340-091299-002-e05 BT0340 Homo sapiens cDNA	7B18H01 Chromosome 7 Fetal Brain cDNA Library Homo sapiens cDNA clone 7B18H01	601479417F1 NIH_MGC_68 Homo sepiens cDNA done IMAGE:3882124 5'	601479417F1 NIH_MGC_68 Homo sapiens cDNA done IMAGE:3882124 5	IL0-HT0205-071199-142-901 HT0205 Homo sapiens cDNA	ys90g08.r1 Soares retina N2b5HR Homo saplens cDNA clone IWAGE:222110 5' similar to SP:A53491 A53491 BUMETANIDE-SENSITIVE NA-K-C1 COTRANSPORTER - SPINY;
Top Hit Database Source	뉟	EST HUMAN	EST HUMAN	EST_HUMAN	L	EST_HUMAN	EST HUMAN	뉟	TN	EST HUMAN	EST HUMAN	EST HUMAN	EST_HUMAN	F	EST_HUMAN	EST_HUMAN	EST_HUMAN	T_HUMAN		TN	NT	NT	EST_HUMAN	T_HUMAN	⊥N	EST_HUMAN	Г	EST_HUMAN		EST_HUMAN	EST_HUMAN
Top Hit Acession No.	4504208 NT	E-109 N85190.1	E-109 AW893192.1	E-109 AW893192.1	E-109 AF240698.1	E-109 BE146144.1	E-109 AI655417.1	4504206 NT	7662083 NT	E-109 BE293673.1			E-109 BF673718.1	74622			E-109 BE179356.1		11024711 NT	11024711 NT		32574				1.0E-109 AW749130.1					
Most Similar (Top) Hit BLAST E Value	1.0E-109	1.0E-109 I	1.0E-109	1.0E-109	1.0E-109	1.0E-109	1.0E-109	1.0E-109	1.0E-109	1.0E-109	1.0E-109	1.0E-109	1.0E-109	1.0E-109	1.0E-109 BE179356.1	1.0E-109	1.0E-109	1.0E-109 A1221385.1	1.0E-109	1.0E-109	1.0E-109 AB046811.1	1.0E-109	1.0E-109 BF182707.1	1.0E-109 BF182707.1	1.0E-109 AL049784.1	1.0E-109	1.0E-109	1.0E-109 BE787540.1	1.0E-109 BE787540.1	1.0E-109	1.0E-109 H84860.1
Expression Signal	2.68	3.37	2.08	2.08	1.1	1.31	4.35	2.67	1.7	0.72	0.72	0.67	0.92	2.92	1.23	1.23	1.41	0.85	0.69	0.69	0.67	3.75	4.91	4.91	1.35	1.39	2.84	4.36	4.36	0.57	1.65
ORF SEQ ID NO:	28925	29314	29661	29962	29785		30395	30650	30839	31252	31253	31480	31445	31604		32556		33269	33651	33652	33933	34288	34290	34291	34970	35098		35549	35550	35797	36077
Exon SEQ ID NO:	15808	16301		16642		17104	17409	17663	17857	18287	18287	18564	18577	18628	18917	25817	18917	19878	20222	20222	20467	20789	2884 884	20801	21447	21561	21936	22011	22011	22255	22613
Probe SEQ ID NO:	2688	3125	3475	3475	3606	3945	4264	4254	4722	5165	5165	5361	5374	5428	5724	6050	6119	6721	6907	2009	7389	7738	740	7740	8366	8480	8857	8932	8932	9177	9439

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Single Exon Probes Expressed in Placenta

hh23105.x1 NCi\_CGAP\_Lu24 Homo sapiens cDNA clone IMAGE:2955989 3' similar to TR:Q9Z124 Q9Z124 Homo sapiens Bruton's tyrosine kinase (BTK), alpha-D-galactosidase A (GLA), L44-like ribosomal protein (L44L) and FTP3 (FTP3) genes, complete cds zb08b12.r1 Soares\_fetal\_lung\_NbHL19W Homo sapiens cDNA clone IMAGE:301439 5' similar to Homo sapiens BAZIB mRNA for bromodomain adjacent to zinc finger domain 1B, complete cds 601237545f7 NIH MGC\_44 Homo sapiens cDNA done IMAGE.3809683 5' ULH-BI4-acs-b-05-b-UI.st NCI\_CGAP\_SubB Homo sapiens cDNA done IMAGE.38095784 3' Homo sapiens chondratin sulfate proteoglycan 4 (melanome-associated) (CSPG4), mRNA DKFZp76111124\_r1 761 (synonym: hamy2) Homo sapiens cDNA clone DKFZp76111124 5' Homo sapiens deiodinase, iodothyronine, type II (DiO2), transcript variant 2, mRNA 601289760F1 NIH\_MGC\_8 Homo sapiens cDNA clone IMAGE:3820030 5' HSC1EC121 normalized infant brain cDNA Homo caplens cDNA clone c-1eo1 Homo sapiens leucine-zipper-like transcriptional regulator, 1 (LZTR1), mRNA 601063030F1 NIH\_MGC\_10 Homo sapiens cDNA clone IMAGE:349599 5\* 601063030F1 NIH\_MGC\_10 Homo sapiens cDNA clone IMAGE:349599 5\* 602080724F2 NIH\_MGC\_81 Homo sapiens cDNA clone IMAGE:4245341 5 Homo sepiens deiodinase, iodothyronine, type II (DIO2), transcript variant 2, Human autoimmune antigen small nuclear ribonucleoprotein E pseudogene Homo sapiens single-minded (Drosophila) homolog 1 (SIM1), mRNA Homo sapiens leucine-zipper-like transcriptional regulator, 1 (LZTR1) AU121370 HEMBB1 Homo sepiens cDNA clone HEMBB1002690 5 PIR:S43969 S43969 p54-beta stress-activated protein kinases - rat Human mRNA for inward rectifier potassium channel, complete cds Top Hit Descriptor Homo sapiens Chedlak-Higashi syndrome 1 (CHS1) mRN Homo saplens calcitonin receptor-like (CALCRL) mRNA Homo sapiens mRNA for KIAA0463 protein, partial cds YGR163W MRNA HOMOLOGUE, COMPLETE CDS. Homo sapiens pregnancy zone protein (PZP), mRNA Homo sapiens pregnancy-zone protein (PZP), mRNA Homo sapiens SNF5/INH gene, exon 6 Homo sapiens gene for AF-6, complete cds Human dystrobrevin (DTN) gene, exon 20 Homo sapiens SNF5/INI1 gene, exon 6 EST\_HUMAN | EST\_HUMAN | EST\_HUMAN | EST\_HUMAN | EST\_HUMAN | EST\_HUMAN | EST\_HUMAN | EST\_HUMAN | EST\_HUMAN | EST\_HUMAN | EST\_HUMAN | EST\_HUMAN | EST\_HUMAN | EST\_HUMAN | EST\_HUMAN | EST\_HUMAN | EST\_HUMAN | EST\_HUMAN | EST\_HUMAN | EST\_HUMAN | EST\_HUMAN | EST\_HUMAN | EST\_HUMAN | EST\_HUMAN | EST\_HUMAN | EST\_HUMAN | EST\_HUMAN | EST\_HUMAN | EST\_HUMAN | EST\_HUMAN | EST\_HUMAN | EST\_HUMAN | EST\_HUMAN | EST\_HUMAN | EST\_HUMAN | EST\_HUMAN | EST\_HUMAN | EST\_HUMAN | EST\_HUMAN | EST\_HUMAN | EST\_HUMAN | EST\_HUMAN | EST\_HUMAN | EST\_HUMAN | EST\_HUMAN | EST\_HUMAN | EST\_HUMAN | EST\_HUMAN | EST\_HUMAN | EST\_HUMAN | EST\_HUMAN | EST\_HUMAN | EST\_HUMAN | EST\_HUMAN | EST\_HUMAN | EST\_HUMAN | EST\_HUMAN | EST\_HUMAN | EST\_HUMAN | EST\_HUMAN | EST\_HUMAN | EST\_HUMAN | EST\_HUMAN | EST\_HUMAN | EST\_HUMAN | EST\_HUMAN | EST\_HUMAN | EST\_HUMAN | EST\_HUMAN | EST\_HUMAN | EST\_HUMAN | EST\_HUMAN | EST\_HUMAN | EST\_HUMAN | EST\_HUMAN | EST\_HUMAN | EST\_HUMAN | EST\_HUMAN | EST\_HUMAN | EST\_HUMAN | EST\_HUMAN | EST\_HUMAN | EST\_HUMAN | EST\_HUMAN | EST\_HUMAN | EST\_HUMAN | EST\_HUMAN | EST\_HUMAN | EST\_HUMAN | EST\_HUMAN | EST\_HUMAN | EST\_HUMAN | EST\_HUMAN | EST\_HUMAN | EST\_HUMAN | EST\_HUMAN | EST\_HUMAN | EST\_HUMAN | EST\_HUMAN | EST\_HUMAN | EST\_HUMAN | EST\_HUMAN | EST\_HUMAN | EST\_HUMAN | EST\_HUMAN | EST\_HUMAN | EST\_HUMAN | EST\_HUMAN | EST\_HUMAN | EST\_HUMAN | EST\_HUMAN | EST\_HUMAN | EST\_HUMAN | EST\_HUMAN | EST\_HUMAN | EST\_HUMAN | EST\_HUMAN | EST\_HUMAN | EST\_HUMAN | EST\_HUMAN | EST\_HUMAN | EST\_HUMAN | EST\_HUMAN | EST\_HUMAN | EST\_HUMAN | EST\_HUMAN | EST\_HUMAN | EST\_HUMAN | EST\_HUMAN | EST\_HUMAN | EST\_HUMAN | EST\_HUMAN | EST\_HUMAN | EST\_HUMAN | EST\_HUMAN | EST\_HUMAN | EST\_HUMAN | EST\_HUMAN | EST\_HUMAN | EST\_HUMAN | EST\_HUMAN | EST\_HUMAN | EST\_HUMAN | EST\_HUMAN | EST\_HUMAN | EST\_HUMAN | EST\_HUMAN | EST\_HUMAN | EST\_HUMAN | EST\_HUMAN | EST\_HUMAN | EST\_HUMAN | EST\_HUMAN | EST\_HUMAN | EST\_HUMAN | EST\_HUMAN | EST\_HUMAN | EST\_HUMAN | EST\_HUMAN | EST\_HUMAN | EST\_HUMAN | EST\_HUMAN | EST\_HUMAN | EST\_HUMAN | EST\_HUMAN | EST\_HUMAN | EST\_HUMAN | EST\_HUMAN | EST\_HUMAN | EST\_HUMAN | EST\_HU EST\_HUMAN EST\_HUMAN EST\_HUMAN HUMAN HUMAN Top Hit Database Source EST\_HUMAN EST\_HUMAN 11418618 NT 7932.1 NT 23.1 NT 23.1 NT 1399.1 NT 7549804 NT 5803073 NT 5803073 NT 7549804 NT 눋 눋 11436041 NT 11436041 4502838 4503098 Top Hit Acession BE540909.1 1.0E-109 BE045560.1 AB007932.1 BF694831.1 1.0E-109 BE397068.1 AL119824.1 ģ 1.0E-109 W 16510.1 387291.1 M15918.1 U78027.1 **U84550.1** 1.0E-109 1.0E-109 1.05-110 1.0E-109 1.0E-109 .0E-109 1.0E-109 1.0E-109 1.0E-110 1.0E-110 1.06-110 1.0E-109 1.0E-109 1.0E-109 1.0E-110 (Top) Hit BLAST E **Most Simila** 1.09 19.68 3.86 84. 232 8,36 3.96 2 8 2.66 0.64 ĕ Expression Signal 32036 26242 26281 26282 26242 29458 30449 38673 36184 38382 36185 37757 28589 26555 26757 29457 ORF SEQ 38109 38422 Ö 13276 13242 13733 16438 SEQ ID 24092 24123 24691 24872 24969 13276 14369 15116 15256 16331 16438 13521 2261 ë 11984 3156 3264 3264 4320 Probe SEQ ID 38 112 305 540 11013 11046 11693 11884 1973 9550 11387 11651 11948 9685 ë

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Top Hit Descriptor	ou32b10.X1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1627963 3' similar to SW:N121_RAT P52591 NUCLEAR ENVELOPE PORE MEMBRANE PROTEIN POM 121;	AU117812 HEMBA1 Homo sapiens cDNA clone HEMBA1002241 5	Homo sepiens KIAA1002 protein (KIAA1002), mRNA	801118710F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3028538 5'	601493677F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3895795 5'	Homo sapiens hypothetical protein FLJ10300 (FLJ10300), mRNA	Homo sapiens hypothetical protein FLJ10300 (FLJ10300), mRNA	Human cystic fibrosis transmembrane conductance regulator (CFTR) gene, exon 7	601109388F1 NIH_MGC_16 Homo sepiens cDNA clone IMAGE:3350277 5'	Human GS2 gene, exon 2	Human GS2 gene, excn 2	tn12d08.x1 NCI_CGAP_Bm25 Home sapiens cDNA clone IMAGE:2167407 3' similar to SW:ETV1_HUMAN P50549 ETS TRANSLOCATION VARIANT 1:	AV714278 DCB Homo sapiens cDNA done DCBCGE01 5'	AV714276 DCB Homo septens cDNA clone DCBCGE01 5'	Homo sapiens mRNA for KIAA0868 protein, partial cds	AU137923 PLACE1 Homo sapiens cDNA clone PLACE1007511 5	ba88f01.y1 NIH_MGC_20 Homo septens cDNA clone IMAGE:2805581 5' similar to TR:O77258 O77258 EG:114D9.2 PROTEIN.;	QV2-LT0053-020400-119-e04 LT0053 Hamo sapiens cDNA	Homo saplens galactokinase 2 (GALK2), mRNA	H. sepiens mRNA for myctonic dystrophy protein kinase like protein	601565604F1 NIH_MGC_21 Homo sepiens cDNA clone IMAGE:3840433 5'	601565604F1 NIH_MGC_2: Homo sapiens cDNA clone IMAGE:3840433 5'	Human insulin receptor mRNA, complete cds	zw67g02.r1 Soares_tests_NHT Homo sepiens cDNA clone IMAGE:781288 5' similar to TR:G1145816	G1145816 FKBP54;	601439784F1 NIH_MGC_72 Homo sepiens cDNA clone IMAGE:3924548 5'	LD-BT0163-040899-094-g10 BT0163 Homo sapiens cDNA	Homo sapiens gene for AF-6, complete cds	PM3-NN1082-140900-006-f12 NN1082 Homo sapiens cDNA	UI-H-BI4-aos-b-05-0-UI.s1 NCI_CGAP_Sub8 Homo sapiens cDNA done IMAGE:3085784 3'	Human ribosomal protein L23a mRNA, complete cds
Top Hit Dafabase Source	EST_HUMAN	EST_HUMAN	N	EST_HUMAN	EST_HUMAN	IN	NT	N	EST_HUMAN	FZ	Ŋ	EST HUMAN	EST HUMAN	EST HUMAN	Z	EST_HUMAN	EST HUMAN	EST HUMAN	N	IN	EST_HUMAN	EST_HUMAN	LN L		EST_HUMAN	EST_HUMAN	EST_HUMAN	NT	EST HUMAN	EST_HUMAN	LN
Top Hit Acession No.	1.0E-110 AI017213.1	1.0E-110 AU117812.1	7882441	1.0E-110 BE299406.1	1.0E-110 BE621069.1	11419323 NT	11419323 NT	M55112.1	1.0E-110 BE251496.1	J08888.1	J08888.1	1.0E-110 AI560289.1	1.0E-110 AV714276.1	.0E-110 AV714276.1	.0E-110 AB020675.1	.0E-110 AU137923.1	.0E-110 BE302694.1	.0E-110 AW838394.1	11432732	/12337.1	.0E-110 BE734357.1	.0E-110 BE734357.1			.0E-110 AA448529.1	.0E-110 BE897218.1	.0E-110 AW062258.1	.0E-110 AB011399.1		.0E-110 BF508896.1	
Most Similar (Top) Hit BLAST E Value	1.0E-110	1.0E-110 /	1.0E-110	1.0E-110	1.0E-110 E	1.0E-110	1.0E-110	1.0E-110 M55112.1	1.0E-110 E	1.0E-110 U0888B.1	1.0E-110 U08888.1	1.0E-110	1.0E-110 /	1.0E-110	1.0E-110	1.0E-110	1.0E-110	1.0E-110	1.0E-110	1.0E-110 Y12337.1	1.0E-110	1.0E-110	1.0E-110 M10051.1		1.0E-110 /	1.0E-110 E	1.0E-110	1.0E-110	1.0E-110	1.0E-110	1.0E-111 U43701.1
Expression Signal	2.04	3.01	2.28	2.23	0.78	8.61	8.61	5.43	0.59	0.85	0.85	0.78	16.19	16.19	2.87	96.0	1.09	2.46	3.38	3.2	3.64	3.64	1.89		1.7	2.47	2.86	2.98	6.01	1.16	11.92
ORF SEQ ID NO:	30872	30897		31583		32358			33754	33782	33783	34025		34132		34293	36174	36395	37171	37700	37916				37539						
Exen SEQ ID NO:	17893	17912	18216	18611	l I	19050			20311	20334	20334	20552	20655	20655	20683	20804	22601	22817	23564	24065	24278	24278			23914	25164	25246		ΙI	15256	13402
Probe SEQ ID NO:	4758	4777	5088	5409	5843	9890	5860	6858	7179	7251	7251	7477	7583	7583	7813	7743	9236	7778	10529	10986	11209	11209	11608		11728	12211	12341	12594	12746	13071	621

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Table 4
Single Exon Probes Expressed in Placenta

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	Top Hit Descriptor	Homo saplens ras GTP ase activating profess 12.0 (NOAD)DNA	601458631F1 NIH MGC 68 Home canbon Charles Into the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the 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the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the	Homo sapiens cat awardows willing teachers and 1/05/01/1	Human cardiac alruha-mwalin heavy chair // M/Lish cardiac alruha-mwalin heavy chair // M/Lish	Homo sapiens DKFZP434D158 pmtein (DKFZD434D458) DNA	Human enkephalin B (enkB) dene exon 4 and 3' flank and complete odd	247b07.r1 Soares pregnant uterus NbHPU Homo sapiers CDNA clore IMAGE:505045 5' similar to ob/A23575 PREGNANCY-SPECIFIC BETA GY YOOPPOTEIN C DECRIDED OF ALL MANY.	247b07.rf Soares pregnant uterus NbHPU Hono sepiens CONA cione IMAGE: 505045 6' similar to	601443890F1 NIH MGC 65 Home series of NA class (MACE 2947655 51	Human two-handed zinc finder protein ZEB mRNA partial case	opolog12.x1 NCI_CGAP_Kid5 Homo sapiens cDNA clone IMAGE:1917574 3' similar to gb:M29893 RAS- RELATED PROTEIN RAL-A (HI IMAN)	DKF20434C1815 r1 434 (synonym: 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	Expression Signal	1.64	1.99	4.13	2.5	1.15	4.59	0.75	0.75	0.88	0.66	2.09	96.0	1.31	3.04	0.7	0.83	0.8	0.8	0.63	3.56	96.0	0.64	8.43	15.93	15.93	3.37	0.54
	ORF SEQ ID NO:	26455		26989	27185	30419	30570	31835	31836	32242	32359	32678	33379	33697	34149	34264	34340	34888	34889	34989	35047	35492	35597		35708	35709	35914	36152
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	Probe SEQ ID NO:	201	753	762	950	4286	4449	5593	5593	5749	5862	6156	6818	6945	7605	7704	7791	8286	8286	8383	8435	8878	8975	8008	9085	9085	9289	9518

Page 455 of 550 Table 4 Single Exon Probes Expressed in Placenta

Probe   Exm   Oper SEC   Expression (Tray) Hit   Top Hit According   Top Hit   Top Hit Descriptor   Signal   BLAST   No. 5 mine   BALON   Top Hit   Source   Signal   BLAST   No. 5 mine   BALON   Top Hit   Source   Signal   BLAST   No. 5 mine   Signal   Signal   Signal   Signal   Signal   Signal   Signal   Signal   Signal   Signal   Signal   Signal   Signal   Signal   Signal   Signal   Signal   Signal   Signal   Signal   Signal   Signal   Signal   Signal   Signal   Signal   Signal   Signal   Signal   Signal   Signal   Signal   Signal   Signal   Signal   Signal   Signal   Signal   Signal   Signal   Signal   Signal   Signal   Signal   Signal   Signal   Signal   Signal   Signal   Signal   Signal   Signal   Signal   Signal   Signal   Signal   Signal   Signal   Signal   Signal   Signal   Signal   Signal   Signal   Signal   Signal   Signal   Signal   Signal   Signal   Signal   Signal   Signal   Signal   Signal   Signal   Signal   Signal   Signal   Signal   Signal   Signal   Signal   Signal   Signal   Signal   Signal   Signal   Signal   Signal   Signal   Signal   Signal   Signal   Signal   Signal   Signal   Signal   Signal   Signal   Signal   Signal   Signal   Signal   Signal   Signal   Signal   Signal   Signal   Signal   Signal   Signal   Signal   Signal   Signal   Signal   Signal   Signal   Signal   Signal   Signal   Signal   Signal   Signal   Signal   Signal   Signal   Signal   Signal   Signal   Signal   Signal   Signal   Signal   Signal   Signal   Signal   Signal   Signal   Signal   Signal   Signal   Signal   Signal   Signal   Signal   Signal   Signal   Signal   Signal   Signal   Signal   Signal   Signal   Signal   Signal   Signal   Signal   Signal   Signal   Signal   Signal   Signal   Signal   Signal   Signal   Signal   Signal   Signal   Signal   Signal   Signal   Signal   Signal   Signal   Signal   Signal   Signal   Signal   Signal   Signal   Signal   Signal   Signal   Signal   Signal   Signal   Signal   Signal   Signal   Signal   Signal   Signal   Signal   Signal   Signal   Signal   Signal   Signal   Signal					_		_	_	_		_	Γ	Γ.	Г	Т	T	Т	Т	Γ	Т	Γ	_	Г	П	Τ	Τ	Γ	T	T	T	T	1		
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Page 456 of 550 Table 4 Single Exon Probes Expressed in Placenta

Top Hit Descriptor	П			DKFZp434M0523_J1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434M0523 5'	Homo saplens solute carrier family 6 (neurotransmitter transporter, L-proline), member 7 (SLC6A7), mRNA	Homo sapiens solute carrier family 6 (neurotransmitter transporter, L-proline), member 7 (SLC6A7), mRNA	AU118051 HEMBA1 Homo sapiens cDNA clone HEMBA1002773 5	Г	Т	7130g07.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sepiens cDNA clone IMAGE:3523020 3' similar to TR:Q9VW35 Q9VW35 CC6743 PROTEIN ;	MR3-SN0009-100400-106-b12 SN0009 Homo sapiens cDNA	yd38d10.s1 Soares fetal liver spleen 1NFLS Homo septens cDNA clone IMAGE:112243 3' similer to ISP:C40H1.1 CE00109 OVARIAN PROTEIN:	vd56d10.s1 Soares fetal livar spleen 1NFLS Homo sapiens cDNA clone IMAGE:112243 3' similar to	SP:C40H1.1 CE00109 OVARIAN PROTEIN;	Homo sapiens mRNA for secreted modular calcium-binding protein (smoc1 gene)	П	qk24008.y5 NCI_CGAP_Kid3 Homo sapiens cDNA clone IMAGE:1869902 5' similar to TR:Q64362 Q64362- FUSED TOES :	qk24c08.y6 NCI_CGAP_Kid3 Homo sapiens cDNA clone IMAGE:1869902 5' similar to TR:Q64362 Q64362		PM0-CT0237-141099-001-h02 CT0237 Homo sepiens cDNA		٦	qk24c08.y5 NC  CGAP Kid3 Homo saplens cDNA cicine IMAGE:1868902 5 similar to 1 K:054362 Q64362   F19FD TOFS	T	T	Ī		ac95f01 x1 Schiller meningioma Homo sapiens cDNA clone IMAGE:1953625 3'
Top Hit Database Source	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	. TN	L	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	NAM HIMAN		EST_HUMAN	F	EST_HUMAN	EST HUMAN	1	EST_HUMAN	EST_HUMAN		EST_HUMAN	NAMILI TOT	L	FST HUMAN	EST HUMAN	F	EST_HUMAN
Top Hit Acession No.	DE-112 BE273103.1	DE-112 BE273103.1	DE-112 BF574235.1	E-112 AL043299.1	11416777 NT	11416777 NT	DE-112 AU118051.1	DE-112 BE867635.1	E-112 BE867635.1	1.0E-112 BF111413.1	DE-112 AW863327.1	E-112 T03967 1		T93967.1	1.0E-112 AJ249900.1	DE-112 BE280479.1	F-112 A1792603.1		0E-112 AI792603.1	DE-112 AW377670.1		DE-112 AI 792603.1	110 AIZO2603 1	0F-112 AF106656 1	0F-113 Al365586.1	0E-113 Al365586.1	0E-113 M11965.1	0E-113 AI365586.1
Most Similar (Top) Hit BLAST E Value	1.0E-112	1.0E-112	1.0E-112	1.0E-112	1.0E-112	1.0E-112	1.0E-112	1.0E-112	1.0E-112	1.0E-112	1.0E-112	1 OE-112	11.1	1.0E-112 T93967.1	1.0E-112	1.0E-112	[ =		-	1.1		-	Ť	-	1 0F-113	-	-	1.0E-113
Expression Signal	0.83	0.83	1.51	0.68	1.49	1.49	1.79	2.64	2.64	237		1 21		1.31	3.14	2.24	2.28		2.28	4.78		1.66	4	131	682			3.23
ORF SEQ ID NO:	33323		23637	33847	34037		34995		35782	ł					37896		38153	L	38154	_		38783	20704	L	26987		27199	
Exen SEG ID NO:	19928		50209	20387	20566	20566	L		22236		Ι.	Į .	L		i	24421			24489	24519	l	25076	25078	1		1_		ll
Probe SEQ ID NO:	6773	6773	6981	2067	7491	7491	8387	9158	9158	10097	11017	11103	3	11103	11191	11359	11428		11428	11460		12096	13008	12727	784	781	965	1572

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Top Hit Descriptor	Homo sapiens elF4E-transporter mRNA, complete cds	UI-H-BW1-ant-f-03-0-UI s1 NC CGAP Sub7 Homo sapiens cUNA done imAGE: 3002070 3	Homo saplens mRNA for putative RNA helicase, 3' end	Homo saplens activating transcription factor B (6-A1F), mrtnA	Homo sapiens activating transcription factor B (B-ATF), mMVA	601469465F1 NIH_MGC_67 Homo sapiens cDNA clone IMACE:3872530 5	AU127214 N T2RP2 Homo sepiens cuind cione in 12KP 2000007 3	AU140291 PLACE2 Homo capiens atinA done PLACEZUOUZ/4 3	Homo sapiens P-glycoprotein (mart) mktvA, complete cus	Homo sapiens UDP-N-acetyl-alpha-D-galactosamine;polypeptide N-acetylgalactusaminyulansura eve o (GaluAc-T8) (GALNT8), mRNA	Homo appiens ATP-binding cassette, sub-family B (MDR/TAP), member 4 (ABCB4), transcript variant B,	пRNA	Homo sapiens ATP-binding cascette, sub-family B (MDR/TAP), member 4 (ABCB4), transcript variant B,	mRNA SA (GBINJA) mRNA	Homo sapiens glutamate receptor, ionotropic, N-metriyi D-aspariate 24 (Chinza) mRnia	Homo sapiens glutamate receptor, lonotropic, N-merry ID-aspea	601152078F1 NIH MGC 19 Homo saplens count invace 3005000 5	601152078F1 NIH MGC_19 Home sapiens culvA done invalor. Sociology	Homo sapiens hypothetical protein FLJ11006 (FLJ11009), mRNA	601297709F1 NIH MGC 19 Homo sepiens GUNA Gone IMANCE 3027 334 3	601297709F1 NIH MGC 19 Homo sapiens cunA digne invite 3027 504 5	RC1+F0134-280800-021-002 F10134 F10110 September 20197	Homo sapiens transmembrane procent z ( ) Michael, (michael), michael		Homo sapiens RAN binding protein / (RANbr /), mixiva	UI-HF-BNO-aK-b-10-0-UI-TI NIH MGC 30 Homo sapiens curis invace 3077228 5	UI-HF-BN0-ag-b-12-0-UI.11 NIH MGC 50 Homo sapiens out A date indee: 307 7250	hh81e09.y1 NCI_CGAP_GU1 Homo saplens cDNA clone IMAGE:2869176 5 similer to TR:060327 C0003444 KIAA0584 PROTEIN ;	hastario vi NGI CGAP GU1 Homo saplens cDNA clone IMAGE:2969176 5' similar to TR:060327 060321		601105529F1 NIH_MGC_15 Homo sapiens cDNA cione IMAGEE:2983300 5	Homo sapiens mkna 10 muluang resistance protein 5 (Abovo)
Top Hit Database Source	۲	EST_HUMAN	TN	NT	M	EST HUMAN	EST_HUMAN	EST HUMAN	٦	Į.		노		ĮN.	N	NT	EST HUMAN	EST_HUMAN		EST_HUMAN	EST_HUMAN	EST_HUMAN	ZINT	Z NT	7 NT	EST HUMAN	EST_HUMAN	FST H IMAN		EST_HUMAN	EST_HUMAN	E/
Tap Hit Acession No.	.0E-113 AF240775.1	.0E-113 BF515218.1	.0E-113 AJ223948.1	5453562 NT	5453562 NT	.0E-113 BE780858.1	.0E-113 AU127214.1	.0E-113 AU140291.1	.0E-113 AF016535.1	11525737 NT		· 9961249 NT		9961249 NT	6006002 NT	6006002 NT	1.0E-113 BE262161.1	1.0E-113 BE262161.1	8922819 NT	1.0E-113 BE382842.1	1.0E-113 BE382842.1	1.0E-113 BE772967.1	11429367 NT	5453997 NT	5453997 NT	1.0E-113 AW500517.1	1.0E-113 AW 500519.1	4 OE 442 AMESON204 4	A 14 COOK 50 1.1	1.0E-113 AW630291.1	1.0E-113 BE292968.1	Y17151.2
Most Similar (Top) Hit BLAST E Value	1.0E-113 A	1.0E-113 B	1.0E-113 A	1.0E-113	1.0E-113	1.0E-113 B	1.0E-113	1.0E-113 A	1.0E-113 A	1 0F-113		1.0E-113		1.0E-113	1.0E-113	1.0E-113	1.0E-113	1.0E-113	1.0E-113	1.0E-113	1.0E-113	1.0E-113	1.0E-113	1.0E-113	1.0E-113	1.0E-113	1.0E-113	10.1	1.00-118	1.0E-113	П	1.0E-114 Y17151.2
Expression Signal	1.63	04.	2.08	36.66	36.66	2.4	6.37	3.54	1.02	25.0		80		8.0	89.0	99.0	0.63	0.63	0.5	2,91	2.91	0.62	1.27	1.01	1.01		1.89		24.6	5.42		0.75
ORF SEQ ID NO:	28240	28422	29385	31263	31264		31870				35125	32800		32810					Ŀ				36674	L	L	37495		1_	38119	38120		
SEQ ID	15994	15297	16375	18300	18300	25930	18805	19228	19254	1	1	10458	1	19458	1	L	L	L	L	1	1	L	1	L	١_	L	_	1_	24457	24457	1	
Probe SEQ ID NO:	1003	2161	3200	5178	5178	5350	5610	6045	6072	200	CEIO	200		6285	6446	8448	7474	7474	9093	928	9236	9601	10036	10256	10256	10842	14385	3	11396	1306	1540	29

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Mact Similar	Most Similar	Most Similar	Most Similar		ì	# ·	
E I U e	Most Similar Expression (Top) Hit Signal BLAST E Value	Most Similar (Top) Hit BLAST E	E I U e	Top Hit	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
						E.	Homo saplens mRNA for multidrug resistance protein 3 (ABCC3)
- ]	0.75	0.75	- ]	7101/17			Home carians mRNA for muliding resistance protein 3 (ABCC3)
13297 26316 0.75 1.0E-114 Y1/151.2	0.75	0.75	1	71/1512	1		
	7	7		T.70554 1		EST HUMAN	yd15c01.st Scares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:108288 3' similar to gb:A21187 ALPHA-2-MACROGLOBULIN PRECURSOR (HUMAN):contains Alu repetitive element
1.0E-114	254 1.05-114	254 1.05-114	1,0E-114		8923087 NT	NT.	Homo saplens hypothetical protein FLJ20080 (FLJ20080), mRNA
27569 4.65 1.0E-114	4.65 1.0E-114	4.65 1.0E-114	1.0E-114		g	LN	Homo saplens rhabdoid tumor deteron region protein 1 (N.15.1.1), in trush Homo saplens rhabdoid tumor deferion (S. cereviste) 3 (MCM3), mRNA
27909 1.9 1.0E-114	1.9 1.0E-114	1.9 1.0E-114	1.0E-114		क्र	Į.	Homo saptens minich of the first content of the Things of the content of the Content of the Content of the Content of the Content of the Content of the Content of the Content of the Content of the Content of the Content of the Content of the Content of the Content of the Content of the Content of the Content of the Content of the Content of the Content of the Content of the Content of the Content of the Content of the Content of the Content of the Content of the Content of the Content of the Content of the Content of the Content of the Content of the Content of the Content of the Content of the Content of the Content of the Content of the Content of the Content of the Content of the Content of the Content of the Content of the Content of the Content of the Content of the Content of the Content of the Content of the Content of the Content of the Content of the Content of the Content of the Content of the Content of the Content of the Content of the Content of the Content of the Content of the Content of the Content of the Content of the Content of the Content of the Content of the Content of the Content of the Content of the Content of the Content of the Content of the Content of the Content of the Content of the Content of the Content of the Content of the Content of the Content of the Content of the Content of the Content of the Content of the Content of the Content of the Content of the Content of the Content of the Content of the Content of the Content of the Content of the Content of the Content of the Content of the Content of the Content of the Content of the Content of the Content of the Content of the Content of the Content of the Content of the Content of the Content of the Content of the Content of the Content of the Content of the Content of the Content of the Content of the Content of the Content of the Content of the Content of the Content of the Content of the Content of the Content of the Content of the Content of the Content of the Content of the Content of the Content of the Content of the Cont
27945 5.08	5.08 1.0E-114	5.08 1.0E-114	1.0E-114	66790	2	NAME TO THE	MRA-HT0559-250200-002-007 HT0559 Homo sapiens cDNA
28406 2.52	2.52	2.52	١	BE171984.1	Т	FIGURE 1	Himan mRNA for KIAA0376 gene, partial cds
-	0.99	0.99	- 1	AB002374.1	T	2 2	Home senions mRNA for KIAA1276 protein, partial cds
26290 0.6	9.0	9.0		AB033102.1	П	Z	Homo sanlens mRNA for KIAA1276 protein, partial cds
26291 0.6	9.6	9.6		AB033102.1		Z	Human gene for catalase (EC 1.11.1.6) exon 2 mapping to chromosome 11, band p13
2.6	2.6	2.6		X04086.1			EAGREGATE NIH MGC 19 Homo sapiens CDNA clone IMAGE: 4100214 5
1.03	1.03	1.03		BF206374.1	ı	EST HUMAIN	Home semilens NOD1 protein (NOD1) gene, exons 1, 2, and 3
3.27	3.27	3.27	_]	4 AF149773.1	١.	2 2	Himan Interferon alpha receptor (HulFN-elpha-Rec) mRNA, complete cds
0.7 1.0	0.7 1.0	0.7 1.0	2	1 103171.1	- 1	NAME TO T	THE RICE AND A TOTAL OF SUP Sub4 Homo sapiens cDNA clone IMAGE 2726424 3
18401 31370 1.1 1.0E-114 AW 294203.1	1.1	1.1	2	4 AW 294203.1	1	בים שחואים	Home sablens same domain, seven thrombospondin repeats (type 1 and type 1-like), transmembrane domain
1.68 1.0E-114 4506880 NT	1.68 1.0E-114	1.68 1.0E-114	1.0E-114		ଯା	N	(TM) and short cytoplasmic domain, (semaphorin) 5A (SEMA5A) mRNA  (TM) and short cytoplasmic domain, (semaphorin) repeats (Moc 1 and Moc 1-like), transmembrane domain
4506880 NT 4506880 NT	1.0E-114	1.0E-114	1.0E-114		8	LN	Homo septents sentia dunient, servery (servery for the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of
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33931 1.09	1.09	1.09	-	4 AU134187.1	- 1	EST HUMAN	AU 134 101 OVANO 1 ISSUE CAPITAL CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF
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33983 8.2	8.2 1.	8.2 1.	1,	4 Y18000.1		LN.	Homo sapiens Nr.z gene
33984 8.2 1.0E-114 Y18000.1	8.2 1.0E-114 Y18000.1	8.2 1.0E-114 Y18000.1	1.0E-114 Y18000.1		١	LN	Homo sapiens INTZ yerre
34675 1.94 1.0E-114	1.94 1.0E-114	1.94 1.0E-114	1.0E-114	4 455	9	4557600 NT	Homo sapiens garring are Homo saniens cDNA clone IMAGE:2017163 3
34963 1.85 1.	1.85	1.85	1.	4 Al363139.1		EST HUMAN	GOOGUD XI INCLOCATE DILEGE HOME SAPING CON COME IMAGE: 2017163 3
L	1.85	1.85	-	4 AI363139.1	ļ	EST HUMAN	gyésdűexti Nol Júszicz malez itente sapiero com complete cds
35516 2.99 1	2.99	2.99	-	14 U63041.1	١	Į.	Human neural der autresion indexate ober in the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of
35589 5.81 1	5.81	5.81		14 AB011133.1	١	Z	Home saplens mRNA for KIAA0561 protein, partial cds
ļ	_	5.81	_	14 AB011133	-	ξ	חסוחס שקומוס וויינים ימי ימי ימי ימי ימי ימי ימי ימי ימי י

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	Top Hit Descriptor	7169g12.x1 Sogres_NSF_FB_9W_OT_PA_P_S1 Homo saplens oDNA clone IMAGE:3526847 3' sImilar to TR.Q9UHN6 Q9UHN6 TRANSMEMBRANE PROTEIN 2 ·	dq03f05.x1 NIH MGC 2 Homo sapiens cDNA clone INAGE-2846744 F	Homo septens knostne kinase endito-src (SRC) crave away 42 and restitle cde	Human ceruloplasmin mRNA	601449752F1 NIH MGC 65 Homo sepiens cDNA clone IMA GE 38R3500 S	Homo septens chromosome 21 segment HS21C027	MR0-HT0559-250200-002-d07 HT0559 Homo seplens cDNA	ba73g12.y1 NIH_MGC_20 Homo saplens cDNA clone IMAGE:2906086 6' similar to gb;X17206 40S	INDOSOWAL PRO LEIN S4 (FIOWAN); 90:MZ0632 Mouse LL.Rep3 protein mRNA from a repetitive element, complete (MOUSE):	AV733454 cdA Homo sepiens cDNA clone cda Rank 5'	AV733454 cdA Homo sapiens cDNA clone cdABA08 6'	AV733454 cdA Homo sapiens cDNA clone cdARA08 5	AV733464 cdA Homo saplens cDNA clone cdABA08 5'	Homo saplens TNF-inducible protein CG12-1 (CG12-1) mRNA	Homo saplens hypothetical protein (DJ1042K10.2) mRNA	Homo saplens hypothetical protein (D.)1042K10.2) mRNA	Homo saplens HLA-B associated transcript-1 (D6S81E) mRNA	Homo saplens polymerase (RNA) II (DNA directed) polypeptide A (220kD) (POLR2A) mRNA	Homo sapiens keratin 18 (KRT18) mRNA	QV4-UM0094-300300-156-b08 UM0094 Homo sapiens cDNA	qt06f01.x1 NCI_CGAP_GC4 Homo sapiens cDNA clone IMAGE:1946809 3' similar to TR:000536 O00536. TTF-I INTERACTING PEPTIDE 6:	q06f01.x1 NCI_CGAP_GC4 Homo sapiens cDNA clone IMAGE:1946809 3' sImilar to TR:000536 000536	Homo saplens transforming growth factor heta-activated kinas-a-kinding protein 4 /TAB41	Homo sapiens transforming growth facility beta-epiticated kinaso-binding protein 1 (1AB1), IIINNA	Homo saplens ferritin heavy behaven 14 (FTH4) mRNA	Homo sapions albha-aminosalioste semialdehvile synthese mRNA commiste and	Homo sapiens alpha-aminoadipate semialdehyde synthase mRNA complete cols	Homo saplens Bruton's tyrosine kinase (BTK), alpha-D-galactosidase A (GLA), L44-like ribosomal protein (144L) and FTP3 ferres, complete rds	601579838F1 NIH_MGC_9 Homo saplens cDNA clone IMAGE:3928832 5	
	Top Hit Database Source	EST HUMAN	EST HUMAN	Į.	¥	EST HUMAN	ΙN	EST_HUMAN		EST HUMAN	EST HUMAN	EST HUMAN	EST HUMAN	EST HUMAN	LN	F	L'N	μN	NT	TN	EST_HUMAN	EST HUMAN	EST HIMAN	IN	NT	IN	LX	ĻΝ	L	EST_HUMAN	
	Top Hit Acession No.	1.0E-114 BF109832.1	1.0E-114 AW327455.1	1.0E-114 AF077754.1	1.0E-114 M13536.1	1.0E-114 BE870004.1	1.0E-114 AL163227.2	1.0E-114 BE171984.1		1.0E-114 BE302666.1	1.0E-114 AV733454.1	1.0E-114 AV733454.1	1.0E-114 AV733454.1	1.0E-114 AV733454.1	11418041 NT	11034850 NT	11034850 NT	4758111 NT	4505938 NT	4557887 NT	.0E-115 AW804759.1	.0E-115 Al339208.1	.0E-115 Al339206.1	5174702INT	5174702 NT	4603794 NT	.0E-115 AF229180.1	,0E-115 AF229180.1	J78027.1	.0E-115 BE745469.1	
	Most Similar (Top) Hit BLAST E Value	1.0E-114	1.0E-114	1.0E-114	1.0E-114	1.0E-114	1.0E-114	1.0E-114		1.0E-114	1.0E-114	1.0E-114	1.0E-114	1.0E-114	1.0E-114	1.0E-114	1.0E-114	1.0E-115	1.0E-115	1.0E-115	1.0E-115	1.0E-115	1.0E-115	1.0E-115	1.0E-115	1.0E-115	1.0E-115	1,0E-115	1.0E-115 U78027.1	1.0E-115	
	Expression Signal	0.87	1.3	2.67	1.36	1.02	1.11	1.18		4.31	8.11	8.11	628	6.28	4.63	2.75	2.75	3.06	1.09	18.42	2.02	1.68	1.68	9	m	15.24	1.15	1.15	1.31	1.13	
	ORF SEQ ID NO:	36022		34621		36989	37010	37415			38197	38198	38522	38523		31975	31976	26264	26391		26552	26766	26767	27041	27042	27044	27823	27824	28140	28400	
	Exan SEQ ID NO:	22459		21104		23378	23399	23795		24106	24525	24525	24831	24831		25616		13262	13358	13362	13519	13742	13742	13988	13988	13990	14742	14742	15032	15278	
	Probe SEQ ID NO:	9384	9614	9662	9748	10343	10364	10762		11027	11466	11466	11842	11842	12643	12936	12936	24	132	138	88	549	549	608	809	811	1590	1590	1888	2142	

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Table 4
Single Exon Probes Expressed in Placenta

esion	Most Similar Expression (Top) Hit Top Hit Acession Signal BLAST E No.	Top Hit Acession No.	esion	ĭ B ŏ	Top Hit Database Source	Top Hit Descriptor
EST	1.13 1.0E-115 BE745489.1 EST	EST	EST		HUMAN	601579838F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3928832 5'
28411	1.1 1.0E-115 AB007902.1			느		Homo sapiens KIAA0442 mRNA, partial cds
1.0E-115 AF231124.1	1.11 1.0E-115 AF231124.1	E-115 AF231124.1		닑		Homo sapiens testican-1 mRNA, complete cds
1.03 1.0E-115 AW804759.1	1.0E-115 AW804759.1	1.0E-115 AW804759.1		ကျ	EST HUMAN	QV4-UM0094-300300-150-b08 UM0094 Homo sapiens cDNA
16359 29365 2.88 1.0E-115 AJ245922.1 NT	2.88 1.0E-115 AJ245922.1	1.0E-115 AJ245922.1		닑		Homo saplens mRNA for alpha-tubulin 8 (TUBA8 gene)
29366 2.88 1.0E-115 A.245922.1	2.88 1.0E-115 AJ245922.1	1.0E-115 AJ245922.1		닐		Homo sepiens mRNA for alpha-tubulin 8 (TUBA8 gene)
29742 1.8 1.0E-115 AJ277392.1	1.8 1.0E-115 AJ277392.1	1.0E-115 AJ277892.1		닑		Homo sapiens partial TTN gene for titin
30299 4.2 1.0E-115 AB00234	4.2 1.0E-115 AB002348.2	1.0E-115 AB002348.2		닑		Homo sapiens mRNA for KIAA0350 protein, partial cds
	2.49 1.0E-115	1.0E-115		닐		Homo sapiens sir2-like 3 (SIRT3), mRNA
30674 4.28 1.0	4.28 1.0E-115	1.0E-115		늘		Homo sapiens EphA4 (EPHA4) mRNA
30918 2.86 1.0E-115 AL096857.1	2.86 1.0E-115 AL096857.1	1.0E-115 AL096857.1		닐		Novel human mRNA from chromosome 1, which has similarities to BAT2 genes
30919 2.86 1.0E-115 AL096857.1	2.86 1.0E-115 AL096857.1	1.0E-115 AL096857.1		늘		Novel human mRNA from chromosome 1, which has similarities to BAT2 genes
31132	2.99 1.0E-115 AL163268.2	1.0E-115 AL163268.2		닐		Homo eapiens chromosome 21 segment HS21C068
31133	2.99 1.0E-115 AL163268.2	1.0E-115 AL163268.2		늘		Homo sapiens chromosome 21 segment HS21C068
31149 1.01 1.0E-115 Y19215.1	1.01 1.0E-115 Y19215.1	1.0E-115 Y19215.1	Y19215.1	닑		Homo sepiens putative psihHbC pseudogene for hair keratin, exons 1 to 9
31391 1.23 1.0	1.23 1.0E-115	1.0E-115		5		Homo saplens interieukin 1 receptor, type I (IL1R1) mRNA
31425 0.92 1.0E-115 AB018311.1	0.92 1.0E-115 AB018311.1	1.0E-115 AB018311.1		닑		Homo saplens mRNA for KIAA0768 protein, partial cds
31642 2.8 1.0E-115 AW970335.1	2.8 1.0E-115 AW970335.1	1.0E-115/AW970335.1	1	ဌ	EST_HUMAN	EST382416 MAGE resequences, MAGK Homo saplens cDNA
18737 31754 0.97 1.0E-115 BF665387.1 [ES	0.97 1.0E-115 BF665387.1	1.0E-115 BF665387.1		띪	EST_HUMAN	602119346F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4276738 5'
32136 1.74 1.0E-115 11425128	1,74 1.0E-115 11425128	1.0E-115 11425128	11425128	יבו	_	Homo sapiens similar to ER to nucleus signalling 1 (H. sapiens) (LOC63433), mRNA
	1.74 1.0E-115	1.0E-115		2	1	Homo sapiens similar to ER to nucleus signalling 1 (H. sapiens) (LOC63433), mRNA
18998 32304 1.15 1.0E-115 Al928799.1 E	1.15 1.0E-115 Al928799.1	1.0E-115 AI928799.1		ŭí	EST_HUMAN	au64g01.x1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2519568 3' similar to gb:L0780 <u>7</u> DYNAMIN-1 (HUMAN);
18008 3230F 115 10E-115 DI928790 1	1 15 1 0E-115 AI928799 1	1 0F-115 A1928799.1		ŭ	EST HIMAN	au84g01.x1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2519568 3' similar to gb:L07807 DYNAMIN-1 (HUMAN):
32919 0.68 1.0E-115 11426788	0.68 1.0E-115 1142678B	1.0E-115 11426786	11426786	ΙZ	1	Homo sapiens sperm surface protein (HSS), mRNA
32920 0.68	0.68 1.0E-115	1.0E-115		Ιz		Homo sapiens sperm surface protein (HSS), mRNA
33064 9.49	9.49 1.0E-115	1.0E-115		12		Homo saplens similar to ribosomal protein S26 (H. sapiens) (LOO63436), mRNA
1.68	1.68 1.0E-115	1.0E-115		I۶		Homo sapiens KIAA0054 gene product, Helicase (KIAA0054), mRNA
1.68	1.68 1.0E-115	1.0E-116		ľΖ		Homo capienc KIAA0054 gene product; Helicase (KIAA0064), mRNA
200000 ALT TOTAL TOTAL	0 25 4 0E 44 8 T9877.4 4	4 OE 446 T98774 4		l u	POT LINABAN	yd86b08.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:115095 5' similar to spinoporo yEAST P15801 TNA POI YMFRASE GAMMA.
1.24 1.0E-115 AI076598.1	1.24 1.0E-115 AI076598.1	1.0E-115 At076598.1			EST HUMAN	cDNA clone IMAGE:1676914 3'
33976 1.24	1.24	F	A1076598.1		EST HUMAN	
			1			

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	Top Hit Descriptor	DKFZp43400127 r1 434 (syngnym: htes3) Homo sepiens cDNA clone DKF7n43400127 F	Homo sapiens chromosome 2 open reading frame 3 (C20RF3) mRNA	Homo sapiens very long chain acyl-CoA dehydrogenase gane, expos 1-20, complete cyc	801469159F1 NIH MGC 67 Home sablens cDNA clone IMAGE:3872247 5	QV0-BT0263-090200-097-h03 BT0263 Horno saniens cDNA	QV0-BT0263-090200-097-h03 BT0263 Home saplens cDNA	2x88d07.r1 Soares NHMPu S1 Homo segiens cDNA clane IMAGE:811789 5	ze8d07.r1 Soares NhHMPu S1 Home sapiens cDNA clone IMAGE:811789 5	Human mRNA for KIAA0383 gene, partial cds	Human mRNA for KIAA0383 gene, partial cds	Homo sepiens latent transforming growth factor beta binding protein 2 (LTBP2) mRNA	Homo saplens latent transforming growth factor beta binding protein 2 (LTBP2) mRNA	601144863F2 NIH_MGC_19 Homo sepiens cDNA clone IMAGE:3160502 5'	DKFZp586K1824 r1 586 (synonym: hute1) Homo sablens cDNA clone DKFZp586K1824	Homo sapiens hypothetical protein (DJ328E19.C1.1), mRNA	601307146F1 NIH_MGC_39 Homo sepiens cDNA clone IMAGE:3641603 5	601307146F1 NIH_MGC_39 Homo saplene dDNA clone IMAGE:3641603 5	7n17e09.x1 NCI_CGAP_Bm23 Home sapiens cDNA cione IMAGE:3584785 3' similar to SW:ZP3A_HUMAN P21754 ZONA PELLUCIDA SPERM-BINDING PROTEIN 3A PRECURSOR:	UI-H-BW0-eio-a-07-0-UI.s1 NCI_CGAP_Sub6 Homo saplens cDNA clone IMAGE:2729772 3'	EST186814 HCC cell line (matastasis to liver in mouse) II Homo sapiens cDNA 5 end similar to dynein, lighter chain 1 cultodescrip	601499514F1 NIH MGC 70 Homo saniens cDNA clone IMA CE Rontsea 51		hy36a06.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3176474 3' similar to TR:Q9Z2H4 — POS72H4 G PROTEIN COI ISI ED DECEDENDE I GDA	ope of and	Homo sapiens CGI-105 profein (LOC51011), mRNA	Homo sapiens mRNA for KIAA0930 protein, partial cds	Homo saplens hypothetical protein FLJ10052 (FLJ10052), mRNA	1556241 3' similar to WP:E04F6.2	Homo saplens glutamate receptor, ionotropic, kalnate 1 (GRIK1) mRNA	AU133399 NT2RP4 Homo sapiens cDNA clone NT2RP4001991 5'
	Top Hit Database Source	EST_HUMAN	LN LN	LN	EST HUMAN	EST HUMAN	EST HUMAN	EST HUMAN	EST HUMAN	LN LN	FZ	LN	LN	EST_HUMAN	EST HUMAN	F	EST_HUMAN	EST_HUMAN	EST HUMAN	EST_HUMAN	EST HIMAN	EST HUMAN	EST HUMAN	TOT INVAN	TN-	Ę	TN	トフ	EST HUMAN	Þ	T_HUMAN
`    	Top Hit Acession No.	1.0E-118 AL043761.1	11431050 NT	1.0E-118 L46590.1	1.0E-118 BE781223.1	1.0E-118 BE062855.1	1.0E-118 BE062855.1	1.0E-118 AA443024.1	1.0E-118 AA443024.1	1.0E-118 AB002381.1	1.0E-118 AB002381.1	4557732 NT	4557732 NT	.0E-118 BE263134.1	.0E-118 AL048474.2	7857016 NT		1.0E-118 BE736213.1	.0E-118 BF195407.1	1.0E-118 AW296351.1	.0F-118 AA315C07 1	T		0F-118 BF2182351	T	35607	.0E-119 AB023147.1	8922205 NT	.0E-119 AA916760.1	4116	.0E-119 AU133399.1
	Most Similar (Top) Hit BLAST E Value	1.0E-118	1.0E-118	1.0E-118	1.0E-118	1.0E-118	1.0E-118	1.0E-118	1.0E-118	1.0E-118	· 1.0E-118	1.0E-118	1.0E-118	1.0E-118	1.0E-118	1.0E-118	1.0E-118	1.0E-118	1.0E-118	1.0E-118	1.0F-118	1.0E-118	1.0E-118	1 0F-118	1.0E-119	1.0E-119	1.0E-119	1.0E-119	1.0E-119	1.0E-119	1.0E-119 /
	Expression Signal	+	4.7	0.72	1.95	7	7	1.1	1.1	0.94	0.94	1.94	1.94	5.15	0.55	1.07	1.23	1.23	1.75	0.59	3.75	2.92	2.92	181	2.46	0.93	2.96	1.01	2.17	1.22	3.96
	ORF SEQ ID NO:			34339	34761					35488	35489	35536	35537	35855	35894	36411	37184	37186	37228	37399	38290	38539	38540	38761	27007	27284	28232	29353		30227	31632
	Exen SEQ ID NO:	20329		20846	21241	21658	1 1		21664		١.	- 1			. 1		23576	23578	23621			24843	24843	25052	13956	16029	15129	16348	16485	17219	18653
	Probe SEQ ID NO:	7246	7776	7790	8159	8577	8577	8583	8583	8873	8873	8918	8918	9236	9286	9792	5	10541	10586	10752	11555	11855	11855	12071	776	1062	1987	3171	3312	4063	5453

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Top Hit Descriptor	Human neurofibromin (NF1) gene, complete cds	RC1-NN0073-250800-018-g06 NN0073 Homo saplens cDNA	AV693731 GKC Homo sapiens cDNA done GKCDHB03 5'	DKFZp762M0710_r1 762 (synonym: hmel2) Homo sapiens cDNA clone DKFZp762M0710 5	DKFZp76ZM0710_r1 762 (synonym: hmcl2) Homo sapiens cDNA clone DKFZp76ZM0710 5	qb77c09.x1 Soeres_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:1706128 3' similar to exa.st.c. i мот ise possas кеватти турет сустовкетета и о	Homo senions matrix metallonroleinase 28 (MMP28) mRNA complete cds	Jones casions matrix metallamplaines 28 (MMD28) mRNA complete orte	THE SAPING SAPING INDUSTRIBUTE OF SA HOME SAPING AT A CHORD IMAGE: 21574513	In the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the 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protein-5 (MDA5), mRNA	Homo sapiens KIAA0477 gene product (KIAA0477), mRNA	qf43a11.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1752764 3' similar to TR:Q13458	Q13458 GUANINE NUCLEOTIDE EXCHANGE FACTOR PROTEIN TRIO.;	aa32f05.r1 NCI_CGAP_GCB1 Homo saplens cDNA clone IMAGE:814977 5'	Homo sapiens partial IL-12RB1 gene for IL-12 receptor beta1 chain, exons 16-17	Homo sapiens hypothetical protein FLJ10206 (FLJ10206), mRNA	Homo sapiens hypothetical protein FLJ10206 (FLJ10206), mRNA	601347190F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3687887 67	Homo sapiens Scd mRNA for stearcy/-CoA desaturase, complete cds	Homo sapiens partial IL-12RB1 gene for IL-12 receptor beta1 chain, exons 16-17	Homo sapiens partial IL-12RB1 gene for IL-12 receptor beta1 chain, exons 16-17	602186072F1 NIH_MGC_45 Homo sapiens cDNA clone IMAGE:4310633 5'	RC3-CT0212-240999-011-f03 CT0212 Homo sapiens cDNA	H. sapiens DNA for endogenous retroviral like element	Homo sapiens mRNA for KIAA0758 protein, partial cds	Homo sapiens synaptojanin 1 (SYNJ1), mRNA	Homo sapiens intersectin 2 (SH3D1B) mRNA, complete cds	Homo sapiens intersectin 2 (SH3D1B) mRNA, complete cds	yy40g12.r1 Scares melanccyte 2NbHM Homo sapiens cDNA clone IMAGE:273766 5
Top Hit Database Source	F	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	MALAI II TOT	EST TIONAIN	15	NI CCT CE MAN	NEWDE TO	I LOT	ES HOMAIN	EST_HUMAN	EST_HUMAN	NT	NT		EST_HUMAN	EST_HUMAN	NT	N IN	Ę	EST_HUMAN	TN	NT	NT.	EST_HUMAN	EST_HUMAN	E	Į.	ΨŁ	Ā	NT	EST_HUMAN
Top Hit Acession No.	JE-119 M89914.1		0E-119 AV693731.1	0E-119 AL134603.1	0E-119 AL134903.1	7 001037	0E-119 AIT30/03.1				,			0E-119 BE615150.1	11545921 NT	11036843 NT		0E-119 AI149796.1	0E-119 AA465124.1	0E-119 AJ297701.1	11425837 NT	41425837 NT	0E-119 BE561967.1	0E-119 AB032261.1	.0E-119 AJ297701.1	0E-119 AJ297701.1	.0E-119 BF569571.1		0E-119 X89211.1	.0E-120 AB018301.1	4507334 NT	0E-120 AF248540.1	.0E-120 AF248540.1	.0E-120 N44873.1
Most Similar (Top) Hit BLAST E Value	1.0E-119	1.0E-119	1.0E-119 A	1.0E-119	1.0E-119	10	1.0E-119	7 707	1.0E-1197	1.00-119	1.0E-119 X06292.1	1.05-1797	1.0E-119	1.0E-119	1.0E-119	1.0E-119		1.0E-119	1.0E-119	1.0E-119	1.0E-119	1.0E-119	1.0E-119	1.0E-119	1.0E-119	1.0E-119	1.0E-119	1.0E-119	1.0E-119	1.0E-120	1.0E-120	1.0E-120	1.0E-120	1.0E-120
Expression Signal	15.48	3.29	1.61	98.0	0.86	·	0.73	200	0.7	7 6	2.39	10.4	1.09	0.93	0.46	96.0		19.0	2.29	1.13	0.77	0.77	0.59	0.73	1.58	1.58	6.62	5.48	3.03	0.68	76.0	2.74		3.26
ORF SEQ ID NO:	31645	31650			32195	-	27/72		1	١	33133	١	34116		36592			36952			37420										26561			
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Table 4
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Acession<br>No.         Top Hit Acession<br>No.         Top Hit<br>Signal<br>Signal<br>Flass         Top Hit Acession<br>Value         Top Hit Acession<br>No.         Top Hit Acession<br>No.         Top Hit Acession<br>Source           14783         228098         6.58         1.0E-120         AF167706.1         NT           15309         228438         1.83         1.0E-120         AB011399.1         NT           15528         26561         1.81         1.0E-120         AB011399.1         NT           17617         30598         2.05         1.0E-120         AF056490.1         NT           17617         30599         2.05         1.0E-120         AF056490.1         NT           17619         30906         3.11         1.0E-120         AF058483.1         NT | Exon<br>NO:         ORF SEQ<br>SIGNAL         Expression<br>Signal         (Top) Hit<br>PLASTE<br>Value         Top Hit Acession<br>PLASTE<br>Value         Top Hit Acession<br>No.         Top Hit Acession<br>No.         Top Hit Acession<br>Source           14783         27869         11.19         1.0E-120         AF167706.1         NT           16309         28437         1.83         1.0E-120         AB011399.1         NT           15328         26561         1.81         1.0E-120         AB011399.1         NT           17617         30598         2.05         1.0E-120         AF055490.1         NT           17617         30590         2.06         1.0E-120         AF055490.1         NT           17619         30906         3.11         1.0E-120         AF058483.1         NT           17919         30907         3.11         1.0E-120         AF098483.1         NT | Exon<br>NO:         ORF
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| Exon<br>NO:         ORF SEQ<br>10 NO:         Expression<br>Signal         (Top) Hit<br>Pales         Top Hit Acession<br>Value         Top Hit Acession<br>No:         Top Hit Acession<br>Value         Top Hit Acession<br>No:         Top Hit Acession<br>Value         Top Hit Acession<br>No:         Top Hit Acession<br>No:         Top Hit Acession<br>No:         Top Hit Acession<br>Source         Top Hit Acession<br>Source         Top Hit Acession<br>Source         Top Hit Acession<br>Acid Acid Acid Acid Acid Acid Acid Acid | Exon<br>NO:         ORF SEQ<br>10 NO:         Expression<br>Signal         (Top) Hit<br>Pales         Top Hit Acession<br>Value         Top Hit Acession<br>No:         Top Hit Acession<br>Value         Top Hit Top Hit Acession<br>No:         Top Hit Acession<br>No:         Top Hit Acession<br>Value         Top Hit Acession<br>No:         Top Hit Acession<br>Source           14763         27869         6.58         1.0E-120         AF167706.1         NT           16309         28437         1.83         1.0E-120         AB011399.1         NT           15309         28438         1.68         1.0E-120         AB011399.1         NT           17617         30598         2.05         1.0E-120         AF058490.1         NT           17617         30599         2.05         1.0E-120         AF098483.1         NT           17619         305906         3.11         1.0E-120         AF098483.1         NT           17619         30249         16.08         1.0E-120         AF098483.1         NT           19043         32349         16.08         1.0E-120         AF088483.1         NT           20809         34296         1.84         1.0E-120         BF688222.1         EST HUMAN           20809         34296         1.84         1.0E-120         D346 | Exon<br>NO:         ORF SEQ<br>Signal<br>14783         Expression<br>Signal<br>14895         (Top) Hit<br>BLAST E<br>PLAST E<br>14895         Top Hit Acession<br>Plane         Top Hit Acession<br>Plane     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Spring and BLASTER (No.)         No.         Spring and BLASTER (No.)         No.         Spring and BLASTER (No.)         No.         No.         No.         No.         No.         No.         No.         No.         No.         No.         No.         No.         No.         No.         No.         No.         No.         No.         No.         No.         No.         No.         No.         No.         No.         No.         No.         No.         No.         No.         No.         No.         No.         No.         No.         No.         No.         No.         No.         No.         No.         No.         No.         No.         No.         No.         No.         No.         No.         No.         No.         No.         No.         No.         No.         No.         No.         No.         No.         No.         No.         No.         No.         No.         No.         No.         No.</td><td>Exon         ORF SEQ         Expression (Top) Hit Top Hit Acession         Top Hit Acession (Top) Hit Top Hit Acession         Top Hit Acession         Top Hit Acession         Top Hit Acession         Top Hit Acession         Top Hit Acession         Top Hit Acession         Top Hit Acession         Top Hit Acession         Top Hit Acession         Top Hit Acession         Top Hit Acession         Top Hit Acession         Top Hit Acession         Top Hit Acession         Top Hit Acession         Top Hit Acession         Top Hit Acession         Top Hit Acession         Top Hit Acession         Top Hit Acession         Top Hit Acession         Top Hit Acession         Top Hit Acession         Top Hit Acession         Top Hit Acession         Top Hit Acession         Top Hit Acession         Top Hit Acession         Top Hit Acession         Top Hit Acession         Top Hit Acession         Top Hit Acession         Top Hit Acession         Top Hit Acession         Top Hit Acession         Top Hit Acession         Top Hit Acession         Top Hit Acession         Top Hit Acession         Top Hit Acession         Top Hit Acession         Top Hit Acession         Top Hit Acession         Top Hit Acession         Top Hit Acession         Top Hit Acession         Top Hit Acession         Top Hit Acession         Top Hit Acession         Top Hit Acession         Top Hit Acession         Top Hit Acession         Top Hit Acession         Top Hit Acession         Top Hit Acession</td></td> | Exon<br>NO:         ORF SEQ<br>SIgnal         Expression<br>Signal         (Top) Hit<br>Place         Top Hit Acession<br>Place         Top Hit Acession<br>Place         Top Hit Acession<br>Place         Top Hit Acession<br>Place         Top Hit Acession<br>Place         Top Hit Acession<br>Place         Top Hit Acession<br>Place         Top Hit Acession<br>Place         Top Hit Acession<br>Place         Top Hit Acession<br>Place         Top Hit Acession<br>Place         Top Hit Acession<br>Place         Top Hit Acession<br>Place         Top Hit Acession<br>Place         Top Hit Acession<br>Place         Top Hit Acession<br>Place         Top Hit Acession<br>Place         Top Hit Acession<br>Place         Top Hit Acession<br>Place         Top Hit Acession<br>Place         Top Hit Acession<br>Place         Top Hit Acession<br>Place         Top Hit Acession<br>Place         Top Hit Acession<br>Place         Top Hit Acession<br>Place         Top Hit Acession<br>Place         Top Hit Acession<br>Place         Top Hit Acession<br>Place         Top Hit Acession<br>Place         Top Hit Acession<br>Place         Top Hit Acession<br>Place         Top Hit Acession<br>Place         Top Hit Acession<br>Place         Top Hit Acession<br>Place         Top Hit Acession<br>Place         Top
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| Exon<br>NO:         ORF SEQ<br>Signal<br>10 NO:         Expression<br>Signal<br>Place         (Top) Hit<br>Value<br>Place         Top Hit Acession<br>Value         Top Hit Acession<br>No:         Top Hit Top Hit Acession<br>Value         Top Hit Acession<br>Place         Top Hit<br>No:         Top Hit<br>No:         Top Hit<br>No:         Top Hit<br>No:         Top Hit Acession<br>Value         Top Hit<br>Source           14783         27869         11.19         1.0E-120         AF167706.1         NT         NT           16309         28437         1.83         1.0E-120         AB011399.1         NT         NT           15526         26561         1.83         1.0E-120         AB011399.1         NT         NT           17617         30598         2.05         1.0E-120         AF056490.1         NT         NT           17617         30598         2.05         1.0E-120         AF056490.1         NT         NT           17619         30500         3.11         1.0E-120         AF056490.1         NT         NT           17619         30500         3.11         1.0E-120         AF056493.1         NT         NT           17619         30500         3.11         1.0E-120         AF056493.1         NT         NT           18043         3.2349         16.08 <td>Exon<br/>NO:         ORF SEQ<br/>SIgnal         Expression<br/>Figure<br/>From<br/>Signal         (Top) Hit<br/>From<br/>From<br/>From<br/>From<br/>From<br/>From<br/>From<br/>From</td> <td>Exon<br/>NO:         ORF SEQ<br/>SIgnal         Expression<br/>Figure<br/>From<br/>Policy         Top Hit Acession<br/>Figure<br/>From<br/>Figure<br/>From<br/>From<br/>From<br/>From<br/>From<br/>From<br/>From<br/>From</td> <td>Exon<br/>No:         ORF SEQ<br/>Signal         Expression<br/>Signal         (Top) Hit<br/>BLAST E<br/>PLAST E<br/>Signal         Top Hit Acession<br/>Top Hit Acession         Top Hit Acession<br/>Top Hit Acession         Top Hit Acession<br/>Deathase<br/>Source           14783         27869        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<td>SPC DR SEC DR (NO.)         Spring and BLASTER (No.)         Top HR Accessory (No.)         Top HR Descriptor         Top HR Descriptor           14782 (NO.)         Spring and BLASTER (No.)         No.         Spring and BLASTER (No.)         Top HR Descriptor         Top HR Descriptor           14782 (NO.)         Spring and BLASTER (No.)         No.         Spring and BLASTER (No.)         No.         Spring and BLASTER (No.)         No.         No.         No.         No.         No.         No.         No.         No.         No.         No.         No.         No.         No.         No.         No.         No.         No.         No.         No.         No.         No.         No.         No.         No.         No.         No.         No.         No.         No.         No.         No.         No.         No.         No.         No.         No.         No.         No.         No.         No.         No.         No.         No.         No.         No.         No.         No.         No.         No.         No.         No.         No.         No.         No.         No.         No.         No.         No.         No.         No.         No.         No.         No.         No.         No.         No.         No.</td> <td>Exon         ORF SEQ         Expression (Top) Hit Top Hit Acession         Top Hit Acession (Top) Hit Top Hit Acession         Top Hit Acession         Top Hit Acession         Top Hit Acession         Top Hit Acession         Top Hit Acession         Top Hit Acession         Top Hit Acession         Top Hit Acession         Top Hit Acession         Top Hit Acession         Top Hit Acession         Top Hit Acession         Top Hit Acession         Top Hit Acession         Top Hit Acession         Top Hit Acession         Top Hit Acession         Top Hit Acession         Top Hit Acession         Top Hit Acession         Top Hit Acession         Top Hit Acession         Top Hit Acession         Top Hit Acession         Top Hit Acession         Top
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      Top Hit Acession<br>Figure<br>From<br>Figure<br>From<br>From<br>From<br>From<br>From<br>From<br>From<br>From                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       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      Expression<br>Signal         (Top) Hit<br>BLAST E<br>PLAST E<br>Signal         Top Hit Acession<br>Top Hit Acession         Top Hit Acession<br>Top Hit Acession         Top Hit Acession<br>Deathase<br>Source           14783         27869         11.19         1.0E-120         AF167706.1         NT           14396         28437         18.58         1.0E-120         AB011399.1         NT           15309         28438         1.83         1.0E-120         AB01399.1         NT           15509         28438         1.83         1.0E-120         AB01399.1         NT           15309         28438         1.83         1.0E-120         AB01399.1         NT           15509         28438         1.83         1.0E-120         AF055490.1         NT           17617         30598         2.06         1.0E-120         AF098463.1         NT           17617         30596         3.11         1.0E-120         AF098463.1         NT           17619         33590         1.0E-120         AF098463.1   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Spring and BLASTER (No.)         No.         Spring and BLASTER (No.)         No.         Spring and BLASTER (No.)         No.         No.         No.         No.         No.         No.         No.         No.         No.         No.         No.         No.         No.         No.         No.         No.         No.         No.         No.         No.         No.         No.         No.         No.         No.         No.         No.         No.         No.         No.         No.         No.         No.         No.         No.         No.         No.         No.         No.         No.         No.         No.         No.         No.         No.         No.         No.         No.         No.         No.         No.         No.         No.         No.         No.         No.         No.         No.         No.         No.         No.         No.         No.         No.         No.         No.         No. | Exon         ORF SEQ         Expression (Top) Hit Top Hit Acession         Top Hit Acession (Top) Hit Top Hit Acession         Top Hit Acession         Top Hit Acession         Top Hit Acession         Top Hit Acession         Top Hit Acession         Top Hit Acession         Top Hit Acession         Top Hit Acession         Top Hit Acession         Top Hit Acession         Top Hit Acession         Top Hit Acession         Top Hit Acession         Top Hit Acession         Top Hit Acession         Top Hit Acession         Top Hit Acession         Top Hit Acession         Top Hit Acession         Top Hit Acession         Top Hit Acession         Top Hit Acession         Top Hit Acession         Top Hit Acession         Top Hit Acession         Top Hit Acession         Top Hit Acession         Top Hit Acession         Top Hit Acession         Top Hit Acession         Top Hit Acession         Top Hit Acession         Top Hit Acession         Top Hit Acession         Top Hit Acession         Top Hit Acession         Top Hit Acession         Top Hit Acession         Top Hit Acession         Top Hit Acession         Top Hit Acession         Top Hit Acession         Top Hit Acession         Top Hit Acession         Top Hit Acession         Top Hit Acession         Top Hit Acession         Top Hit Acession         Top Hit Acession         Top Hit Acession         Top Hit Acession         Top Hit Acession         Top Hit Acession         Top Hit Acession         Top Hit Acession |

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	Top Hit Descriptor	Homo sepiens Inostiol polyphosphate-4-phosphatase, type I, 107kD (INPP4A), splice variant a, mRNA	Homo sepiens inositol polyphosphate-4-phosphatase, type I, 107kD (INPP4A), splice variant a, mRNA	Homo sapiens metabotropic glutamate receptor 1 beta (mGluR1beta) mRNA, complete cds	602014759F1 NCL_CGAP_Brn64 Horno saplens cDNA clone IMAGE:4150286 5'	602014759F1 NCI_CGAP_Brn64 Homo sapiens cDNA done IMAGE:4150286 5	Homo sapiens hHb3 gene for hair keratin, exons 1 to 9	Homo saplens hHb3 gene for hair keratin, exons 1 to 9	Homo sapiens mRNA for KIAA1337 protein, partial cds	Homo saplens mRNA for KJAA1337 protein, partial cds	Homo sapiens adaptor-related protein complex AP-4 epsilon subunit mRNA, complete cds	qx57b01.x1 NCI_CGAP_Pan1 Homo sapiens cDNA clane IMAGE:2005417.31	H.saplens ECE-1 gene (exon 17)	hu09f08.x1 NCI_CGAP_Lu24 Homo saplens cDNA clone IMAGE:3166119 3'	601140483F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3049820 5'	Human glucose transporter (GLUT4) gene, complete ods	Homo saplens Xq pseudoautosomal region; segment 2/2	RC3-NN0066-270400-011-f02 NN0066 Homo sapiens cDNA	RC3-NN0066-270400-011-f02 NN0066 Homo sapiens cDNA	Homo sapiens gamma-aminobutyric acid (GABA) A receptor, alpha 2 (GABRA2), mRNA	Homo saplens DNA for prostacyclin synthase, excn 8	Homo saplens DNA for prostacyclin synthase, exon 8	ia05g05.y1 Human Pancreatic Islets Homo sapiens cDNA 5' sImilar to TR:075457 075457 CYTOSOLIC	its Homo sapiens cDNA 5' similar to TR:075457 075457 CYTOSOLIC	PHOSPHOLIPASE A2-GAMMA.;	Homo saplens COX11 (yeast) homolog, cytochrome c oxidase assembly protein (COX11), mRNA	Homo sapiens UDP-glucuronosyltransferase 2B4 precursor (UGT2B4) mRNA, UGT2B4*E458 allele,		Homo sapiens chloride intracellular channel 4 like (CLIC4L), mRNA	y/74c01.s1 Soares fetal fiver spleen 1NFLS Homo sapiens cDNA clone IMAGE:248448 3	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1), mRNA	Homo sapiens intersectin short isoform (ITSN) mRNA, complete cds
	Top Hit Database Source	TN	TN	M	EST_HUMAN	EST_HUMAN	NT	Þ	NT	IN	IN	EST_HUMAN	Ę	EST HUMAN	EST_HUMAN	TN	IN	EST_HUMAN	EST HUMAN	ΙN	TN	TN	EST HUMAN		EST_HUMAN	NT		NT	NT	EST_HUMAN	NT	IN
	Top Hit Acession No.	4755139 NT	4755139 NT	.0E-121 L76631.1	.0E-121 BF344378.1	.0E-121 BF344378.1	.0E-121 Y19208.1	.0E-121 Y19208.1	.0E-121 AB037758.1	.0E-121 AB037758.1	.0E-121 AF155156.2	.0E-121 AI263294.1	.0E-121 X91937.1	.0E-121 BE222250.1	.0E-121 BE271424.1	.0E-121 M91463.1	.0E-121 AJ271736.1	.0E-121 AW898086.1	.0E-121 AW898088.1	11436217 NT	.0E-121 D84122.1	.0E-121 D84122.1	0E-121 AW 683858.1		.0E-121 AW 683858.1	11427788[NT		.0E-121 AF064200.1	7330334 NT	.0E-121 N59624.1	11526176 NT	.0E-122 AF114488.1
	Most Similar (Top) Hit BLAST E Value	1.0E-121	1.0E-121	1.0E-121	1.0E-121	1.0E-121	1.0E-121	1.0E-121	1.0E-121	1.0E-121	1.0E-121	1.0E-121	1.0E-121	1.0E-121	1.0E-121	1.0E-121	1.0E-121	1.0E-121	1.0E-121	1.0E-121	1.0E-121	1.0E-121	1.0E-121		1.0E-121	1.0E-121		1.0E-121	1.0E-121	1.0E-121	1.0E-122	1.0E-122
Ì	Expression Signal	1	-	1.22	1.07	1.07	6.8	5.8	1.23	. 1.23	8.25	1.76	3.42	0.84	0.73	0.64	96.0	0.79	0.79	1.07	2.51	2.51	1.02		1.02	3.45		1.94	5.74	1.93	2.64	2.33
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	ORF SEQ Exp ID NO: S	28269	28270					29337	. 1				31189			33308		31483		34725			36702			37733				37950		
		15164 28269	15164 28270	15304		15766	16325	16325	16790	16790	16929	17590	18219		18873	19913		18529	18529		21209	21209 34730	10062 23100 36702			24094			24280 37919		278 13496 26526	13557

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Top Hit Descriptor	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1), mRNA	Homo saplens intersectin short Isoform (ITSN) mRNA, complete cds	Human kappa-immunoglobulin germline pseudogene (Chr22.4) variable region (subgroup V kappa II)	Homo sapiens cystelne-rich repeat-containing protein S52 precursor, mRNA, complete cds	Homo sapiens callagen, type XII, alpha 1 (COL12A1), mRNA	Homo sapiens collagen, type XII, apha 1 (COL12A1), mRNA	601497032F1 NIH_MGC_70 Homo saplens cDNA clone IMAGE:3899368 5'	601896173F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4125234 5'	601896173F1 NIH_MGC_19 Homo saplens cDNA clone IMAGE:4125234 5'	Homo sapiens FYVE domain-containing dual specificity protein phosphalase FYVE-DSP2 mRNA, complete eds	Homo canione amulald hafa (AA) praemins or profein (professe poolin. II Alsheimer disease) (ADD) mBNA	THEERON SHE AND ALL I'M MIN MICE SO HAVING SOND A CHARACTER THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT	Unit - Drogging Control   Min_Wico_Control september Control Invoced to September 1	601113567F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3354232 5	601113567F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3354232 5'	ak49h06.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1409339 3'	Homo sapiens mRNA for doublesex and mab-3 related transcription factor 1 (DMRT1)	Homo sapiens lethal glant larvae (Drosophila) homolog 2 (LLGL2), mRNA	qy32h07.x1 NCL_CGAP_Bm23 Homo sapiens cDNA done !MAGE:2013757.3' similar to SW:wTA1 HUMAN 013330 METASTASIS-ASSOCIATED PROTEIN MTA1.	qy32h07.x1 NCI_CGAP_Bm23 Homo sapiens cDNA done IMAGE:2013757 3' similar to	SW:MTA1_HUMAN Q13330 METASTASIS-ASSOCIATED PROTEIN MTA1.;	Novel human gene mapping to chomosome X, isoform of dbl (proto-oncogene)	EST367904 MAGE resequences, MAGD Homo sapiens cDNA	Homo sapiens gene for B120, exon 10	Homo sapiens phosphomannomutase 1 (PMM1), mRNA	602018058F1 NCI_CGAP_Bm67 Homo saplens cDNA clone IMAGE:4153670 5'	602018058F1 NCL_CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4153670 5	Homo sapiens chromosome 21 segment HS21C049	Homo sapiens inner membrane protein, mitochondrial (mitofilin) (IMMT), mRNA	Homo sapiens phosphatidylinositol-4-phosphate 5-ktrase, type II, beta (PIP5K2B) mRNA, and translated products
Top Hit Database Source	LN	NT	TN	L	N	NT	EST_HUMAN	EST_HUMAN	EST_HUMAN	I	FX	EST LIMAN	EST TOWAR	EST_HUMAN	EST HUMAN	EST_HUMAN	NT	NT	EST HIMAN		EST_HUMAN	NT	EST_HUMAN	NT	TN	EST_HUMAN	EST_HUMAN	NT	NT	NT
Top Hit Acession No.	11526176 NT	.0E-122 AF114488.1	0E-122 M20707.1	.0E-122 AF167706.1	11418424 NT	11418424 NT	0E-122 BE906024.1	0E-122 BF316170.1	0E-122 BF316170.1	0E-122 AF264717.1	TM 894COAK	OE 123 AWE04645 1	]	.0E-122 BE256039.1	0E-122 BE256039.1	0E-122 AA868671.1	.0E-122 AJ276801.1	11424216 NT	0F-122 AI35961R 1		0E-122 Al359618.1	.0E-122 AL117234.1	.0E-122 AW955834.1	AB024068.1	11418187 NT	.0E-123 BF345274.1	.0E-123 BF345274.1	.0E-123 AL163249.2	5803114 NT	4505818 NT
Most Similar (Top) Hit BLAST E Value	1.0E-122	1.0E-122	1.0E-122	1.0E-122	1.0E-122	1.0E-122	1.0E-122	1.0E-122	1.0E-122	1.0E-122	100	4 05 422	1.UE-122	1.0E-122	1.0E-122	1.0E-122	1.0E-122	1.0E-122	1 0F-122		1.0E-122	1.0E-122	1.0E-122	1.0E-122	1.0E-122	1.0E-123	1.0E-123	1.0E-123	1.0E-123	1.0E-123
Expression Signal	2.56	3.34	5.19	18.7	1.61	1.61	6.92	7.43	7.43	4.87	000	7	-	1.2	6.8	0.64	9.0	1.17	96.0		0.96	0.64	212	1.83	5.28	1.53	1.53	6.18	3.36	3.83
ORF SEQ ID NO:		27146					28110			29096	<u>L</u> _					ĺ			36159		36160	36983				27019				27491
Exon SEQ ID NO:	13577	14080	14406	14878	14899	14899	15003	15685	15685	16080	10,00	40222	7670	18875	18875	20442	22075	22306	22580		22589	23373	24302	24744	- 25178	13968	13968	14206	14213	14424
Probe SEQ ID NO:	368	905	1247	1728	1750	1750	1857	2560	2560	2901	7007	7	9104	5681	9689	7363	9668	9228	9524		9524	10338	11233	11667	12231	789	789	1038	1047	1267

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Top Hit Descriptor	Homo sapiens phosphatidyfinositol-4-phosphate 5-kinase, type II, beta (PIPGK2B) mRNA, and translated products	Homo sapiens similar to sex comb on midleg (Drosophila)-like 2 (H. sapiens) (LOC63782), mRNA	Human amelogenin (AMELY) gene, 3' end of cds	Human amelogenin (AMELY) gene, 3' end of cds	Human amelogenin (AMELY) gene, 3' end of cds	Homo sapiens RAB9-like protein (LOC51209), mRNA	Homo sapiens glutaminyl-peptide cyclotransferase (glutaminyl cyclase) (QPCT), mRNA	Homo sapiens retinaldehyde-binding protein (CRALBP) gene, complete, cds	Homo sapiens retinaldehyde-binding protein (CRALBP) gene, complete, cds	601591108F1 NIH MGC_7 Homo sapiens cDNA clone IMAGE:3945433 5'	AU118435 HEMBA1 Homo sapiens cDNA clone HEMBA1003591 5'	yqb4e03.r1 Soeres fotal liver spicen 1NFLS Homo sepiens oDNA clone IMAGE:202444 5' similar to SP:YAK1 YEAST P14880 PROTEIN KINASE YAK1	Human growth hormone releasing hormone gene, exon 7	Human hBRAVO/Nr-CAM precursor (hBRAVO/Nr-CAM) gene. complete cds	Homo sapiens heparan sulfate (glucosamine) 3-O-sulfotransferase 2 (HS3ST2), mRNA	Homo saplens 2'-5'oligoadenylate synthetase 2 (OAS2), mRNA	601152815F1 NIH_MGC_19 Homo saplens cDNA clone IMAGE:3509162 5	Homo sapiens hypothetical protein FLJ20184 (FLJ20184), mRNA	yx89d11.r1 Soares melanocyte 2NbHM Homo sapiens cDNA clone IMAGE:288917 3' similar to PIR:S49611 S46611 protein kinase PkpA - Phycomyces blakesleeanus ;	y89411.r1 Soeres melanocyte 2NbHM Homo sapiens cDNA clone IMAGE:268917 5' similar to PIR:S49611 S46811 protein threes Plond - Physical September Holoripagning	AU131881 NT2RP3 Home sepiens cDNA clone NT2RP3nn34ng 5	AU131881 NT2RP3 Homo sapiens cDNA clone NT2RP3003409 5	RC4-BT0311-251199-012-a07 BT0311 Homo saplens cDNA	Homo sapiens mRNA for KIAA0454 protein, partial cds	Address to the following the following the following the following the following the following the following the following the following the following the following the following the following the following the following the following the following the following the following the following the following the following the following the following the following the following the following the following the following the following the following the following the following the following the following the following the following the following the following the following the following the following the following the following the following the following the following the following the following the following the following the following the following the following the following the following the following the following the following the following the following the following the following the following the following the following the following the following the following the following the following the following the following the following the following the following the following the following the following the following the following the following the following the following the following the following the following the following the following the following the following the following the following the following the following the following the following the following the following the following the following the following the following the following the following the following the following the following the following the following the following the following the following the following the following the following the following the following the following the following the following the following the following the following the following the following the following the following the following the following the following the following the following the following the following the following the following the following the following the following the following the following the following the following the following the f	602086791F1 NIH MGC 83 Homo sepiens cDNA clane IMAGE-4250879 5:	602086791F1 NIH MGC 83 Homo sapiens cDNA clone IMAGE:4250879 5	UI-H-BI3-all-f-10-0-UI.s1 NCI_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2737291 3'	101-H-Bis-ail-f-10-0-Uls 1 NCI CGAP Sub5 Homo seniens cDNA clone IMAGE 2737291 3
Top Hit Database Source			N F					N7	NT	EST_HUMAN 601	Γ		Т				EST HUMAN 601		EST_HUMAN S46	PST HIMAN SAG		EST HUMAN AU		1	į	T HUMAN	Т		EST HUMAN UH
Top Hit Acession No.	4505818 NT	11422479 NT	.0E-123 M55419.1		.0E-123 M55419.1	7705962 NT	6912617 NT	0E-123 L34219.1	0E-123 L34219.1	0E-123 BE799746.1	0E-123 AU118435.1	0E-123 H53198.1			11525833 NT	11436439 NT	BE263001.1	7202	0E-123 N35841.1	0E-123 N35841 1	-	0E-123 AU131881,1	ĺ		DE-423	-		0E-123 AW450931.1 E	0E-123 AW450931.1
Most Similar (Top) Hit BLAST E Value	1.0E-123	1.0E-123	1.0E-123	1.0E-123	1.0E-123	1.0E-123	1.0E-123	1.0E-123	1.0E-123	1.0E-123	1.0E-123	1.0E-123	1.0E-123	1.0E-123	1.0E-123	1.0E-123	1.0E-123	1.0E-123	1.0E-123	1 0F-123		1.0E-123	1.0E-123 /	1.0E-123	1 OF 123		1.0E-123	1.0E-123	1.0E-123
Expression Signal	3.83	0.94	3.21	32	32	4.21	0.71	1.62	1.62	1.76	1.93	P6.0	1.39	0.71	0.83	1.31	222	9:0	9.0		0.79	Ø.70	0.7	2.07	18 77	4.91	4.91	2.71	2.71
ORF SEQ ID NO:	27492	28286	28427	28428	28429		29512	31799	31800	32185	33146	33718	33733	33887	34109	34374	34386	34393	34538	34539	34701	34702		36279	36324	38705	38706	38798	38799
Exan SEQ ID NO:	14424	1		15301			16495	18760	18760	18893	19758	20278	20290	20424	20634	20875	20884	20891	21025	21025	21182	21182	21812	22711		25004		25094	25094
Probe SEQ ID NO:	1267	2035	2166	2166	2166	2389	3322	5563	5563	9999	6598	7143	7156	7344	7562	7820	7829	7836	7976	7975	8100	8100	8732	9569	9705	12020	12020	12114	12114

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Probe SEα ID S SEα ID S SEα ID S SEα ID S SEα ID S SEα ID S SEα ID S SEα ID S SEα ID S SEα ID S SEα ID S SEα ID S SEα ID S SEα ID S SEα ID S SEα ID S SEα ID S SEα ID S SEα ID S SEα ID S SEα ID S SEα ID S SEα ID S SEα ID S SEα ID S SEα ID S SEα ID S SEα ID S SEα ID S SEα ID S SEα ID S SEα ID S SEα ID S SEα ID S SEα ID S SEα ID S SEα ID S SEα ID S SEα ID S SEα ID S SEα ID S SEα ID S SEα ID S SEα ID S SEα ID S SEα ID S SEα ID S SEα ID S SEα ID S SEα ID S SEα ID S SEα ID S SEα ID S SEα ID S SEα ID S SEα ID S SEα ID S SEα ID S SEα ID S SEα ID S SEα ID S SEα ID S SEα ID S SEα ID S SEα ID S SEα ID S SEα ID S SEα ID S SEα ID S SEα ID S SEα ID S SEα ID S SEα ID S SEα ID S SEα ID S SEα ID S SEα ID S SEα ID S SEα ID S SEα ID S SEα ID S SEα ID S SEα ID S SEα ID S SEα ID S SEα ID S SEα ID S SEα ID S SEα ID S SEα ID S SEα ID S SEα ID S SEα ID S SEα ID S SEα ID S SEα ID S SEα ID S SEα ID S SEα ID S SEα ID S SEα ID S SEα ID S SEα ID S SEα ID S SEα ID S SEα ID S SEα ID S SEα ID S SEα ID S SEα ID S SEα 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18178 18178 18178 18178 18178 18178 18178 18178 18178 18178 18178 18178 18178 18178 18178 18178 181	R =	Signal	Most 8	Top Hit Acession No. No. 4607500 4607500 AA397651.1 AA397551.1 AA397551.1 AA397551.1 AA397551.1 AA397551.1 AA397551.1 AA397551.1 AA397551.1 AA397551.1 AA397551.1 AA397551.1 AA397551.1 AA397561.1 AA397561.1 AA397561.1 AA397561.1 AA397561.1 AA397561.1 AA39764.1 AA3784.1 AA3784.1 AA3784.1 AA3784.1 AA3784.1 AA3784.1 AA3784.1 AA3784.1 AA3784.1 AA3784.1 AA3784.1 AA3784.1 AA3784.1 AA3784.1 AA3784.1 AA3784.1 AA3784.1 AA3784.1 AA3784.1 AA3784.1 AA3784.1 AA3784.1 AA3784.1 AA3784.1 AA3784.1 AA3784.1 AA3784.1 AA3784.1 AA3784.1 AA3784.1 AA3784.1 AA3784.1 AA3784.1 AA3784.1 AA3784.1 AA3784.1 AA3784.1 AA3784.1 AA3784.1 AA3784.1 AA3784.1 AA3784.1 AA3784.1 AA3784.1 AA3784.1 AA3784.1 AA3784.1 AA3784.1 AA3784.1 AA3784.1 AA3784.1 AA3784.1 AA3784.1	Top Hit Database Source Source NIT NIT NIT NIT NIT NIT NIT NIT NIT NIT	Homo saplens T-cell lymphoma invasion and metastasis ( TIAMI) mRNA Homo saplens T-cell lymphoma invasion and metastasis ( TIAMI) mRNA Homo saplens T-cell lymphoma invasion and metastasis ( TIAMI) mRNA Homo saplens T-cell lymphoma invasion and metastasis ( TIAMI) mRNA Homo saplens DNA for amyloid precureor protein, complete of a 2390.0432 POL=REVERSE TRANSCRIPTASE HOMOLOG (RETROVIRAL ELEMENT); Human putative ribosomate protein S1 mRNA Homo saplens schizo brain S11 Homo saplens GDNA clore INAGE:728719 5' similar to TR:G300482 G300.432 POL=REVERSE TRANSCRIPTASE HOMOLOG (RETROVIRAL ELEMENT); Human putative ribosomate protein S1 mRNA Homo saplens protein complete protein (ISPC068), mRNA Homo saplens inpotrated protein S1 mRNA Homo saplens inpotrated grain a semporal 3 gane, sexte 5, 10, and complete ods Homo saplens putative ribosomaly rectifying K-channel subunit (KCNJ6/BIR1) gene, exon Homo saplens gene for 6 B120, exon 11 Homo saplens gene for 6 B120, exon 11 Homo saplens gene for 8 B120, exon 11 Homo saplens ATP-sensitive invarially rectifying K-channel subunit (KCNJ6/BIR1) gene, exon Homo saplens and S10, exon 11 Homo saplens gene R1D, exon 11 Homo saplens gene for 8 B120, exon 11 Homo saplens gene for 8 B120, exon 11 Homo saplens gene for 8 B120, exon 11 Homo saplens gene for 8 B120, exon 11 Homo saplens gene for 8 B120, exon 11 EST374838 MAGE resequences, MAGH Homo saplens cDNA Homo saplens putentical protein FL10300 (FL1/3030), mRNA Homo saplens putentical protein R1/10300 (FL1/3030), mRNA Homo saplens in pacificational invasion and metastesis 1 (TRNA) mRNA Homo saplens putentical protein R1/10300 (FL1/3030), mRNA Homo saplens in pacificational invasion control (CL1/3030), mRNA Homo saplens in pacificational invasion and metastesis 2 (TRNA) mRNA Homo saplens putentical protein R1/10300 (FL1/3030), mRNA Homo saplens in pacificational protein CR1/20300 (FL1/3030), mRNA Homo saplens in pacificational protein CR1/20300 (FL1/3030), mRNA Homo saplens in pacificational protein contents (EDII), exern x+1 EST3734644F
7152	19725		3.15	-	Y11717	LN	M.musculus mRNA for hoxe3 gene.
7367	20280	331.20		-	0E-124 RF 271295 1	EST HUMAN	600943771F1 NIH MGC_8 Homo seplens cDNA clone IMAGE:2966585 5'
7287	280				- C		

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Top Hit Descriptor	600943771F1 NIH_MGC_B Homo sapiens cDNA clone IMAGE:2966585 5'	ac08h05.s1 Stratagene HeLa cell s3 937216 Homo sapiens cDNA clone IMAGE:855897 3'	Homo sapiens ribosomal protein L5 (RPL6) mRNA	hg94a09.x1 NCI_CGAP_Kld11 Homo sapiens cDNA clone IMAGE;2853240 3' simitar to TR:O95162 095162 PEROXISOMAL SHORT-CHAIN ALCOHOL DEHYDROGENASE.;	hg94a09.xt NCI_CGAP_Kid11 Homo saplens dDNA clone IMAGE:2853240 3' similar to TR:095162 095162 PEROXISOMAL SHORT-CHAIN ALCOHOL DEHYDROGENASE.;	wc43g03.x1 NCI_CGAP_Pr28 Homo sapiens cDNA clone IMAGE;2321428 3'	wc43g03.x1 NCI_CGAP_P/28 Homo sapiens cDNA clone IMAGE:2321428 3'	AV645633 GLC Homo saplens cDNA clone GLCACE04 3'	AV645633 GLC Homo saplens cDNA clone GLCACE04 3'	w193102.x1 NCI_CGAP_KId12 Homo sapiens cDNA clone IMAGE:2400891 3'	wi93f02x/1 NCI_CGAP_Kd12 Homo saplens cDNA clone IMAGE:2400891 3'	UI-HF-BNO-akz-b-04-0-UI-r1 NIH_MGC_60 Homo sapiens cDNA clone IMAGE:3078846 5'	Human muscle glycogen phosphorylase (PYGM) gene, exons 6 through 17	hj05c08.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2980906 3'	t/19e03.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2141980 3' similar to TR:O31662 031662 YKRS PROTEIN.;	#19e03.x1 NCI_CGAP_Gas4 Homo saplens cDNA clone IMAGE:2141980 3' similar to TR:O31662 O31662 YKRS PROTEIN.;	zt81b04.r1 Strategene schizo brain S11 Homo saptens cDNA clone IMAGE:728719 5' similar to TR:G300482	G300482 POL=REVERSE TRANSCRIPTASE HOMOLOG (RETROVIRAL ELEMENT);	z/81b04.r1 Stratagene schizo brain S11 Homo saplens cDNA clone IMAGE:728719 5' similar to TR:G300482 G300482 POL=REVERSE TRANSCRIPTASE HOMOLOG (RETROVIRAL ELEMENT) ;	Homo sapiens mRNA for KIAA1093 protein, partial cds	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA	Homo saplens mRNA for KIAA1172 protein, partial cds	601577981F1 NIH_MGC_9 Homo saplens cDNA clone IMAGE:3926685 5'	HA0086 Human fetal liver cDNA library Homo sapiens cDNA	HA0086 Human fetal liver cDNA library Homo sapiens cDNA	Homo sapiens ALR-like protein mRNA, partial cds	zk53c07.s1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:486540 3' similar to gb:X65857_cds1 OLFACTORY RECEPTOR-LIKE PROTEIN HGMP07E (HUMAN);
Top Hit Database Source	EST_HUMAN	EST_HUMAN		EST_HUMAN	EST HUMAN	Г	EST_HUMAN	EST_HUMAN	EST_HUMAN		EST_HUMAN	EST_HUMAN	Г	EST_HUMAN	EST_HUMAN	EST HUMAN		EST_HUMAN	EST HUMAN	F						_	NT	EST_HUMAN
Top Hit Acession No.	.0E-124 BE271295.1	.0E-124 AA630331.1	4506654 NT	.0E-124 AW612106.1	.0E-124 AW612106.1		.0E-124 AI799864.1	.0E-124 AV645633.1	.0E-124 AV645633.1		.0E-124 AI767133.1	.0E-124 AW 503755.1	.0E-124 U94778.1	.0E-124 AW 685863.1	.0E-124 AI448456.1	.0E-124 AI446455.1		.0E-124 AA397551.1	.0E-124 AA397551.1	.0E-124 AB029016.1	11417862 NT	11417862 NT	.0E-125 AB032998.1		.0E-125 Al110656.1	.0E-125 A1110656.1	.0E-125 AF284750.1	.0E-125 AA042813.1
Most Similar (Top) Hit BLAST E Value	1.0E-124	1.0E-124	1.0E-124	1.0E-124	1.0E-124	1.0E-124	1.0E-124	1.0E-124	1.0E-124	1.0E-124	1.0E-124	1.0E-124	1.0E-124	1.0E-124	1.0E-124	1.0E-124		1.0E-124	1.0E-124	1.0E-124	1.0E-124	1.0E-124	1.0E-125	1.0E-125	1.0E-125	1.0E-125	1.0E-125	1.0E-125
Expression Signal	96.0	2.38	2.73	1.24	124	0.68	0.68	1.72	1.72	77.7	77.7	1.46	1.57	3.9	2.18	2.18		4.6	4.6	96:1	2.36	2.36	7.32	4.69	2.02	2.02	2,42	1.45
ORF SEQ ID NO:	33825	34278		35277		35996	36997					36717	38009		37575	37576		26926	26927	32004								27124
Exan SEQ ID NQ:	20370	l	21634	21737	21737	22438	22438	22740	22740	22848	22848	23113	24368	24668	23947	23947		13891	13891	J``		26038	l.,	L_	13847	13847	13927	14059
Probe SEQ ID NO:	7287	7725	8453	8657	8657	9363	8363	9894	9691	9808	9808	10075	11302	11617	11761	11761		12310	12310	12780	13080	13080	329	439	681	661	746	883

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ORF SEQ ID NO:	ő ö ö	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
	27252	1.54	1.0E-125	.0E-125 AL163210.2	NT	Homo saplens chromoscane 21 segment HS21C010
	27394	1.73	1.0E-125	7662279 NT	ΝΤ	Homo sapiens KIAA0744 gene product; histone deacetylase 7 (KIAA0744), mRNA
	27948		1.0E-125	7661867 NT	LN	Homo sapiens KIAA0022 gene product (KIAA0022), mRNA
	28106		1.0E-125	.0E-125 AF015450.1	LN	Homo sapiens Usurpin-apha mRNA, complete cds
	28107	16.3	1.0E-125		NT	Homo sapiens Usurpin-alpha mRNA, complete cds
	28687	4.81	1.0E-125	.0E-125 AA011278.1	EST_HUMAN	zi01g09.r1 Scares_fetal_liver_spleen_1NFLS_S1 Homo saplens cDNA clone IMAGE:429368 5'
	28820		1.0E-125	.0E-125 AA042813.1	EST_HUMAN	2k53c07.s1 Soares_pregrant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:486540 3' similar to gb:X65857_cds1 OLFACTORY RECEPTOR-LIKE PROTEIN HGMP07E (HUMAN);
	28898		1.0E-125	4696	ž	Homo sapiens inhibin, alpha (INHA) mRNA
ŀ	28899	2.34	1.0E-125	4504696 NT	۲	Homo sapiens inhibin, alpha (INHA) mRNA
	30123		1.0E-125	.0E-125 AA042813.1	EST_HUMAN	2463c07.s1 Soares_pregnant_uterus_NbHPU Homo sepiens cDNA clone IMAGE:486540 3' similar to gb:X65867_cds1 OLFACTORY RECEPTOR-LIKE PROTEIN HGMP07E (HUMAN);
	30796		1.0E-126	11426114 NT	Ī	Homo sapiens zinc finger protein ZNF287 (ZNF287), mRNA
l	30797		1.0E-125	11425114 NT	Z	Homo sapiens zinc finger protein ZNF287 (ZNF287), mRNA
	30857		-	.0E-125 BE315412.1	EST_HUMAN	601141152F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3140796 5
	32375	0.65	٦	.0E-125 BF683645.1	EST_HUMAN	602139874F1 NIH_MGC_46 Hamo sapiens cDNA clane IMAGE:4300770 5'
ı	32501		1.0E-125	11436448 NT	LN L	Homo sapiens KIAA0985 protein (KIAA0985), mRNA
ı	32514		[	.0E-125 BE175169.1	EST_HUMAN	QV2-HT0577-010500-165-b06 HT0577 Homo seplens cDNA
	32561	3.53	1.0E-125	.0E-125 BE892660.1	EST_HUMAN	601433472F1 NIH_MGC_72 Homo sapiens cDNA done IMAGE:3918952 5'
l	32606	1 _	1.0E-125	.0E-125 AI679904.1	EST HUMAN	w67c07x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2256108 3' similar to WP:C45G9.2 CE01854 :
ı	32942		1.0E-125	.0E-125 BE736055.1	EST_HUMAN	601305670F1 NIH_MGC_39 Homo saplens cDNA done IMAGE:3640087 5
ı	33259		1.0E-125	.0E-125 BE562526.1	EST_HUMAN	601335826F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3689790 5'
1	33260		1.0E-125	.0E-125 BE562526.1	EST_HUMAN	601335826F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3689790 5'
ı	33483		1.0E-125	.0E-125 X03427.1	F	Homo sapiens IGF-II gene, exon 5
l	33484		1.0E-126	.0E-126 X03427.1	N	Homo saplens IGF-II gene, exon 5
	34249		1.0E-125	.0E-125 BE278823.1	EST_HUMAN	601159076F1 NIH_MGC_21 Homo sapiers cDNA clane IMAGE:3505603 5'
	34491		1.0E-125	11425572 NT	ΤN	Homo saplens adaptor-related protein complex 2, beta 1 subunit (AP2B1), mRNA
	35357	1.49	1.0E-125	.0E-125 U90288.1	NT	Human chromosome 10 duplicated adrenoleukodystrophy (ALD) gene segment containing exons 8-10
	35358	1.49	1.0E-125	.0E-125 U90288.1	L	Human chromosome 10 duplicated adrendeukodystrophy (ALD) gene segment containing exons 8-10
	35945		1.0E-125	.0E-125 BE181640.1	EST_HUMAN	QV1-HT0638-070500-191-d12 HT0638 Homo sapiens cDNA
ı	35946	4.15	1.0E-125	.0E-125 BE181640.1	EST_HUMAN	QV1-HT0638-070500-191-d12 HT0638 Homo sepiens cDNA

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Probe SEQ ID S NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
9581	22723	36293	1.06	1.06	-125 AI565998.1	EST_HUMAN	t <u>n52b03.x1 NC _CGAP_Kid11</u> Homo saplens cDNA clone IMAGE:2171981 3' similar to TR:Q14089 Q14089 HYPOTHETICAL PROTEIN ;
10670	23704			1.0E		EST HUMAN	601590345F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3844531 5
10712	23745		1.06	L		LN	Human mRNA for KIAA0300 gene, partial cds
10921	24004	Ŀ			1.0E-125 AF043458.1	LNT	Homo sapiens I-REL gene, exon 5
11091	24165		1.34	1.0E-125	11425570 NT	LN	Homo saplens ryanodine receptor 1 (skeleta) (RYK1), mKNA
11357	24419	38076	2.42			EST_HUMAN	DKFZp434N2414_r1 434 (synonym: ntess) Homo sapiens curve cigne DNr 2p+3+N2+1+3
11401	24462				1.0E-125 AB014567.1	NT	Homo sapiens mRNA for KIAA0667 protein, partial cds
11538	24594		1.63		R61450.1	EST_HUMAN	wh15a12.r1 Soares Intant brain 1NIB Homo sapiens count during www.co.co.co.co.co.co.co.co.co.co.co.co.co.
11568	24623				7669505 NT	٦	Home saplens myosin, neavy polypeptide II, swerdal indeed, audit (with II), Illings
11575	24630	38309			1.0E-125 AF026029.1	Z	Homo saplens poly(A) binding protein II (FAbr Z) gene, configure cos
11686	24685	38375			1.0E-125 AW812899.1	EST HUMAN	RC3-ST0186-250200-018-c11 S10180 Homo sapiens cDNA
11793	24783	38479			1.0E-125 BE074267.1	EST_HUMAN	QV3-BT0569-020200-075-g09 BT Tobe From 0 septens outs
11793	24783		4.71	L	1.0E-125 BE074267.1	EST_HUMAN	QV3-BT0566-020200-075-g09 BT0569 Homo saptens cDNA
795	13974		2.16		4758007 NT	LΝ	Homo sapiens CDC-like kinase (CLK) mKNA
86/	13977	27030	1.74		1.0E-126 M61938.1	LN	Human laminin B1 chain gene, exon 20
942	14116	3 27175	1.53		X68735.1	LN	H.saplens gene for alpha1-antichymoutpasir, axon 2
2663	15785	28900			1.0E-126 6382078 NT	. 1	Homo sapiens KAN binding protein 2 (KANDEZ), mKNA
3140	16316	5 29329	9 8.12		1.0E-126 AA160709.1	EST HUMAN	2072c03.r1 Strategene pencreas (#93/200) norno sapiens curva cicile introduce con con contra introduce con contra contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction o
3140	1		8.12		1.0E-126 AA160709.1	EST_HUMAN	2072c03.r1 Stratagene pancreas (#837208) nomo sapiens conva dure invade
3719	16880	29885			1.0E-126 X53941.1	ΝΤ	H.sapiens DNA for liver cytochrome be pseudogene
3745					3 7657038 NT	LNT NT	Homo saplens death receptor 6 (DRb), mRNA
<b>498</b>	Ĺ		1.08		1.0E-126 AF101108.1	LN	Homo sapiens collagen type XI apha-1 (COL11A1) gene, exon to
4908	I	31027			1.0E-126 AF101108.1	LN-T	Homo sapiens collagen type XI alpha-1 (COL11A1) gene, exon os
4956	18086	8 31062	1.81		1.0E-126 N34078.1	EST_HUMAN	yx78c06.r1 Soares melanocyte zindtim nomo sapiens colina cione image. 2000 c
5820	1_	32316	0.68		1.0E-126 T68998.1	EST_HUMAN	ye52b12.s1 Soares fetal liver spiecen 1NFLS Homo sapiens cunna universative granter
1 8	<u> </u>		į		1 OE -128 4 4 4 60 07 5 1	EST HUMAN	2x66e03.r1 Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:/90444 3 Similar to TR:G1145880 G1145880 TITIN ;
202	19332			L	E-126 AB040958.1	L	Homo sapiens mRNA for KIAA 1525 protein, pertial cda
2 6	L			L	1.0E-126 AB040958.1	¥	Homo sapiens mRNA for KIAA 1525 protein, partial cds
7860	1	L		L	E-126 AF257737.1	L	Homo saplens cliary dynein heavy chain 9 (DNAH9) mRNA, complete cds
7869	L			L	1.0E-126 AF257737.1	Ā	Homo sapiens ciliary dynein heavy chain 9 (DNAH9) mRNA, complete cds
9082					E-126 AB037715.1	F	Homo sapiens mRNA for KIAA1294 protein, partial cds
2000	1			L	1 0F-126 AB037715.1	¥	Homo sapiens mRNA for KIAA1294 protein, partial cds
2000	-						

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	Top Hit Descriptor	Human mRNA for ankyrin (varient 2.1)	ne74b12.s1 NCL_CGAP_Ew1 Homo sapiens cDNA clone IMAGE:909983 similar to SW:TSGG_HUMAN P98066 TUMOR NECROSIS FACTOR INDUCIRIE PROTEIN TSGA PDER I IDSOP	Homo sapiens neuro-oncolonical ventral antinen 1 (NIOVA1) salice ventant 4 mich A	602/39138F1 NIH MGC 46 Home septens cDNA clope IMAGE 4208240 F	801149404F1 NIH MGC 19 Home sabiens cDNA clone IMAGE 3502120 51	601577981F1 NIH MGC 9 Homo saplens cDNA clone IMAGE:392885 5	Homo sapiens mRNA for casein kinase I eosilon, complete cds	Homo sapiens mRNA for casein kinase I epsion, complete cds	Homo sapiens mRNA for casein kinase I epsilon, complete cds	Homo sapiens mRNA for casein kinase   epsilon complete cds	Homo sapiens DNA for amyloid precursor protein, complete cds	Homo saplens DNA for amyloid precursor protein, complete orls	Homo sapiens intersectin short isoform (TSN) mRNA complete cds	Homo sapiens lost on transformation LOT1 mRNA, complete cds	Homo saplens ubiquitin specific protease 8 (USP8) mRNA	Homo sapiens leukocyte immunoglobulin-like receptor, subfamily A (with TM domain), member 1 (LILRA1), mRNA mRNA	Homo saplens leukocyte immunoglobulin-like receptor, subfamily A (with TM domain), member 1 (ULRA1), mRNA mRNA	Homo sapiens ribosomal protein L26 (RPL26) mRNA	Homo sapiens adlican mRNA, complete cds	Human mRNA for cytokeratin 18	Homo saplens intersectin short isoform (ITSN) mRNA, complete cds	eu80e06.yl Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE.2782394 5' similar to TR.015170 Q15170 TRANSCRIPTION FACTOR S-II-RELATED PROTEIN :contains element MER22	repetitive element;	Homo sapiens delayed rectifier potassium channel subunit IsK mRNA, complete ods	Homo saplens neuroblastoma-amplified protein (LOC51594), mRNA	Homo saplens neuroblastoma-amplified protein (LOC51594), mRNA	Homo saplens cytochrome P450 retinoid metabolizing protein P450RAI-2 mRNA, complete cds	Homo sapiens RAD1 (S. pombe) homdog (RAD1) mRNA, and translated products	Homo saplens chromosome 21 segment HS21C068
	Top Hit Database Source	NT	EST HUMAN	LN	EST HUMAN	EST HUMAN	Т	П	NT	LZ	LN				LN	LN L					Į.	IN		HOMAN	NT			LN		- L
,	Top Hit Acession No.	.0E-126 X16609.1	.0E-126 AA483368.1	4505424 NT	.0E-126 BF683175.1	.0E-126 BE281680.1	.0E-126 BE743922.1	.0E-127 AB024597.1	.0E-127 AB024597.1	.0E-127 AB024597.1	.0E-127 AB024597.1	0E-127 D87675.1	.0E-127 D87675.1	-	.0E-127 U72621.2	4827053 NT	1N 2903089	5803065 NT	4506620 NT	0E-127 AF245505.1		0E-127 AF114488.1			0E-127 AF135188.1	7706239 NT	7706239 NT	0E-127 AF252297.1	4506384 NT	DE-127 AL163268.2
	Most Similar (Top) Hit BLAST E Value	1.0E-126	1.0E-128	1.0E-126	1.0E-126	1.0E-126	1.0E-126	1.0E-127	1.0E-127	1.0E-127	1.0E-127	1.0E-127	1.0E-127	1.0E-127	1.0E-127	1.0E-127	1.0E-127	1.0E-127	1.0E-127	1.0E-127	1.0E-127	1.0E-127	100	1.05-12/ /	1.0E-127 #	1.0E-127	1.0E-127	1.0E-127 /	1.0E-127	1.0E-127
	Expression Signal	2.42	0.8	0.67	2.01	2.2	6.48	292	2.92	2.75	2.75	214	2.14	1.17	4.81	2.22	1.97	1.97	17.46	3.12	21.46	0.61		,	0.59	24.93	24.93	0.83	6.74	2.69
	ORF SEQ ID NO:	34781	34082				31536	26429	26430	26429		i	26536	27145	27174	27967	28382	28383	28535	28675	28911	29948	0000	0/000	30368	30491	30492	30737	30842	
	Exen SEQ ID NO:	21259	21458	L				13400		1	13400	13502	13502	14079	14113	14876	15263	15263	15406	15547	15794	16942	17072	7	17379	17511	17511	17756	17860	17890
	Probe SEQ ID NO:	8177	8377	10000	1 1099	11806	12823	178	176	177	177	284	284	904	939	1726	2127	2127	2273	2418	2674	3781	30.0	2 5	4232	4368	4368	4618	4725	4755

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			1268 5' similar to PHOSPHODIESTERASE													ilicad, complete cds	liced, complete cds		0.00	(LOC63184), mRNA	(LOC63184), mRNA	1-45								1		
	Top Hit Descriptor	Homo sapiens Ring1 and YY1 binding protein (RYBP), mRNA	za01a10.r1 Soares molanocyte 2NbHM Homo sepiens cDNA clone IMAGE:291268 6' similar to SW:PIP6_RAT P10688 1-PHOSPHATIDYLINOSITOL-4,5-BISPHOSPHATE PHOSPHODIESTERASE	DELTA 1;	Homo saplens neuronal cell adhesion molecule (NRCAM) mRNA	H. saplens NOS2 gene, exon 8	H.sapiens TCF11 gene, exon 3-6	Homo saplens integrin, beta 8 (ITGB8) mRNA	Homo sapiens immunoglobulin superfamily, member 3 (IGSF3), mRNA	Homo septens reetin (RELN) mRNA	Homo sapiens Pendred syndrome (PDS), mRNA	Homo sapiens Pendred syndrame (PDS), mRNA	602151232F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4292575 5'	Homo sapiens Chediak-Higashi syndrome 1 (CHS1), mRNA	Homo sapiens Chediak-Higashi syndrome 1 (CHS1), mRNA	Homo sapiens secretory pathway component Sec31B-1 mRNA, alternatively spliced, complete cds	Homo sapiens secretory pethway component Sec31B-1 mRNA, affematively spliced, complete cds	qm94h09.x1 NCI_CGAP_Lu5 Homo sapiens cDNA clane IMAGE:18964493'	Homo sapiens Chediak-Higashi syndrome 1 (CHS1), mRNA	Homo sapiens similar to heat shock 70kD protein 9B (mortalin-2) (H. sapiens) (LOC63184), mRNA	Homo saplens similar to heat shock 70kD protein 9B (mortalin-2) (H. sapiens) (LOC63184), mRNA	601434784F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3919917 5'	601434784F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3919917 5'	Homo sapiens mRNA for casein kinase I epsilon, complete cds	Homo sapiens mRNA for caseln kinase I epsilon, complete cds	Horno saplens gene for AF-6, complete cds	Homo sapiens gene for AF-6, complete cds	601278127F1 NIH_MGC_20 Homo sapiens oDNA clone IMAGE:3618822 5	Homo sapiens chondroitin sulfate proteoglycan 2 (versican) (CSPG2) mRNA	Homo sapiens chandrottin sulfate proteoglycan 2 (versican) (CSPG2) mRNA	Human FAU1P pseudogene, trinucleotide repeat regions	
	Top Hit Database Source			T HUMAN									EST HUMAN			TN	Ę	EST HUMAN					r_HUMAN		N		IN.	EST_HUMAN (			i k	
6	Top Hit Acession No.	6912639 NT		0E-127 W03547.1	4826863		0E-127 X84060.1	4504778 NT	11421595 NT	4826977 NT	11421914 NT	11421914 NT	0E-127 BF671355.1	11427235 NT	11427235 NT	0E-127 AF274863.1	0E-127 AF274863.1	0E-127 AI298932.1	11427235 NT	11417339 NT	17339				DE-127 AB024597.1	0E-127 AB011399.1	0E-127 AB011399.1	0E-128 BE385617.1	4758081 NT	4758081		
	Most Similar (Top) Hit BLAST E Value	1.0E-127		1.0E-127	1.0E-127	1.0E-127	1.0E-127	1.0E-127	1.0E-127	1.0E-127	1.0E-127	1.0E-127	1.0E-127	1.0E-127	1.0E-127	1.0E-127	1.0E-127	1.0E-127	1.0E-127	1.0E-127	1.0E-127	1.0E-127	1.0E-127	1.0E-127	1.0E-127	1.0E-127	1.0E-127	1.0E-128	1.0E-128	1.0E-128	1.0E-128	
	Expression Signal	4.36		1.57	0.91	4.18	223	5.73	1.09	0.81	1.31	1.31	0.63	0.81	0.81	3.73	3.73	98.0	66.0	5.64	5.64	1.55	1.55	3.03	3.03	1.74	1.64	1.56	96.0	96:0	18.07	
	ORF SEQ ID NO:	30916		32320	32351	1			33352			34526	34536	36713	35714	36462	36463	36718	37194	38150	38151	38614	38615	26429	26430	32037			27396	27397	28387	
	Exon SEQ ID NO:	17930		19014	19044	1910	19464	19618	19952	20073	21014	21014	21023	22167	22167	22880	22880	23115	23586	24487	- 1	· [	- 1	- 1	13400	25507	26044	13667	14342	1	15268	ĺ
	Probe SEQ ID NO:	4795	i	5824	2854	5923	6291	6451	6797	7208	7964	7964	7973	9088	9088	9840	9840	10077	10551	11426	11426	11927	11927	12539	12539	12763	13170	472	1179	1179	2132	

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Top Hit Descriptor	Homo sapiens ribosomal protein S2 (RPS2) mRNA		Homo sapiens chromatin-specific transcription elongation factor, 140 kDa subunit (FACTP140), mRNA	Homo sapiens minna tot intervited by the control management of PROX1) mRNA	Homo sapiens prosper created from the homo chain H1 exon 12	H.sapiens gene ror inter-alpharu yosin iliniarian iliangement (70kD) (PDE1C), mRNA	Homo sapiens procedures and 10, commoduling and MAGE: 3	I Good Lux I NOT COUNTY To the County of the County of the County of the County of the County of the County of the County of the County of the County of the County of the County of the County of the County of the County of the County of the County of the County of the County of the County of the County of the County of the County of the County of the County of the County of the County of the County of the County of the County of the County of the County of the County of the County of the County of the County of the County of the County of the County of the County of the County of the County of the County of the County of the County of the County of the County of the County of the County of the County of the County of the County of the County of the County of the County of the County of the County of the County of the County of the County of the County of the County of the County of the County of the County of the County of the County of the County of the County of the County of the County of the County of the County of the County of the County of the County of the County of the County of the County of the County of the County of the County of the County of the County of the County of the County of the County of the County of the County of the County of the County of the County of the County of the County of the County of the County of the County of the County of the County of the County of the County of the County of the County of the County of the County of the County of the County of the County of the County of the County of the County of the County of the County of the County of the County of the County of the County of the County of the County of the County of the County of the County of the County of the County of the County of the County of the County of the County of the County of the County of the County of the County of the County of the County of the County of the County of the County of the County of the County of the County of the County of the County of the County of the County of the County of the	Homo sapiens minuta to Natarata process, person	Homo sapiens minitar to introduce process, par series contact in MAGE:1182620 similar to TR:0951338 0951338	OHROMOSOME SEGREGATION GENE HOMOOGOGS;  OHROMOSOME SEGREGATION OF HOMOOGOGS;	Homo sapiens glutamate receptor, idnoucipic, invitiouly brasparator (CCIII)	om68h08 s1 NCI, CGAP, GC4 Homo saplens CLNX cluis mixtor	1604511912F1 NIH MGC / I Tolilo Sapiens Con Civil III Con Civil III Con Civil III Con Civil III Con Civil III Con Civil III Con Civil III Con Civil III Con Civil III Con Civil III Con Civil III Con Civil III Con Civil III Con Civil III Con Civil III Con Civil III Con Civil III Con Civil III Con Civil III Con Civil III Con Civil III Con Civil III Con Civil III Con Civil III Con Civil III Con Civil III Con Civil III Con Civil III Con Civil III Con Civil III Con Civil III Con Civil III Con Civil III Con Civil III Con Civil III Con Civil III Con Civil III Con Civil III Con Civil III Con Civil III Con Civil III Con Civil III Con Civil III Con Civil III Con Civil III Con Civil III Con Civil III Con Civil III Con Civil III Con Civil III Con Civil III Con Civil III Con Civil III Con Civil III Con Civil III Con Civil III Con Civil III Con Civil III Con Civil III Con Civil III Con Civil III Con Civil III Con Civil III Con Civil III Con Civil III Con Civil III Con Civil III Con Civil III Con Civil III Con Civil III Con Civil III Con Civil III Con Civil III Con Civil III Con Civil III Con Civil III Con Civil III Con Civil III Con Civil III Con Civil III Con Civil III Con Civil III Con Civil III Con Civil III Con Civil III Con Civil III Con Civil III Con Civil III Con Civil III Con Civil III Con Civil III Con Civil III Con Civil III Con Civil III Con Civil III Con Civil III Con Civil III Con Civil III Con Civil III Con Civil III Con Civil III Con Civil III Con Civil III Con Civil III Con Civil III Con Civil III Con Civil III Con Civil III Con Civil III Con Civil III Con Civil III Con Civil III Con Civil III Con Civil III Con Civil III Con Civil III Con Civil III Con Civil III Con Civil III Con Civil III Con Civil III Con Civil III Con Civil III Con Civil III Con Civil III Con Civil III Con Civil III Con Civil III Con Civil III Con Civil III Con Civil III Con Civil III Con Civil III Con Civil III Con Civil III Con Civil III Con Civil III Con Civil III Con Civil III Con Civil III Con Civil III Con Civil III Con Civil III Con	EST 30/ 300 NIACE resolutions, which is a second of the segment 2 of 4]	Insum-like grown recome mining present - premium processite Genomic, 1019 nt, segment 2 of 4]	Insulin-like growth ractor britaing protein - trainming from C2H2 type domains	Home sanlens glutathione S-transferase theta 2 (OSTT2) and glutathione S-transferase theta 1 (OSTT1)	genes, complete cds genes, complete cds	genes, complete ods	Homo sapiens zinc finger protein 76 (expressed in testis) (ZNF / 0), Illining	Homo sapiens platelet-derived growth factor receptor, beta polypeptude (FDGF13D) mixtor.	Homo sapiens platelet derived growth factor receptor, beta pulypeptude (r. Don hay have	ZING FINGER PROTEIN HZF10	ZING FINGER PROTEIN HZF-10	ZING FINGER PROTEIN HZF10	Home saniens mRNA for KIAA1459 protein, partial cds	CMAVAS Human cardiac muscle excression library Homo sapiens cDNA clone 4151935 similar to CMYA5	Cardiomyopathy associated gene 5
Top Hit Database Source	L		Ę	LN.	Ę	LN.	- 1	EST_HUMAN	L	LN	98.1 EST_HUMAN	LN	EST_HUMAN	EST HUMAN	EST HUMAN	NT.	Ļ.	Ž	Ę	Ž	N	TN	N.	SWISSPROT	SWISSPROT	TOGOSSIWS	- AMERICAN	Z	EST_HUMAN
Top Hit Acession No.	4506718 NT		17455	E-128 AB033073.1	1426673		20965				A639198.1	11425254	1.0E-128 AA928959.1	E-128 BE887554.1	JE-128 AW955290.1	E-129 S37722.1	DE-129 S37722.1	E-129 AL096880.1	DE-129 AF240786.1	DE-129 AF240786.1	11418522 NT	4505682 NT	4505682 NT		OE 420 044585	201100	.0E-129 Q14380	.0E-129 AB040892.1	.0E-129 AW766254.1
Most Similar (Top) Hit BLAST E Value	4 OF 128	1.00-120	1.0E-128	1.0E-128 A	1.0E-128	1.0E-128 X69539.1	1.0E-128	1.0E-128 BF224345.1	1.0E-128 AB007923.1	1.0E-128 AB007923.1	1.0E-128 AA639198.1	1.0E-128	1.0E-128	1.0E-128	1.0E-128 /	1.0E-129	1.0E-129	1.0E-129	1.0E-129		-								_
Expression Signal	27.04	18.70	1.11	1.17	7.27	0.75	1.5	6.26	29.0	29:0	84	3.54	3.51	1.98	4.26	1.93		3.74	1.66	1 68								2.37	2.32
ORF SEQ ID NO:	100	28547		29664	30909	32139		33538	L							26663		27999	28004	20000						3 29381		4 30413	30517
Exen SEQ ID NO:		15415	15642	16648	17821	18856	19710	20123	21824	21824	23376	24031	24038	24279	25282	13621	1		14910	2,0,7	1	13037	L	- 1	-1		16373	17424	4.75.30
Probe SEQ ID NO:		2283	2516	3484	4788	5662	6548	7070	8745	8745	10241	10040	10057	11210	12402	124	428	1756	1761		19/1	185	8 8	2838	3198	3198	3198	4279	13057

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		-					
Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acesslon No.	Top Hit Database Source	Top Hit Descriptor
	1						CMYAS Human cardiac muscle expression library Homo sapiens cDNA clone 4151935 similar to CMYA5
4395				1.0E-129		EST HUMAN	Caldion I) Ord April
6216				1.0E-129	T	Т	Homo sapiens NVLV 11 gene combons contains NAACE 3015350 5
9854		33201	0.61		٦	LHUMAN	601513861F1 NIH MGC_71 Homb sapiens curva cione invade, 3513350
7277		33814	3.99	-	.0E-129 AJ006345.1	NT	Homo sapiens KVLU I1 gene
7340	<u> </u>	L	4.03	1.0E-129	11420850 NT	NT	Homo sapiens similar to ribosomal protein S26 (H. sapiens) (LOCosoe4), missivA
7697		L	1.04		.0E-129 AF041056.1	NT	Homo sapiens WSCR4 gene, exons 3 and 4
7697	L	L			.0E-129 AF041056.1	LN	Homo sapiens WSCR4 gene, exons 3 and 4
8513	1 _		3.57	٦	.0E-129 AB014534.1	NT	Homo sapiens mRNA for KIAA0634 protein, partial cds
10284	L	36920		1.0E-129	11437282 NT	NT	Homo sapiens solute carrier family 21 (organic anion transporter), member 9 (SECZIA9), minuth
10284	1_			1.0E-129	11437282 NT	TN	Homo sapiens solute carrier family 21 (organic anion transporter), member 9 (SLCZ1A9), mixiwa
10.730					0E-129 AI199117.1	EST HUMAN	qi40408.x1 NCI_CGAP_Bm25 Homo espiens cDNA clone IMAGE:1858959 3' similar to I K:U 14640 U 14650 MITOGEN INDUCIBLE GENE MIG-2;
2							qi40d08.x1 NCI_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:1858959 3' similar to TR:Q14840 Q14840
10730	23783	37371	0.52	_	.0E-129 Al199117.1	EST_HUMAN	MITOGEN INDUCIBLE GENE MIG-2;
11497	L		3,32		1.0E-129 AA625526.1	EST_HUMAN	af72f07.r1 Soares_NhHMPu_S1 Homo sapiens CDNA clone IMAGE:1047 309 3
11578	1	33882		1.0E-129	11420850 NT	IN	Homo sapiens similar to nbosomal protein 52to (H. sapiens) (L. C. Coodey), into the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract o
12387		i	4.28		1.0E-129 H83155.1	EST_HUMAN	yq49c05.r1 Soares fetal liver splean 1NFLS Homo septens cUNA come livAcE: 1991 12.9 strilled to SP:B48150 B48150 BH-25=HIBERNATION-RELATED PROTEIN - TAMIAS ASIATICUS=ASIAN; SP:B48150 B48150 HP-25=HIBERNATION-RELATED PROTEIN - TAMIA SECONDARY 51
12817	L		1.97	L	1.0E-129AL120739.1	EST_HUMAN	DKFZp762K171_r1 762 (synonym: hmelz) Homo sapiens culvin ciglie DNFZp762K171_v
78	L	1 26341	1.01		7705530 NT	TN	Homo saplens hypothetical protein (HSF C242), mKNA
1197	┖				1.0E-130 AB037835.1	NT	Homo sapiens mRNA for KIAA1414 protein, partial cos
18	L	2 27939			1.0E-130 BE275192.1	EST_HUMAN	601121995F1 NIH MGC Z0 Homo sapiens culvA clone liviAGE 3346366 5
1700	14852	Ì	"		1.0E-130 BE275192.1	EST HUMAN	601121995F1 NIH MGC ZO Homo sapiens CLINA citate invitorio control del national del national del national del national del national del national del national del national del national del national del national del national del national del national del national del national del national del national del national del national del national del national del national del national del national del national del national del national del national del national del national del national del national del national del national del national del national del national del national del national del national del national del national del national del national del national del national del national del national del national del national del national del national del national del national del national del national del national del national del national del national del national del national del national del national del national del national del national del national del national del national del national del national del national del national del national del national del national del national del national del national del national del national del national del national del national del national del national del national del national del national del national del national del national del national del national del national del national del national del national del national del national del national del national del national del national del national del national del national del national del national del national del national del national del national del national del national del national del national del national del national del national del national del national del national del national del national del national del national del national del national del national del national del national del national del national del national del national del national del national del national del national del national del national del national del national del national del national del national del national del national del national del
2040					1.0E-130 X04092.1	Z	Human gene for catalasse (EC 1.11.1.0) exon 8 mapping to continuosonio 11, warm P.19
2830	15944	+	7.23		1.0E-130 AJ010230.1	N	Homo sepiens KE I finger protein-like 1 anusense transcript, paruar
294	l	29132	1.36	ļ	1.0E-130 BE564219.1	EST_HUMAN	601343016F1 NIH MGC 53 Homo sapiens cuiva cione image: 3000400 5
82	ı				1.0E-130 BE564219.1	EST HUMAN	601343016F1 NIH MGC 53 Homo sapiens cunna cione imaner 300343016F1 NIH MGC 53 Homo sapiens cunna in a constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant constant
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	Top Hit Descriptor	8 Homo sapiens cOMA	Homo sarlane child	Jono sariens CINA	Septions CIVA	(FBBP) mRNA	Homo sapiens solithe certier familis & from reviews transmittee transmittee transmittee transmittee transmittee	disponder, L-proline), member / (SLC6A7), mRNA	A complete cas	orniprete cus	ens.		2505877.91	:687590 5' similar to TR:G222811	667590 5' sImflar to TR: G222811									mRNA			DNA clone GEN-516H08 5'	cDNA clone GEN-516H08 5'		BMSC cr48e07 3'	BMSC cr48e07 3'	s 23 through 34
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	Expression Signal	1.49	1.49	1.03	1.03	0.85	1.85	0.83	0.63	0.53	2.06	1.82	0.63	2.52	2.52	1.14	3.34	3.34	3.17	3.17	6	0.62	0.89	4.6	1.77	1.77	1.45	1.45	9.83	16.36	16.36	2.48
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(Think A.)	Homo sapiens actin, beta (ACLB) mkinA	Human polyhomeotic 1 homolog (HPH1) mr.NA, paries Cas	HA1347 Human fetal liver oDNA library Homo sapiens cDNA	Homo sapiens mRNA for KIAA1363 protein, partial cds	H.sapiens ncx1 gene (exon 2)	FE3RD5.x1 NCI CGAP Ut4 Home saplens cDNA clone IMAGE:2230833 3' similar to 1 R:Q99551 Q99551	MITOCHONDRIAL TRANSCRIPTION TERMINATION FACTOR PRECURSOR.	ts38b05,x1 NCI_CGAP_Ut4 Homo sapiens cDNA clone IMAGE:2230833 3' similar to 1R. 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cos	Homo sapiens mRNA for KIAA0721 protein, partial cds	Mus musculus testis-specific protein, Y-encoded-Ilka (†1spyl), mKNA	TCBAP1E4466 Pediatric pre-B cell acute fumphoblastic leukemia Baylor-HGSC project= I UBA Homo sapran	cDNA clone TCBAP4466	TCBAP1E4466 Pediatric pre-B cell acute lymphobiastic leukamia baylor-noso project i con nome communication in the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of 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Page 482 of 550 Table 4 Single Exon Probes Expressed in Placenta

Most Similar  Expression (Top) Hit Top Hit Acession Signal BLASTE No. Source	EST_HUMAN	1.17 0.0E+00 AB018301.1 NT	1.17 0.0E+00[AB018301.1 NT	33805 NT	3.79 0.0E+00 AL163201.2 NT	4.65 0.0E+00 AF231919.1  NT	ΙN	6.95 0.0E+00 AF231919.1 NT	1.37 0.0E+00 . 4507500[NT	1.37 0.0E+00 4507500 NT	7706028 NT	0.96 0.0E+00 D83327.1 NT	1.2 0.0E+00 D83327.1 NT	2	1.41 0.0E+00 AW845293.1 EST_HUMAN	28553 5.65 0.0E+00 4557029 NT Homo sapiens potassium inwardiy-rectifying channel, subfamily J. member 15 (KCNJ15) mRNA	029 NT	26664 6.16 0.0E+00 AB028942.1   NT Homo septens mRNA for KIAA1019 protein, paritial cds	4.28 0.0E+00 AB028942.1  NT	8.13 0.0E+00 4506728 NT	AA480002.1 EST_HUMAN	0.0E+00 4507152 NT	24.65 0.0E+00 4507152 NT	88.1 NT	1.15 0.0E+00 O14867 SWISSPROT	1.15 0.0E+00 O14867  SWISSPROT	4.14 0.0E+00 7657213 NT	1.82 0.0E+00 7657213 NT	0.0E+00 5174574 NT	0.74 0.0E+00 4505256 NT	4.58 0.0E+00 4827057 NT	
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Page 483 of 550 Table 4 Single Exon Probes Expressed in Placenta

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Single Exoli Plobes Expressed in Placenta	Top Hit Descriptor	Homo sapiens chromosome 21 unknown mRNA	Homo sapiens chromosome 21 unknown mRNA	Homo sapiens chromosome 21 unknown mRNA	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA	Homo saplens GA-binding protein transcription factor, alpha subunit (60kD) (GARPA), mRNA	Human mRNA for KIAA0184 gene, partial cds	Human mRNA for KIAA0184 gene, partial cds	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA	AU134963 PLACE1 Homo sapiens cDNA clone PLACE1000899 5'	Homo sapiens mRNA for KIAA 1019 protein, partial cds	ay81h05.x1 NC_CGAP_Brn25 Home sapiens cDNA clone IMAGE:2018457 3' similar to gb:X54199	RC2-CTR22C-300100-016-300 CTR230 Long contract CNA	Homo sapiens Ind Echindra profess (FC/GAMMAIRE) HONA	Homo sapiens IaG Fc binding protein (FC(GAMMA)BP) mRNA	Homo sapiens IgG Fc binding protein (FC(GAMMA)BP) mBNA	Homo sapiens IgG Fc binding protein (FC/GAMMA)BP) mRNA	Homo saplens IgG Fc binding protein (FC(GAMMA)BP) mRNA	Homo sapiens IgG Fc binding protein (FC(CAMMA)BP) mRNA	Homo sapiens IgG Fc binding protein (FC(GAMMA)BP) mRNA	Homo sapiens IgG Fc binding protein (FC(GAMMA)BP) mRNA	Homo sapiens igG Fc binding protein (FC(GAMMA)BP) mRNA	H.sepiens gene for RNA pol II largest subunit, exons 23-29	H.sapiens gene for RNA pol II largest subunit, exons 23-29	H.sapiens gene for RNA pol II largest subunit, exons 23-29	H.sapiens gene for RNA pol II largest subunit, exons 23-29	Homo sapiens ribosomal protein L19 (RPL19) mRNA	yg09a02.r1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:31652 5'	Home capiens phosphorbosylglycinamide formyltransferase, phosphoribosylglycinemide synthetase,	prospinatiosydminomidazde synthetace (CART) mRNA Homo saniens ribosomal modelin CE (RDCS) mDNA	Hours capiens making for KIA A1040 and in put in put in put in put in put in put in put in put in put in put in put in put in put in put in put in put in put in put in put in put in put in put in put in put in put in put in put in put in put in put in put in put in put in put in put in put in put in put in put in put in put in put in put in put in put in put in put in put in put in put in put in put in put in put in put in put in put in put in put in put in put in put in put in put in put in put in put in put in put in put in put in put in put in put in put in put in put in put in put in put in put in put in put in put in put in put in put in put in put in put in put in put in put in put in put in put in put in put in put in put in put in put in put in put in put in put in put in put in put in put in put in put in put in put in put in put in put in put in put in put in put in put in put in put in put in put in put in put in put in put in put in put in put in put in put in put in put in put in put in put in put in put in put in put in put in put in put in put in put in put in put in put in put in put in put in put in put in put in put in put in put in put in put in put in put in put in put in put in put in put in put in put in put in put in put in put in put in put in put in put in put in put in put in put in put in put in put in put in put in put in put in put in put in put in put in put in put in put in put in put in put in put in put in put in put in put in put in put in put in put in put in put in put in put in put in put in put in put in put in put in put in put in put in put in put in put in put in put in put in put in put in put in put in put in put in put in put in put in put in put in put in put in put in put in put in put in put in put in put in put in put in put in put in put in put in put in put in put in put in put in put in put in put in put in put in put in put in put in put in put in put in put in put in put in put in put in put in put in put in put in put in put in put in put in put in put in pu	Homo semiens SON DNA hinding protein (SON) wDNA	Homo saplens SON DNA binding protein (SON) mRNA	
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ig.iio	Top Hit Acession No.	0.0E+00 AF231919.1	0.0E+00 AF231919.1	0.0E+00 AF231919.1	4507500 NT	4503854 NT			4507500 NT	0.0E+00 AU134963.1	0.0E+00 AB028942.1	0.05+00.41363014.4		03680	4503680 NT	503680					4506608		4503044 NIT	4506728 NT	0.0E+00 AR028042 1	7152	4507152 NT							
	Most Similar (Top) Hit BLAST E Value	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00 D80006.1	0.0E+00 D80006.1	0.0E+00	0.0E+00	0.0E+00	00+300	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00 X74870.1	0.0E+00 X74870.1	0.0E+00 X74870.1	0.0E+00 X74870.1	0.0E+00	0.0E+00 R17795.1		0.05	00H00	0.01	0.0E+00	
	Expression Signal	2.75	2.75	2.53	1.01	1.59	2	1.43	0.08	3.37	7.56	80	1.32	2.24	234	234	2.18	1.42	1.42	1.98	2.55	2.14	0.98	98.0	1.07	1.07	18.46	1.49	130	3.85	282	17.7	17.7	
	ORF SEQ ID NO:		26608	26609	26611	26615	26616	28616	26618	26629	26673	26674	26836	26639	26640	26641	26642	26643	26644	26645	26646	26647	26648	26649	26648	26649		26233	26675		26676	26677	26678	
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	Probe SEQ ID NO:	366	366	367	369	372	373	374	376	387	38	399	\$	407	408	408	409	<del>2</del>	<del>6</del>	411	412	413	414	414	415	415	419	433	144	44	443	4	44	

Page 484 of 550 Table 4 Single Exon Probes Expressed in Placenta

Single Extil Flobes Expressed in Lagorica	Тор Hit Descriptor	Mus musculus truncated SON protein (Son) mRNA, complete cds	Homo sepiens chromosome 21 segment HS21C001	Homo sapiens interferon gamma receptor 1 (IFNGR1) mRNA	RAT11152PE1 NIH MGC 16 Homo septens cDNA done IMAGE 3352348 5	Home sapiens 5-hydroxytrodamine (serotonin) receptor 1B (HTR1B) mRNA	House assume the second recording records and the second records and the second records and the second records and the second records and the second records and the second records and the second records and the second records and the second records and the second records and the second records and the second records and the second records and the second records and the second records and the second records and the second records and the second records and the second records and the second records and the second records and the second records and the second records and the second records and the second records and the second records and the second records and the second records and the second records and the second records and the second records and the second records and the second records and the second records and the second records and the second records and the second records and the second records and the second records and the second records and the second records and the second records and the second records and the second records and the second records and the second records and the second records and the second records and the second records and the second records and the second records and the second records and the second records and the second records and the second records and the second records and the second records and the second records and the second records and the second records and the second records and the second records and the second records and the second records and the second records and the second records and the second records and the second records and the second records and the second records and the second records and the second records and the second records and the second records and the second records and the second records and the second records and the second records and the second records and the second records and the second records and the second records and the second records and the second records and the second records and the second records and the second records and	Homo sapiens 3-1/9 loxyu ypeaning (co. co. m.)	Homo sapiens retain 18 (XRT18) mRNA	Homo sociona chromosome 21 segment HS21C046	Homo septens directing 1 segment HS21C046	Hallo saples a common 21 segment HS21C046	Homo sapters anonicaline at regiment regiments	Home sapiens mixiva to nixva conject of the NT2RP4000837 5	AU132898 NIZRE 4 Futility Replaced Spring September 2014 Cone IMAGE:3615756 5	BUTZ/4831F1 NITL WISO 20 HOUR CARD Sablens CDNA	PMO-U IUU65-1304UU-40E-1000 U I SUGO I IUIE CHINA CHINA CHINA CHINA CHINA CHINA CHINA CHINA CHINA CHINA CHINA CHINA CHINA CHINA CHINA CHINA CHINA CHINA CHINA CHINA CHINA CHINA CHINA CHINA CHINA CHINA CHINA CHINA CHINA CHINA CHINA CHINA CHINA CHINA CHINA CHINA CHINA CHINA CHINA CHINA CHINA CHINA CHINA CHINA CHINA CHINA CHINA CHINA CHINA CHINA CHINA CHINA CHINA CHINA CHINA CHINA CHINA CHINA CHINA CHINA CHINA CHINA CHINA CHINA CHINA CHINA CHINA CHINA CHINA CHINA CHINA CHINA CHINA CHINA CHINA CHINA CHINA CHINA CHINA CHINA CHINA CHINA CHINA CHINA CHINA CHINA CHINA CHINA CHINA CHINA CHINA CHINA CHINA 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(UQCRFS1), nuclear gene	encoding mitochandrial protein, mRNA
EXOII FIODE	Top Hit Database Source	NT	TN		I١	EST TOWNS	-	5	5			-N	LN.		EST_HUMAN	EST_HUMAN	EST HUMAN	LN	Z	EST HUMAN	TN TOL	EST HOMAN	ESI HOMAIN	2 12	2 2	Z	2 12	2	L	LN	FZ	EST HUMAN	- L		LN T
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	Most Similar (Top) Hit BLAST E Value	0.0E+00	V 00 130 0	0.05	0.0E+00	0.0E+00 B	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.05+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0=+00	0.0=+00	0.0E+00	0.0E+00	0.0E+00	Lo	00-100	0.05-00	0.0=+00	0.0E+00
	Expression Signal	4 23	1	1.45	4.44	0.75	3.38	3.38	21.77	21.77	4.1	6.3	5.9	4.25	1.81	1.66	1.7	1.82	0.95	1.9	4.43	1.57	1.15	1.57	8.39	4.53					,	4.82		5.31	1.85
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Page 485 of 550 Table 4 Single Exon Probes Expressed in Placenta

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Top Hit Descriptor	Human apolipoprotein A-I (ApoA-I) gene, exon 1	601822627F1 NIH_MGC_75 Homo saplens cDNA clone IMAGE:4045447 5	Homo sepiens hypothetical protein FLJ20701 (FLJ20701), mKNA	Homo sapiens hypothetical protein FLJ20701 (FLJ20701), mkNA	Homo sapiens hypothetical protein FLJ20701 (FLJ20701), mRNA	Homo saplens hypothetical protein FLJ20701 (FLJ20701), mtNA	Homo sapiens hypothetical protein FLJ20701 (FLJ20701), mixiva	Homo sepiens hypothetical protein FLJ20/01 (FLJ20/01), mRNA	Homo sapiens acety-Coenzymo A carboxytase beta (ACACB), Illinoral	Homo sapiens Smad- and Oit-Interacting zinc ringer protein minuth, partial cus	Homo sapiens Smad- and Oir-interacting Ziro iniger protein initation, realized and an action of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the 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sapiens low density lipoprotein-related protein 2 (LRF2), mKNA	Homo sapiens low density lipoprotein-related protein 2 (LRF2), mining	260c07.7 Soares, testis, NHT Homo saptens curva cione liwa de	Homo sapiens RGH2 gene, retrovirus-like element	2h51b04.r1 Soares_feta_jlver_spleen_1NFLS_51 Homo sepiens curva clone introductions of similar companies of the sepiens of the sepiens of the sepiens of the sepiens of the sepiens of the sepiens of the sepiens of the sepiens of the sepiens of the sepiens of the sepiens of the sepiens of the sepiens of the sepiens of the sepiens of the sepiens of the sepiens of the sepiens of the sepiens of the sepiens of the sepiens of the sepiens of the sepiens of the sepiens of the sepiens of the sepiens of the sepiens of the sepiens of the sepiens of the sepiens of the sepiens of the sepiens of the sepiens of the sepiens of the sepiens of the sepiens of the sepiens of the sepiens of the sepiens of the sepiens of the sepiens of the sepiens of the sepiens of the 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X-linked (PRKX) mRNA	Home september kniese Kilnked (PRKX) mRNA	Limman and contains abtracting the 1 (FRV9)	Human enougenous removates prints (markistane chromosomal) protein 1 (HMG1) mRNA	Homo sapiens night-mobility group (1971) and the sapiens of the sapiens of the sapiens of the sapiens of the sapiens of the sapiens of the sapiens of the sapiens of the sapiens of the sapiens of the sapiens of the sapiens of the sapiens of the sapiens of the sapiens of the sapiens of the sapiens of the sapiens of the sapiens of the sapiens of the sapiens of the sapiens of the sapiens of the sapiens of the sapiens of the sapiens of the sapiens of the sapiens of the sapiens of the sapiens of the sapiens of the sapiens of the sapiens of the sapiens of the sapiens of the sapiens of the sapiens of the sapiens of the sapiens of the sapiens of the sapiens of the sapiens of the sapiens of the sapiens of the sapiens of the sapiens of the sapiens of the sapiens of the sapiens of the sapiens of the sapiens of the sapiens of the sapiens of the sapiens of the sapiens of the sapiens of the sapiens of the sapiens of the sapiens of the sapiens of the sapiens of the sapiens of the sapiens of the sapiens of the sapiens of the sapiens of the sapiens of the sapiens of the sapiens of the sapiens of the sapiens of the sapiens of the sapiens of the sapiens of the sapiens of the sapiens of the sapiens of the sapiens of the sapiens of the sapiens of the sapiens of the sapiens of the sapiens of the sapiens of the sapiens of the sapiens of the sapiens of the sapiens of the sapiens of the sapiens of the sapiens of the sapiens of the sapiens of the sapiens of the sapiens of the sapiens of the sapiens of the sapiens of the sapiens of the sapiens of the sapiens of the sapiens of the sapiens of the sapiens of the sapiens of the sapiens of the sapiens of the sapiens of the sapiens of the sapiens of the sapiens of the sapiens of the sapiens of the sapiens of the sapiens of the sapiens of the sapiens of the sapiens of the sapiens of the sapiens of the sapiens of the sapiens of the sapiens of the sapiens of the sapiens of the sapiens of the sapiens of the sapiens of the sapiens of the sapiens of the sapiens of the sapiens of the sapiens of the sa
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Most Similar (Top) Hit BLAST E	0.0E+00 J04066.1	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	00130	005+00	00+100	00.100	000-100	20.00	20.00	0.0100	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00
Expression Signal	7.14	1.87	0.95	0.95	0.77	77.0	0.72	0.72	0.64	1.93	1.93	2.19	0.93	1.99	2.34	2.34	96.0	0.98	1.42	6.57	20.7	907.4	4.40								ES		3.92
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Probe SEQ ID NO:	612	615	617	617	618	618	619	619	624	629	629	639	25	643	48	4	645	645	852	656		000		20 6	2/2	2/9	β Q	67 <u>.</u>	3/9	88	685	691	702



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	Top Hit Descriptor	Homo sapiens mRNA for KIAA1089 protein, partial cds	Homo sapiens similar to rat Integral membrane glycoprotein POM121 (POM121L1), mKNA	np49d01.s1 NCI_CGAP_Br1.1 Homo saplens cDNA clone IMAGE:1129633 3' similar to gb:X57352	INTERFERON-INDUCIBLE PROTEIN 1-8U (HUMAN);	Human von Willebrand factor gene, exons 23 prougn 34	Human von Willebrand factor gene, exons 23 through 34	Homo sapiens TNF receptor-associated factor 1 (TRAF1) mRNA	Homo sapiens ALR-like protein mRNA, partial cds	Homo sapiens ALR-like protein mKNA, partial cus	Homo sapiens hypothetical protein FLJZ1634 (FLJZ1634), IIIINNA  "ATABAM Barlor LIDED AviorIIIINA	TCAAP100779 Pediatric acute myelogenous (eukemia ceii (rAb Mi) bayidin isso, project i ozonimisapiens cDNA clone TCAAP0779	Homo capiens MHC class I antigen (HLA-G) mRNA, HLA-G1 allele, complete cds	Homo sapiens MHC class I antigen (HLA-G) mRNA, HLA-G1 allele, complete cds	Human, plasminogen activator inhibitor-1 gene, exons 2 to 9	Human, plasminogen activator inhibitor-1 gene, exons 2 to 9	Homo sapiens mRNA for KIAA1339 protein, partial cds	Homo sapiens zinc finger protein 212 (ZNF212), mRNA	Homo sapiens mRNA for repressor protein, partial cds	601445647F1 NIH_MGC_65 Homo sapiens cDNA cione liwa cE.3043603 3	M69g08.r1 Soares breast ZNDHBst Homo sapiens Conversion MACE. 1550.5	Homo sapiens splicing factor 34, subunit 1, 12000 (31301), misson	Homo sapiens gene for AF-5, complete cas	Homo saplens MARO 170 gene product (Nova 170), minor	Human mKNA for NIAAU184 gene, par ital ous	Human mRNA for KIAA0184 gene, paritial outs	H.sapiens mRNA for interreron alphabaeta receptor (1019 10111)	Homo sapiens mRNA for KIAA0910 protein, partial cus	Homo sapiens mRNA for KIAAU910 protein, partial cus	Homo sapiens pericentrin (PCN1) mRNA	Homo sapiens T-cell lymphoma invasion and metastasis 1 ( 1 MM I ) intolva	Homo sapiens hormonally upregulated neu timor-associated nu lase (1101417), 111,447	Homo sapiens hormonally upregulated neu (umpi-associated nulsae (10011), Illinois	Homo sapiens porassium voluge-gardu originier, lest contact current, manage-gardu originier, lest contact current, manage-gardu originier, lest contact current, manage-gardu originier, lest contact current, manage-gardu originier, lest contact current, manage-gardu originier, lest contact current, manage-gardu originier, lest contact current, lest contact current, lest contact current, lest contact current, lest contact current, lest contact current, lest contact current, lest contact current, lest contact current, lest contact current, lest contact current, lest contact current, lest contact current, lest contact current, lest contact current, lest contact current, lest contact current, lest contact current, lest contact current, lest contact current, lest contact current, lest contact current, lest contact current, lest contact current, lest contact current, lest contact current, lest contact current, lest contact current, lest contact current, lest contact current, lest contact current, lest contact current, lest contact current, lest contact current, lest contact current, lest contact current, lest contact current, lest contact current, lest contact current, lest contact current, lest contact current, lest contact current, lest contact current, lest contact current, lest contact current, lest contact current, lest contact current, lest contact current, lest contact current, lest contact current, lest contact current, lest contact current, lest contact current, lest contact current, lest contact current, lest contact current, lest contact current, lest contact current, lest contact current, lest contact current, lest contact current, lest contact current, lest contact current, lest contact current, lest contact current, lest contact current, lest contact current, lest contact current, lest contact current, lest contact current, lest contact current, lest contact current, lest contact current, lest contact current, lest contact current, lest contact current, lest contact current, lest contact current, lest co
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Sign S	Top Hit Acession No.		7468		1.			5032192 NT			11545800 NT	0.0E+00 BE241577.1			Π		15	12749		5.1		5032086 NT	0.0E+00 AB011399.1	7661965 NT	D80006.1	D80006.1	X89772.1	0.0E+00 AB020717.1	0.0E+00 AB020717.1	5174478 NT	4507500 NT	7657213 NT		4557686 NT
	Most Similar (Top) Hit T BLAST E Value	0 0F+00 AB029012.1	00+100	25	0.0E+00 AA614537.1	0.0E+00 M60675.1	0.0E+00 M60675.1	0.0E+00	0.0E+00 AF264750.1	0.0E+00	0.0E+00	a 00+	O 0E+00	0 0F+00	0.0E+00 J03764.1	0 0F+00 103764 1	0.0E+00	0.0E+00	0.0E+00 D30612.1	0.0E+00		00+30.0				0.0E+00 D80008.1				0.0E+00	0.0E+00	\ _		0.0E+00
	Expression Signal	4 94	383	3	13.13	6.4	6.4	1.35	4.62	4.62	9.17	9000	1 19	1 10				207				2.85	1.64	3.01	1.24	1.24	274			13.47	11.09		5 2.46	1.84
	ORF SEQ ID NO:	08020	20050	05607	20949	26953	26954	26963	26969	26970	26973		2005				27010						27031	_				L	L		L	5 27085		8 27088
	Exon SEQ ID NO:	43000	2005	1388	13909	13013	13913	13023	13928	13928	13930		13936	L			13956		⊥.	1_	L	L	L	13983	ı	L	1	L	L	上	L	L		L
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Top Hit Descriptor	Homo sapiens serine-threonine protein kinase (MNBH) mRNA, complete ods	Homo sapiens serine-threonine protein kinase (MNBH) mRNA, complete cds	Homo sapiens serine-threonine protein kinase (MNBH) mRNA, complete cds	Homo saplens GA-binding protein transcription factor, alpha subunit (60kD) (GABPA), mRNA	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA	Homo sapiens T-cell lymphoma Invasion and metastasis 1 (TIAM1) mRNA	Homo sapiens sodium/myo-inositol cotransporter (SLC5A3) gene, complete cds	Homo sapiens mRNA for KIAA1019 protein, partial cds	Homo sapiens mRNA for KIAA1019 protein, partial cds	Homo sapiens SON DNA binding protein (SON) mRNA	Homo sapiens mRNA for KIAA1019 protein, partial cds	Homo sapiens ribosomal protein S5 (RPS5) mRNA	Homo sapiens mRNA for KJAA0910 protein, partial cds	Homo saplens mRNA for KIAA0910 protein, partial cds	nj66d07.s1 NCI_CGAP_Pr10 Hamo sapiens cDNA clone IMAGE:997453	nj66d07.s1 NCI_CGAP_Pr10 Homo sapiens cDNA clone IMAGE:997453	602085579F1 NIH_MGC_83 Homo saplens cDNA clone IMAGE:4249915 5'	Homo sapiens hormonally upregulated neu fumor-associated kinase (HUNK), mRNA	Homo sapiens hormonally upregulated neu fumor-associated kinase (HUNK), mRNA	Homo saplens hormonally upregulated neu tumor-associated kinase (HUNK), mRNA	Homo sapiens hormonally upregulated neu tumor-associated kinase (HUNK), mRNA	Homo sapiens chromosome 21 segment HS21C003	QV0-BT0703-280400-211-911 BT0703 Homo saplens cDNA	QV0-BT0703-280400-211-g11 BT0703 Homo sapiens cDNA	Homo sapiens chromosome 21 segment HS21C003	Homo saplens laminin receptor 1 (67kD, ribosomal protein SA) (LAMR1), mRNA	Homo sapiens laminin receptor 1 (67kD, ribosomal protein SA) (LAMR1), mRNA	Homo sapiens alpha-1-antichymotrypsin precursor, mRNA, partial cds	protein C inhibitor [human, leukocytes, Genomic, 1216 nt, segment 2 of 5]	protein C Inhibitor [human, leukocytes, Genomic, 1216 nt, segment 2 of 5]	protein C inhibitor [human, leukocytes, Genomic, 1216 nt, segment 2 of 5]	Homo sapiens kallistatin (P14) gene, exons 1-4, complete cds	Homo sapiens of cardiac alpha-myosin heavy chain gene	Homo saplens of cardiac alpha-myosin heavy chain gene
Top Hit Datebase Source	LN.	NT	LNT	FZ	L	TN	LN	LN	NT	LN	NT	ΝT	NT	F	EST_HUMAN	EST_HUMAN	EST_HUMAN	L	L	LN	LN	NT	EST_HUMAN	EST_HUMAN	NT	NT	NT	NT	NT	NT	NT	NT	L	Z
Top Hit Acession No.	0.0E+00 AF108830.1	0.0E+00 AF108830.1	0.0E+00 AF108830.1	4503854 NT	4507500 NT	4507500 NT	0.0E+00 AF027153.1	0.0E+00 AB028942.1	0.0E+00 AB028942.1	4507152NT	0.0E+00 AB028942.1	4506728 NT	0.0E+00 AB020717.1	0.0E+00 AB020717.1	0.0E+00 AA533272.1	0.0E+00 AA533272.1	0.0E+00 BF677694.1	7657213	7857213 NT	7657213 NT	7657213 NT	0.0E+00 AL163203.2	0.0E+00 BE089592.1	0.0E+00 BE089592.1	0.0E+00 AL163203.2	4504958 NT	4504958 NT	0.0E+00 AF089747.1	369364.1	369364.1	569364.1			720656.1
Most Similar (Top) Hit BLAST E Value	0.0E+00/	0.0E+00/	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00/	0.0E+00/	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00/	0.0E+00	0.0E+00	0.0E+00	0.0E+00 S69364.1	0.0E+00 S69364.1	0.0E+00 S69364.1	0.0E+00 L28101.1	0.0E+00 Z20656.1	0.0E+00 Z20656.1
Expression Signal	2.19	2.19	1.45	2.85	1.37	1.37	2.07	5.27	5.27	11.32	4.03	3.87	1.54	1.54	1.82	1.82	8.41	1.4	1.4	2.54	2.54	86.0	1.93	1.93	2.7	90.6	69.6	1.42	69.0	0.69	69.0	1.62	0.71	0.71
ORF SEQ. ID NO:		27095		27101		27107			27119		27121	27122	27125	27128	27127	27128					27132		Ì		27170				27177					27184
Exon SEQ ID NO:	14033	14033	14034	14039	14042	14042	14049	14053	14053	14054	14055	14056	14060	14060	14061	14061	14062	14066	14066	14067	14067	14089	14096		14106	14115	14115	14117	14118	14118	14118	14119	14122	14122
Probe SEQ ID NO:	856	856	857	862	998	998	873	877	877	878	879	880	884	884	882	882	886	890	890	891	891	914	921	921	931	941	943	944	845	945	942	946	949	949

Page 488 of 550 Table 4 Single Exon Probes Expressed in Placenta

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	Top Hit Descriptor	Human ras inhibitor mRNA, 3' end	Human ras inhibitor mRNA, 3' end	Human ras Inhibitor mRNA, 3' end	Homo sapiens thyrotrophic embryonic factor (TEF), mRNA	Homo sapiens thyrotrophic embryonic factor (TEF), mRNA	os98e03.s1 NCI_CGAP_GC3 Homo sapiens cDNA clone IMAGE:1613404.3'	os98e03.s1 NCI_CGAP_GC3 Homo sapiens cDNA clone IMAGE:1613404 3'	Homo sapiens KIAA0929 protein Msx2 interacting nuclear farcet (MINT) homolog (KIAA0929) mRNA	Homo saplens mRNA for PSP24, complete cds	PM2-GN0014-050900-001-f02 GN0014 Homo sapiens cDNA	PM2-GN0014-050900-001-f02 GN0014 Homo sapiens cDNA	PM2-GN0014-050900-001-f02 GN0014 Homo sapiens cDNA	Homo sapiens partial of tr gene, exons 2 and 3	Homo sapiens partial c-fgr gene, exons 2 and 3	Homo sapiens chromodomain protein, Y chromosome-like (CDYL) mRNA	Human beta-tubulin (TUB4q) gene, complete cds	Human beta-tubulin (TUB4q) gene, complete cds	Human beta-tubulin (TUB4q) gene, complete cds	Homo sapiens 8q22.1 region and MTG8 (CBFA2T1) gene, partial cds	Homo saplens 8q22.1 region and MTG8 (CBFA2T1) gene, partial cds	Homo saplens 14q32 Jagged2 gene, complete cds; and unknown gene	Homo sapiens 14q32 Jagged2 gene, complete cds; and unknown gene	Homo sapiens 14q32 Jagged2 gene, complete cds; and unknown gene	Homo saplens 14q32 Jagged2 gene, complete cds; and unknown gene	Horno sapiens DKFZP586M0122 protein (DKFZP586M0122), mRNA	Homo saplens inner membrane protein, mitochondrial (mitofilin) (IMMT), mRNA	ae88g07.st Stratagene fetal retina 937202 Homo expiens cDNA clone IMAGE:838236 3' similar to SW:PRS8_HUMAN P47210 26S PROTEASE REGULATORY SUBUNIT 8	EST51124 WATM1 Homo sapiens cDNA clone 51124 similar to DNA-DIRECTED RNA POLYMERASE II	(alignment Ser and Pro with BLASTx or p)	EST51i24 WATM1 Homo sapiens cDNA chone 51i24 similar to DNA-DIRECTED RNA POLYMERASE II (alignment Ser and Pro with BLASTx or p)	Homo saplens TRAF family member-associated NFKB activator (TANK) mRNA
	Top Hit Database Source	Į.	<u>F</u>	N N	N	<u>L</u> N	EST_HUMAN	EST_HUMAN	ΙN	LΝ	EST HUMAN	EST HUMAN	EST_HUMAN	Z	N <sub>T</sub>	۲	F	F	F	뉟	NT	LN	LN	LN	IN	TN	TN	EST_HUMAN		EST HUMAN	1 EST_HUMAN	LΝ
	Top Hit Acession No.	0.0E+00 M37190.1	0.0E+00 M37190.1	M37190.1	4507430	4507430 NT	0.0E+00 AI001948.1	0.0E+00 A1001948.1	7657266 NT	0.0E+00 AB030565.1	0.0E+00 BF366974.1	0.0E+00 BF366974.1	0.0E+00 BF366974.1	X52207.1	X52207.1	4757969 NT	J83668.1	J83668.1	J83668.1	0.0E+00 AF198490.1	0.0E+00 AF198490.1	0.0E+00 AF111170.3	0.0E+00 AF111170.3	0.0E+00 AF111170.3	0.0E+00 AF111170.3	7661685 NT	5803114 NT	0.0E+00 AA458680.1		443182.1	443182.1	4759249
	Most Similar (Top) Hit BLAST E Value	0.0E+00	0.0E+00	0.0E+00 M37190.1	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00 X52207.1	0.0E+00 X52207.1	0.0E+00	0.0E+00 U83668.1	0.0E+00 U83668.1	0.0E+00 U83668.1	0.0E+00	0.0E+00	0.0E+00	0.0E+00/	0.0E+00/	0.0E+00	0.0E+00	0.0E+00	0.0E+00/		0.0E+00 N43182.1	0.0E+00 N43182.1	0.0E+00
	Expression Signal	0.93	9.11	0.79	1.24	1.24	3.95	3.95	14.34	1.76	43.62	43.62	43.62	202	202	3.97	1.07	5.81	60.6	4	29.56	0.96	4.66	13	1.18	2.11	1.27	1.39	- !	2.43	2.43	16:0
	ORF SEQ ID NO:			27207				27217					27238	27241	27242		27257		27258			27264	27264	27264	27265	27268	27272			27277	27278	27279
	Exon SEQ ID NO:					14149		16027	14158	14168	14177	14177	14177	14179	14179	14188	14199	14200	14200	14203	14203	14207	14207	14207	14208	14211	14215	14217		14220	14220	14221
	Probe SEQ ID NO:	973	974	975	976	976	984	984	986	266	1006	1006	1006	1008	1008	1017	1029	1030	1031	1034	1035	1039	1040	1041	1042	1045	1049	1051	,	1064	1054	1066

Page 489 of 550 Table 4 Single Exon Probes Expressed in Placenta

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Top Hit Descriptor	Homo sapiens TRAF family member-associated NFKB activated (TANA) IIITAAN	Homo sapiens hypothetical protein FLU1 i 190 (TLU) in 190, in 190, in 190, in 190, in 190, in 190, in 190, in 190, in 190, in 190, in 190, in 190, in 190, in 190, in 190, in 190, in 190, in 190, in 190, in 190, in 190, in 190, in 190, in 190, in 190, in 190, in 190, in 190, in 190, in 190, in 190, in 190, in 190, in 190, in 190, in 190, in 190, in 190, in 190, in 190, in 190, in 190, in 190, in 190, in 190, in 190, in 190, in 190, in 190, in 190, in 190, in 190, in 190, in 190, in 190, in 190, in 190, in 190, in 190, in 190, in 190, in 190, in 190, in 190, in 190, in 190, in 190, in 190, in 190, in 190, in 190, in 190, in 190, in 190, in 190, in 190, in 190, in 190, in 190, in 190, in 190, in 190, in 190, in 190, in 190, in 190, in 190, in 190, in 190, in 190, in 190, in 190, in 190, in 190, in 190, in 190, in 190, in 190, in 190, in 190, in 190, in 190, in 190, in 190, in 190, in 190, in 190, 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Most Similar (Top) Hit BLAST E Value	0.0E+00	0.0E+00	0.0日+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00 A	0.0E+00	0.0E+00	0.0E+00	0.0E+00 B	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00 X95826.1	0.0E+00 X95826.1		0.0E+00	0.0E+00	0.0E+00	0.0E+00				0.0E+00
Expression Signal	0.97	3.27	1.51	1.51	1,51	2.74	2.74	13.57	0.92	2.81	2.04	1.91	3.82	3.82	0.82	0.82		1.2	3,95	19.6		4.52		0.71	0.71	1.15		1.22	1.22	1.32	2.19	2.19		8.64
ORF SEQ ID NO:	27280		27295					L		27321		27340												27387	27388		5 27391	4 27400		5 27402	7 27415	7 27416	١.	7 27428
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Page 490 of 550 Table 4 Single Exon Probes Expressed in Placenta

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Top Hit Descriptor	Homo saplens mult. (E. coti) homolog 3 (MLH3), mRNA	Homo sapiens hypothetical protein FLJ10697 (FLJ10697), mKNA	Homo saplens ALR-like protein mRNA, partial cds	Home cardens Al R-like protein mRNA, partial ods	Turns explores A B like rectain mRNA partial cds	Total September 19 Production and the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of th	Homo sepiens ALK-like protein Illinato, yalaan oo l	Homo sapirens circumsums a subsequing a second second second (CSPG4), mRNA	Homo seguens crondrolluli suniare proceedy cert y through the seguents of the seguents of the seguents of the seguents of the seguents of the seguents of the seguents of the seguents of the seguents of the seguents of the seguents of the seguents of the seguents of the seguents of the seguents of the seguents of the seguents of the seguents of the seguents of the seguents of the seguents of the seguents of the seguents of the seguents of the seguents of the seguents of the seguents of the seguents of the seguents of the seguents of the seguents of the seguents of the seguents of the seguents of the seguents of the seguents of the seguents of the seguents of the seguents of the seguents of the seguents of the seguents of the seguents of the seguents of the seguents of the seguents of the seguents of the seguents of the seguents of the seguents of the seguents of the seguents of the seguents of the seguents of the seguents of the seguents of the seguents of the seguents of the seguents of the seguents of the seguents of the seguents of the seguents of the seguents of the seguents of the seguents of the seguents of the seguents of the seguents of the seguents of the seguents of the seguents of the seguents of the seguents of the seguents of the seguents of the seguents of the seguents of the seguents of the seguents of the seguents of the seguents of the seguents of the seguents of the seguents of the seguents of the seguents of the seguents of the seguents of the seguents of the seguents of the seguents of the seguents of the seguents of the seguents of the seguents of the seguents of the seguents of the seguents of the seguents of the seguents of the seguents of the seguents of the seguents of the seguents of the seguents of the seguents of the seguents of the seguents of the seguents of the seguents of the seguents of the seguents of the seguents of the seguents of the seguents of the seguents of the seguents of the seguents of the seguents of the seguents of the seguents of the seguents of the seguents of the	Homo sapiens predictin 4 (TTCN4) illican	Homo sapiens NF2 gene	Homo sapiens ribosomal protein Sz (NY Sz) intrava.	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Homo sapiens zinc finger protein 1/3 (ZNT1/3) mrNAA	Homo sapiens RFB30 gene for Rinks inger protein	Homo sapiens ring finger protein 9 (RNY9), minny	Homo seplens zinc finger protein 173 (ZNF173) mKNA	Homo sepiens mRNA for KIAA05/7 protein, complete cas	Homo sapiens KIAA0170 gene product (KIAA0170), mRNA	Homo sepiens KIAA0170 gene product (KIAA0170), mitNA	Homo sagiens period (Drosophila) homolog 3 (PER3), mRNA	Homo saplens period (Drosophila) homolog 3 (PER3), mRNA	Human endogenous retrovirus HERV-K10	601109792F1 NIH_MGC_16 Homo saplens cDNA clone IMAGE:3350471 5'	En110792F1 NIH MGC 16 Homo saplens cDNA clone IMAGE:3350471 5	
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Expression Signal	1 28	100	6.0	20.3	2.89	3.33				69'0	1.38	29.86		1.83						1.2	12	1.4	1.86	0.83	1.7	1.55										7 1.02
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Probe SEQ ID NO:	1000	3	1250	1254	1254	1255	1256	1275	1276	1286	1295	1303	13.1	1316	1248	1328	430B	13.2B	1320	1339	1339	1345	1346	1347	1349	1350	1354	365	1354		1333	200	1356	1368	1429	142

Page 491 of 550 Table 4 Single Exon Probes Expressed in Placenta

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Top Hit Descriptor	Homo seniens mRNA for Familial Cylindromatosis cyld gene		RAN, member RAS oncogene familyHomo sapiens RAN, member RAS oncogene family (RAN), mRNA	Homo septients propretein converties additionate to the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of	Homo sapiens proprotein convertes succession type 2 (1 cons.)	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Human von Willebrand factor pseudogene corresponding wexters of minds.	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Top Hit Database Source	114		Ę	₽Z	NT	NT	NT	NT	NT	L	L'A	NT	LZ.	LN L	Ę	L	TN	NT	NT	EST_HUMAN	Ę	Z	EST_HUMAN	EST HUMAN	LZ.	F <sub>2</sub>	Į	į	N N	1	Z F	- L	- L	
Top Hit Acession No.	T	00 AJ250014.1	6042208 NT	4505646 NT	4505646 NT	7705565 NT	7705565 NT				.1	+00 D87077.1	6912457 NT	7661965 NT	7661965 NT				7706434 NT	0.0E+00 AA481172.1	0.0E+00 AF023860.1	0.0E+00 AF023860.1	0.0E+00 AW976097.1	0.0E+00 AW976097.1	+00 D40884.1	178027	ASOSAOA NT	10000	TM 204094		TIN 2/8000/			4507720IN
Most Similar (Top) Hit BLAST E		0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00 Y07829.2	0.0E+00	0.0E+00 M60676.1	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00			1		1		0.0		0.0E+00
Expression Signal		1.03	13.57	76.0	0.97	1.99	1.99	29.09	4.63	4.2	1.37	1.73	8.24	2.28	2.28	3.74	6.62	6.62	2.61	2.66	27.8	27.8	1.55	1,55	1.03		3.2						0.97	
ORF SEQ ID NO:		27668	27680											L	L		27742	L			27792		_	27797	27798				27802					1 27812
Exon SEQ ID NO:		14593	14602	1	14810	14512	14812	14615	14625	14643	14844	1_	L	<u>l</u>	L	14654	1	L	L	L	L	L	L	14717	14718	l	- 1	1		14723		3 14729		14731
Probe SEQ ID NO:		1440	1449	1457	1457	1459	1450	1462	1471	1490	1491	1405	1498	150	1500	1501	1507	1507	1541	1555	1562	1562	1564	1564	1565		1587	1558	1568	1570	1571	1578	1578	1578

Page 492 of 550 Table 4 Single Exon Probes Expressed in Placenta

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Top Hit Descriptor	Homo sapiens ribosomal protein L5 (RPL5) mRNA	Human laminin receptor (2H5 epitope) mRNA, 5' end	Homo sapiens titin (TTN) mRNA	Homo sapiens tith (TTN) mRNA	Homo sapiens chandroitin sulfate proteoglycen 4 (melanome-associated) (CSPG4) mRNA	human c-yes-2 gene	H. sapiens hH2B/e gene	Homo sapiens butyrophilin, subfamily 2, member A1 (BTN2A1), mRNA	Homo sapiens butyrophillin, subfamily 2, member A1 (BTN2A1), mRNA	AV690831 GKC Homo sapiens cDNA done GKCBOF02 5	AV690831 GKC Homo sapiens cDNA done GKCBOF02 5	Homo sapiens mRNA for KIAA1472 protein, partial cds	Homo septens DNA polymerase zeta catalytic subunit (REV3) mRNA, complete cds	Homo sapiens KIAA0569 gene product (KIAA0569). mRNA	Homo sapiens KIAA0569 gene product (KIAA0569), mRNA	Homo sapiens heat shock 70kD protein 10 (HSC71) (HSPA10), mRNA	Homo sapiens heat shock 70kD protein 10 (HSC71) (HSPA10), mRNA	Human sodium channel mRNA	yo78c05.s1 Scares adult brain N2b4HB55Y Homo septens cDNA clone IMAGE:183848.3	Homo sapiens mRNA for KIAA1609 protein, partial cds	Homo saplens mRNA for KIAA1609 protein, partial cds	UI-H-Bi3-ajw-c-04-0-UI.s1 NCI_CGAP_Sub5 Homo sepiens cDNA clone IMAGE:27332943'	MR0-HT0166-191199-004-b11 HT0188 Homo sapiens cDNA	MR0-HT0166-191199-004-b11 HT0166 Homo sapiens cDNA	wg81b07.x1 Soares, NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2371477 3' similar to TR:062788 Q62788 CYS2/HIS2 ZINC FINGER PROTEIN.	Homo sapiens hematopoletic-derived zinc finger protein (HD-ZNF1) mRNA	Homo sapiens T-cell receptor gamma V1 gene region	Human zinc-finger protein 7 (ZFP7) mRNA, complete ods	Human zinc-finger protein 7 (ZFP7) mRNA, camplete cds	Homo sapiens keratin 18 (KRT18) mRNA	Homo sapiens vets avian erythroblastosis virus E28 oncogene related (ERG), mRNA	hu11405.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3186281 3' similar to TR:095147 095147 MP-1 LIKE PROTEIN TYROSINE PHOSPHATASE;
Top Hit Database Source	F	NT	N	TN	TN	NT	LN FN	LN	TN	EST HUMAN	EST_HUMAN	NT	NT	NT	TN	N	N	TN	EST_HUMAN	F	TN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST HUMAN		TN	LΝ	N	TN		EST_HUMAN
Top Hit Acession No.	4506654 NT	M14199.1	4507720 NT	4507720 NT		D00333.1	Z83738.1	5921460 NT	5921460 NT	0.0E+00 AV690831.1	0.0E+00 AV690831.1	0.0E+00 AB040905.1	0.0E+00 AF157476.1	7862183 NT	7662183 NT	- 5729876 NT	5729876 NT	M91803.1	0.0E+00 H26973.1	0.0E+00 AB046829.1	0.0E+00 AB046829.1	0.0E+00 AW44637.1	0.0E+00 BE144364.1	0.0E+00 BE144364.1	0.0E+00 AI768104.1	4758513 NT	0.0E+00 AF057177.1	M29580.1	M29580.1	4557887 NT	7657065 NT	0.0E+00 BE222374.1
Most Similar (Top) Hit BLAST E Value	0.0E+00	0.0E+00 M14199.1	0.0E+00	0.0E+00	0.0E+00	0.0E+00 D00333.1	0.0E+00 Z83738.1	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00 M91803.1	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00 M29580.1	0.0E+00 M29580.1	0.0E+00	0.0E+00	0.0E+00
Expression Signal	32.23	27.68	1.43	1.43	13.85	3.25	11.38	2.55	2.55	11.09	11.09	2.1	1.88	6.83	6.83	56.88	56.88	1.53	6.29	1.87	1.87	1.66	2.12	2.12	1.3	1.71	2.8	2.1	2.1	64.4	2.42	1.08
ORF SEQ ID NO:		27813	27828	27829	27830		27844	27845	27846				27852	27855	27856	27857	27858	27860	27876	27887	27888	27903	27936	27937	27941	27942	27943	27947	27948	27950	27951	27954
<i>-</i> ∞	16042	14732	14745	14745	14747	14755	14764	14765	14765	14766	14766			14772	14772	14774	14774	14776	14791	14801	14801	14820	14850	14850	14854	14855	14856	14859	14859	14861	14862	14865
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Page 493 of 550 Table 4 Single Exon Probes Expressed in Placenta

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Top Hit Descriptor	hu11d05.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3166281 3' similar to TR:095147 095147 NRP-1 LIKE PROTEIN TYROSINE PHOSPHATASE;	Homo saplens gamma-aminobutyric acid (GABA) A receptor, gamma と(いわいてく) mivve	yo59e08.r1 Soares broatt 3NbHBst Homo sapiens r.DNA done IMANCE. Io2249.5 Simila IV 95.MD-1005. GAMMA-GLUTAMYLTRANSPEPTIDASE 5 PRECURSOR (HUMAN).	yo59e08.rf Sceres breast 3NbHBst Homo sapiens cDNA clone IMAACE:182240 5 striller to yb., Michosos GAMMA-GLUTAMYLTRANSPEPTIDASE 5 PRECURSOR (HUMAN).	qf43f09.x1 Soares_testis_NHT Homo sapiens cUNA cione liviAcE:17 32ous 3	H. sapiens H2B/h gene	H. sapiens H2B/h gene	Home sapiens ingn-mobility group (floridistance critical processors) processors (floridistance critical processors) and the critical processors (floridistance critical processors) and the critical processors (floridistance critical processors) and the critical processors (floridistance critical processors) and the critical processors (floridistance critical processors) and the critical processors (floridistance critical processors) and the critical processors (floridistance critical processors) and the critical processors (floridistance critical processors) and the critical processors (floridistance critical processors) and the critical processors (floridistance critical 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Top Hit Database Source	EST_HUMAN	ΤN	EST_HUMAN	EST_HUMAN	EST HUMAN	NT	NT	Į.	Į.	LN T	NT	NT	F	۲	Ä	Ę	5	Ę	LN N	N	Į.	LN	L'N	. 1	EST_HUMAN	Ę	Ł	LN T	LN.
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Most Similar (Top) Hit Tell BLAST E Value	0.0E+00 BE222374.1	0.0E+00	0.0E+00 H30132.1	0.0E+00 H30132.1	0.0E+00 A1149880.1	0.0E+00 Z80780.1	0.0E+00 Z80780.1	0.0E+00	0.0E+00	0.0E+00	0.0E+00 M75980.1	0.0E+00.0	0.0E+00	0.0E+00	0.0E+00 M75980.1	0.0E+00	0.0E+00	0.0E+00	0.0E+00/				Ш		0.0E+00			0.0E+00	
Expression Signal	108	3.2	4.3	4.3	0.97	10.28	10.28	21.3				1.85			2.54				3.33	4,		3.2		7.55	1.7	24.06	6	24.99	
ORF SEQ ID NO:	27955	27957	_			27963			27976					27990				28005	28027	L		28074	L		5 28085	١			
Exon SEQ ID NO:	14865	14856	14869	14869	14871	14872	14872	14875	14883	14886	14890	14890	14893	14896	14896	14900	14902	14911	14933	16047	14978	14978		1	١.	<u>L</u> .	14998		<b>1</b>
Probe SEQ ID 8	12.7	17.16	1740	1, 1, 1	1771	1722	1722	1725	1734	1737	1741	1741	1744	1747	1747	1751	1763	1762	1784	1826	1830	1830	1833	1837	1839	1850	1852	1863	1863

Page 494 of 550 Table 4 Single Exon Probes Expressed in Placenta

Top Hit Descriptor  Homo sapiens activating transcription factor 4 (tax-responsive enhancer element B67) (ATF4) mRNA  Homo sapiens immunoglobin superfamily, member 3 (IGSF3) mRNA, and translated products  Homo sapiens Retina-derived POU-domain factor-1 (RPF-1), mRNA  Homo sapiens Retina-derived POU-domain factor-1 (RPF-1), mRNA  Homo sapiens Retina-derived POU-domain factor-1 (RPF-1), mRNA  Homo sapiens Retina-derived POU-domain factor-1 (RPF-1), mRNA  Homo sapiens Retina-derived POU-domain factor-1 (RPF-1), mRNA  Homo sapiens mRNA for KIAA1152 protein, partial cds  Homo sapiens mRNA for KIAA1152 protein, partial cds  Homo sapiens mRNA for KIAA1152 protein, partial cds  Homo sapiens potassium voltage-gated channel, Shab-related subfamily, member 1 (KCNB1) mRNA  Homo sapiens potassium voltage-gated channel, Shab-related subfamily, member 1 (KCNB1) mRNA  Homo sapiens potassium voltage-gated channel, Shab-related subfamily, member 1 (KCNB1) mRNA  Homo sapiens potassium voltage-gated channel, Shab-related subfamily, member 1 (KCNB1) mRNA  Homo sapiens potassium voltage-gated channel, Shab-related subfamily, member 1 (KCNB1) mRNA  Homo sapiens nuclear protein (NPZ20), mRNA  Homo sapiens mRNA for KIAA1367 protein, partial cds  Homo sapiens RAD1 (S. pombe) homolog (RAD1) mRNA, and translated products  Homo sapiens RAD1 (S. pombe) homolog (RAD1) mRNA, and translated products  Homo sapiens RAD1 (S. pombe) homolog (RAD1) mRNA, and translated products  Homo sapiens RAD1 (S. pombe) homolog (RAD1) mRNA, and translated products  Homo sapiens RAD1 (S. pombe) homolog (RAD1) mRNA, and translated products  Homo sapiens RAD1 (S. pombe) homolog (RAD1) mRNA, and translated products  Homo sapiens RAD1 (S. pombe) homolog (RAD1) mRNA, and translated products  Homo sapiens RAD1 (S. pombe) homolog (RAD1) mRNA, and translated products  Homo sapiens RAD1 (S. pombe) homolog (RAD1) mRNA, and translated products										(LLL)				
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Γ		Т	Т	Т	Т	Т	Т	Т	Т	Т	Τ	1	Т	Т	Т	Т	Т	Т	T	т	Τ	Ť	T	Ĺ	Ţ	Ť	۳	1.4	Ť	Ť	7	1	JI SI	T Shart
	Top Hit Descriptor	bb73f11.y1 NIH MGC_12 Homo sapiens cDNA clone IMAGE:3048045 5'	Homo sapiens histidine ammonia-lyase (HAL) mRNA	Homo sapiens histidine ammonia-lyase (HAL) mRNA	Homo sapiens chromosome 21 segment HS21C052	Homo saplens nebulin (NEB), mRNA	Homo sapiens nebulin (NEB), mRNA	Homo sapiens actinin, alpha 4 (ACTN4) mRNA	Homo sapiens actinin, alpha 4 (ACTN4) mRNA	Homo sapiens mRNA for KIAA0790 protein, partial cds	Homo saplens mRNA for KIAA0790 protein, partial cds	Human TFEB protein mRNA, partial cds	Human TFEB protein mRNA, partial cds	x169b01.x1 NCI_CGAP_Part Homo saplens cDNA clone IMAGE:2679913.3	x169b01.x1 NCI_CGAP_Pan1 Homo saplens cDNA clone IMAGE:2679913 3	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA	Homo saplens mRNA for KIAA0577 protein, complete cds	H.sapiens genes for samenogelin I and semenogelin II	H.sapiens genes for semenogelin I and semenogelin II	Homo saplens mRNA for KIAA1513 protein, partial cds	Homo sapiens SMCY (SMCY) gene, complete ods	Homo sepions SMCY (SMCY) gene, complete cds	Homo sapiens chromosome 21 open reading frame 7 (YG81), mRNA	Homo saplens TP53TG3a (TP53TG3a), mRNA	601573895F1 NIH_MGC_9 Hamo sapiens cDNA clone IMAGE:3835198 5'	601573895F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3835198 5'	Homo sapiens coagulation factor IX (plasma thromboplastic component, Christmas disease, hemophilia B)	4 1440834 DI ACEA Warms senions aDNA clara DI ACEA000034 E	Homo canians K18 64144 inchiair (K18 64144), mBNA	Homo sanjons Kiada144 protein (Kiada144) mRNA	7822F10 Chromosome 7 Fedel Brain cDNA Library Home canions cDNA close 2020E10	7B22E10 Chromosome 7 Fetal Brain cDNA Library Homo sapiens cDNA clone 7B22E10	Homo sapiens similar to rat integral membrane glycoprotein POM121 (POM121L1), mRNA
	Top Hit Database Source	EST HUMAN	Ę	LN	LN L	NT.	NT	Z	Z-	LN PA	FZ	FN	FZ	EST HUMAN	EST_HUMAN	N-	LN	LN L	Ę	FN	FZ	۲	LΝ	TN	NT	EST_HUMAN	EST_HUMAN		EST LIBAAN	-1	LV.	EST HIMAN	EST HUMAN	FA
5	Top Hit Acession No.	3.0E+00 BE018066.1	4809282 NT	4809282 NT	3.0E+00 AL163252.2	8400716 NT	8400716 NT	4826638 NT	4826638 NT	3.0E+00 AB018333.1	3.0E+00 AB018333.1			.0E+00 AW193024.1	.0E+00 AW193024.1	6912457 NT	6912457 NT	9.1					0.0E+00 AF273841.1	8394546 NT	7706742 NT	0.0E+00 BE743215.1	.0E+00 BE743215.1	TN 850364B	0.0E+00 A11440824 4	55.05	7705565 NT	0.0E+00 AA077589 1		37468
	Most Similar (Top) Hit BLAST E Value	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.05+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00 M33782.1	0.0E+00 M33782.1	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00 Z47556.1	0.0E+00 Z47556.1	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.05+00	O OF TOO	00+100	00+400	0.0F+00.0	0.0E+00	0.0E+00
	Expression Signal	1.3	1.69	1.69	1.04	1.41	1.41	12.98	12.98	2.11	2.11	1.93	1.93	3.24	3.24	89.6	9.68	1.53	1.09	1.09	5.04	1.85	1.85	1.53	0.98	35.36	35.36	1 02	57.03	78.0	26.0	2.59	2.59	3.79
	ORF SEQ ID NO:	28250	28255					28274					28294			28297		28300	28301	28302			28338	28368		28374		28376	28378	27694	27695	28380	28381	
	Exon SEQ ID NO:	15145	15151	15151		15167		15168	15168	15178	15178	15184	15184	15186	15186	15187			15190			15218			15250	15255	15255	15257	1525g	14612	14612	15260	15260	15262
	Probe SEQ ID NO:	2002	2011	2011	2024	2026	2028	2027	2027	2037	2037	2043	2043	2045	2048	2046	2046	2048	2049	2049	2026	2078	2078	2109	2112	2117	2117	2119	27.21	2122	2122	2124	2124	2126

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Top Hit Descriptor	Hamo sapiens phosphodiesterase 6A. cGMP-specific rod alpha (PDE6A) mRNA	HSCOIC021 normalized infant brain cDNA Homo sapiens cDNA clone c-0ic02	qv90f08.x1 NCI_CGAP_Utz Homo sapiens cDNA clone IMAGE:1988871 3' similar to contains Alu repetitive	element;	00 1465 140FT NITE WISC. 59 HOMO SEPTEMS CLINA CIONE IMAGE: 388 / 147 5	601902804F1 NIH_MGC_19 Hamo sapiens cDNA clone IMAGE:4135320 5'	601802604F1 NIH_MGC_19 Hamo saplens cDNA clone IMAGE:4135320 5'	RC3-CT0413-270700-022-d10 CT0413 Homo saplens cDNA	RC3-CT0413-270700-022-d10 CT0413 Home saplens cDNA	Human plasma membrane calcium ATPase isoform 2 (APT2B2) mRNA, comlete cds	Human plasma membrane calctum ATPase isoform 2 (APT2B2) mRNA, comlete cals	Homo sapiens mRNA for CDC2I 5 protein kinasa (CDC2I 5 gans) isoform 1	Homo sepiens GTP binding protein 1 (GTPBP1) mRNA	783402.x1 NCI_CGAP_GC6 Homo saplens cDNA clone IMAGE 3220610 3' similar to SW:DTD_HUMAN	P50443 SULFATE TRANSPORTER;	QV1-GN0065-140800-318-c10 GN0065 Homo saplens cDNA	Homo sapiens X-linked Juvenile refinoschisls protein (XLRS1) gene, exon 6 and complete cds	601672066F1 NIH_MGC_20 Homo sapiens cDNA cione IMAGE:3954785 5'	PM0-BT0547-210300-004-F04 BT0547 Homo sapiens cDNA	Homo saplens glutathione S-fransferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1)	genes, complete cds	IL3-C10219-271099-022-G10 C10219 Homo sapiens cDNA	QV-BT066-020399-092 BT065 Homo saplens cDNA	QV-BT065-020399-092 BT065 Homo sapiens cDNA	Homo sapiens potassium large conductance calcium-activated channel, subfamily M, beta member 3-like	(KCNMB3L), mRNA	Human DNA-binding protein mRNA, 3'end	601122338F1 NIH_MGC_20 Homo saplens cDNA done IMAGE:3346688 5	Human mRNA for KIAA0244 gene, partial cds	AV738288 CB Homo sapiens cDNA clone CBNBDE08 5	AV738288 CB Homo saplens cDNA clone CBNBDE08 5	oc32e01.s1 NCI_CGAP_Lu5 Hamo sapiens cDNA clone IMAGE:15678963'	602014829F1 NCI_CGAP_Brn64 Homo saplens cDNA clone IMAGE:4150734 5	601572186T1 NIH_MGC_55 Homo saplens cDNA done IMAGE:38390123'
Top Hit Database Source	Ž	EST_HUMAN		EST HUMAN	NIWAIN TO I SE	EST_HUMAN	EST HUMAN	<b>EST_HUMAN</b>	EST_HUMAN	N	NT	NT	TN	1000	EST_HUMAN	EST_HUMAN	N	EST HUMAN	EST_HUMAN		Ν			EST_HUMAN	!	Į.		EST_HUMAN	¥	EST_HUMAN	EST HUMAN	EST_HUMAN		EST_HUMAN
Top Hit Acession No.	4585863 NT	<b>—</b>		0.0E+00 AI244247.1	05011253.1	0.0E+00 BF315325.1	0.0E+00 BF315325.1	3.0E+00 BE697125.1	0.0E+00 BE697125.1	.00620.1	.00620.1	3.0E+00 AJ297709.1	4758489 NT	T COOPE 4	J.UE+UU BESUUSES.1	0.0E+00 BE767964.1	3.0E+00 AF018963.1		0.0E+00 BE072624.1			0.0E+00 AW752708.1	0.0E+00 Al904640.1	0.0E+00 AI904640.1		7657252 NT	.14787.1	.0E+00 BE274696.1	.0E+00 D87685.1	0.0E+00 AV738288.1	.0E+00 AV738288.1	0,0E+00 AA931591.1	BF344434.1	0.0E+00 BE748899.1
Most Similar (Top) Hit BLAST E Value	0.0E+00	0.0E+00 Z42399	00.70	0.01	0.01.00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00 L00620.1	0.0E+00 L00620.1	0.0E+00	0.0E+00	000	0.05+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00		0.0E+00/	0.0E+00	0.0E+00/	0.0E+00 /	ı	0.0E+00	0.0E+00 L14787.1	0.0E+00	0.0E+00[	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00 E
Expression Signal	1.48	2.9	000	2.38		225	225	3.6	3.6	3.43	3.43	1.11	1.16	70,	<u> </u>	3.17	1.26	4.84	1.5		8	3.41	6.48	6.48		1.08	1.52	1.26	0.94	23.12	23.12	2.57	24.38	40.14
ORF SEQ ID NO:		28384		28303	1000	28395	28396	28404	28405				28420	26/32	77-07			28446	28447	-	28448	28450	28452	28453		1		28518	28521	28622	28523	28525	28529	28530
Exen SEQ ID NO:		15265	15057	15272	L	$_{\perp}$	15274				15288		15294	15208	02701	- [		- [	15321		15323	15325	15327	15327	0000	1225	16382	15392	15394	15395	15395	15397	15401	15402
Probe SEQ ID NO:	2128	2129	24.33	2136		7138	2138	2144	2144	2152	2152	2153	2158	2462	2012	2182	2183	2185	2186	-	2188	2190	2192	2192	2226	C777	2249	2259	2261	2262	2262	2264	2268	2269

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	Top Hit Descriptor	GM1-TN0141-250900-439-b08 TN0141 Homo sapiens cDNA	CN41-TN0141-250900-439-b08 TN0141 Homo saplens cDNA	Control of the MCC 10 Home series cONA clone IMAGE 4129622 5	00180020111 Nin Wood 19 10010 September 2008 10 10 10 10 10 10 10 10 10 10 10 10 10	TRANSCRIPTION FACTOR S-IL-RELATED PROTEIN;	2453-07.s1 Soares_pregnant_uterus_NbHPU Homo sapiens cUNA clone involct_recovery 5 similar to darx66867_cds1 OLFACTORY RECEPTORLIKE PROTEIN HOMPORE (HUMAN) approximation of darx66867_cds1 OLFACTORY RECEPTORLIKE PROTEIN PROME SAX SIMILAR TO DARX SIMILAR TO DARX SIMILAR TO DARX SIMILAR TO DARX SIMILAR TO DARX SIMILAR TO DARX SIMILAR TO DARX SIMILAR TO DARX SIMILAR TO DARX SIMILAR TO DARX SIMILAR TO DARX SIMILAR TO DARX SIMILAR TO DARX SIMILAR TO DARX SIMILAR TO DARX SIMILAR TO DARX SIMILAR TO DARX SIMILAR TO DARX SIMILAR TO DARX SIMILAR TO DARX SIMILAR TO DARX SIMILAR TO DARX SIMILAR TO DARX SIMILAR TO DARX SIMILAR TO DARX SIMILAR TO DARX SIMILAR TO DARX SIMILAR TO DARX SIMILAR TO DARX SIMILAR TO DARX SIMILAR TO DARX SIMILAR TO DARX SIMILAR TO DARX SIMILAR TO DARX SIMILAR TO DARX SIMILAR TO DARX SIMILAR TO DARX SIMILAR TO DARX SIMILAR TO DARX SIMILAR TO DARX SIMILAR TO DARX SIMILAR TO DARX SIMILAR TO DARX SIMILAR TO DARX SIMILAR TO DARX SIMILAR TO DARX SIMILAR TO DARX SIMILAR TO DARX SIMILAR TO DARX SIMILAR TO DARX SIMILAR TO DARX SIMILAR TO DARX SIMILAR TO DARX SIMILAR TO DARX SIMILAR TO DARX SIMILAR TO DARX SIMILAR TO DARX SIMILAR TO DARX SIMILAR TO DARX SIMILAR TO DARX SIMILAR TO DARX SIMILAR TO DARX SIMILAR TO DARX SIMILAR TO DARX SIMILAR TO DARX SIMILAR TO DARX SIMILAR TO DARX SIMILAR TO DARX SIMILAR TO DARX SIMILAR TO DARX SIMILAR TO DARX SIMILAR TO DARX SIMILAR TO DARX SIMILAR TO DARX SIMILAR TO DARX SIMILAR TO DARX SIMILAR TO DARX SIMILAR TO DARX SIMILAR TO DARX SIMILAR TO DARX SIMILAR TO DARX SIMILAR TO DARX SIMILAR TO DARX SIMILAR TO DARX SIMILAR TO DARX SIMILAR TO DARX SIMILAR TO DARX SIMILAR TO DARX SIMILAR TO DARX SIMILAR TO DARX SIMILAR TO DARX SIMILAR TO DARX SIMILAR TO DARX SIMILAR TO DARX SIMILAR TO DARX SIMILAR TO DARX SIMILAR TO DARX SIMILAR TO DARX SIMILAR TO DARX SIMILAR TO DARX SIMILAR TO DARX SIMILAR TO DARX SIMILAR TO DARX SIMILAR TO DARX SIMILAR TO DARX SIMILAR TO DARX SIMILAR TO DARX SIMILAR TO DARX SIMILAR TO DARX SIMILAR TO DARX SIMILAR TO DARX SIMILAR TO DARX SIMILAR TO DARX SIMILAR T	2453-07.s1 Soares_pregnant_uterus_NbHPU Homo septens.cUNA cione innAct—Accado Similia Caba.X65867_cds1 OLFACTORY RECEPTOR-LIKE PROTEIN HOMPOTE (HUMAN);	Homo saplens chromosome z i segment noz rocor	Homo sapiens chioilosome z Josephanic Pozicos	Homo capiens KIAAU952 protein (KIAA0952), IIIIXAYA	Homo sapiens Kirkhusuz protein (Kirkhusuz), mikani	Human beta-prime-goagon (PANZZ) gene, com 1.5	2112010:11 NO CON CONTROL OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF T	Homo squens E. 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Coo)	Notice septials in November 27 Home seriens ODIA clone IMAGE:3918607 5	BO 1433225F I NIT MICC 70 Home sapiens CDNA clone IMAGE:3897457 5'	Red 405-206 1 NH MGC 70 Homo sapiens cDNA clone IMAGE 3897457 5	United Services mRNA for KIAA1363 protein, partial cds	Home satiens differentially expressed in FDCP (mouse homolog) 6 (DEF6), mRNA	Homo saniens differentially expressed in FDCP (mouse homolog) 6 (DEF6), mRNA	And 2012 At Spares fetal liver spleen 1NFLS S1 Homo sapiens cDNA clone IMAGE:1674828 3	778-11 r1 Sources total fetus Nb2HF8 9w Homo saplens cDNA clone IMAGE:759740 5	777811 r1 Searce total fetus Nb2HF8 9w Homo saplens cDNA clone IMAGE:759740 5	AND 1848F1 NCI CGAP Brn67 Homo sapiens cDNA clone IMAGE:4157339 5'	Home senions mRNA for KIAA0910 protein, partial cds	Home seniars mRNA for KIAA0910 protein, partial cds	Homo caniabs flavin containing monooxygenase 3 (FMO3), mRNA	7427-02 VA NCI CGAP CLI 1 Homo sapiens cDNA clone IMAGE:3295370 3' similar to TR:094939 094939	KIAA0867 PROTEIN;	Homo sapiens phosphoryase Kinase alpha subulnit (Prinkiz) gene, evol 32	ty57c08.x1 NCI_CGAP_Utz Homo saptens culture clinic livrocizzo. 102	
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Top Hit Descriptor	Homo sapiens gene for AF-8, complete cds	Homo sapiens KIAA0952 protein (KIAA0952), mRNA	Homo septens KIAA0952 protein (KIAA0952), mRNA	Hamme censions energy short and sentition 2 (SSFA2), mRNA	Figure capters open resident (SSEA2) mRNA	HOMO SADIGLIS SPELLING TO THE THE TANK A CRISTO SET OF THE TANK A CRISTO SET OF THE TANK A CRISTO SET OF THE TANK A CRISTO SET OF THE TANK A CRISTO SET OF THE TANK A CRISTO SET OF THE TANK A CRISTO SET OF THE TANK A CRISTO SET OF THE TANK A CRISTO SET OF THE TANK A CRISTO SET OF THE TANK A CRISTO SET OF THE TANK A CRISTO SET OF THE TANK A CRISTO SET OF THE TANK A CRISTO SET OF THE TANK A CRISTO SET OF THE TANK A CRISTO SET OF THE TANK A CRISTO SET OF THE TANK A CRISTO SET OF THE TANK A CRISTO SET OF THE TANK A CRISTO SET OF THE TANK A CRISTO SET OF THE TANK A CRISTO SET OF THE TANK A CRISTO SET OF THE TANK A CRISTO SET OF THE TANK A CRISTO SET OF THE TANK A CRISTO SET OF THE TANK A CRISTO SET OF THE TANK A CRISTO SET OF THE TANK A CRISTO SET OF THE TANK A CRISTO SET OF THE TANK A CRISTO SET OF THE TANK A CRISTO SET OF THE TANK A CRISTO SET OF THE TANK A CRISTO SET OF THE TANK A CRISTO SET OF THE TANK A CRISTO SET OF THE TANK A CRISTO SET OF THE TANK A CRISTO SET OF THE TANK A CRISTO SET OF THE TANK A CRISTO SET OF THE TANK A CRISTO SET OF THE TANK A CRISTO SET OF THE TANK A CRISTO SET OF THE TANK A CRISTO SET OF THE TANK A CRISTO SET OF THE TANK A CRISTO SET OF THE TANK A CRISTO SET OF THE TANK A CRISTO SET OF THE TANK A CRISTO SET OF THE TANK A CRISTO SET OF THE TANK A CRISTO SET OF THE TANK A CRISTO SET OF THE TANK A CRISTO SET OF THE TANK A CRISTO SET OF THE TANK A CRISTO SET OF THE TANK A CRISTO SET OF THE TANK A CRISTO SET OF THE TANK A CRISTO SET OF THE TANK A CRISTO SET OF THE TANK A CRISTO SET OF THE TANK A CRISTO SET OF THE TANK A CRISTO SET OF THE TANK A CRISTO SET OF THE TANK A CRISTO SET OF THE TANK A CRISTO SET OF THE TANK A CRISTO SET OF THE TANK A CRISTO SET OF THE TANK A CRISTO SET OF THE TANK A CRISTO SET OF THE TANK A CRISTO SET OF THE TANK A CRISTO SET OF THE TANK A CRISTO SET OF THE TANK A CRISTO SET OF THE TANK A CRISTO SET OF THE TANK A CRISTO SET OF THE TANK A CRISTO SET OF THE TANK A CRISTO SET OF THE TANK A CRISTO SET OF THE TANK A CRISTO SET OF THE TANK A CRISTO SET OF THE TANK A CRIST	Homo sapiens signal regulatory protein, Deta, 1 (Cirk - PETITY) III www.	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Sycomome P450 A (CYP3A4) genes, complete cds; and cytochrome P450	4 (CTPAA) and Cycell and Care partial cds	AU118082 HEMBA1 Homo sepiens cDNA clone HEMBA1002839 5	AI1/18082 HEMBA1 Homo sepiens cDNA clone HEMBA1002839 5	AI 1418082 HEMBA1 Homo saplens cDNA clone HEMBA1002839 5	A BARBATO ROMEDIA AND BARBATO HOMO Sablens CDNA	NIRG-DIVIDIVE ACCOUNTED A LICENS A LICENS A CHARACTER A TOOR 155 5	AUT19362 HEMBAT TRUIT SALIES COLOR SOLICE TEMPORARY 3' SIMILAR TO TRIO08662	0x80b02.x1 Soares_INHMPu_S1 home saperts curve rune invace 1xxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxx	Homo sapiens hypothetical protein recovery in a system sapiens hypothetical protein recovery in a system sapiens and second system system system system system system system system system system system system system system system system system system system system system system system system system system system system system system system system system system system system system system system system system system system system system system system system system system system system system system system system system system system system system system system system system system system system system system system system system system system system system system system system system system system system system system system system system system system system system system system system system system system system system system system system system system system system system system system system system system system system system system system system system system system system system system system system system system system system system system system system system system system system system system system system system system system system system system system system system system system system system system system system system system system system system system system system system system system system system system system system system system system system system system system system system system system system system system system system system system system system system system system system system system system system system system system system system system system system system system system system system system system system system system system system system system system system system system system system system system system system system system system system system system system system system system system system system system system system system system system system system system system system system system system system system system system system system system system system system system syst	801432608F1 NIH MGC 72 Homo sapiens clond cione image39191030	AB005622 HeLa CUNA (1. 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Page 499 of 550 Table 4 Single Exon Probes Expressed in Placenta

Top Hit Descriptor	III.HF-BP0p-ais-c-07-0-Ulr1 NIH MGC 51 Homo sapiens cDNA clone IMAGE:3072780 5	English Strate Strate Strate Strate Strate Strate Strate Strate Strate Strate Strate Strate Strate Strate Strate Strate Strate Strate Strate Strate Strate Strate Strate Strate Strate Strate Strate Strate Strate Strate Strate Strate Strate Strate Strate Strate Strate Strate Strate Strate Strate Strate Strate Strate Strate Strate Strate Strate Strate Strate Strate Strate Strate Strate Strate Strate Strate Strate Strate Strate Strate Strate Strate Strate Strate Strate Strate Strate Strate Strate Strate Strate Strate Strate Strate Strate Strate Strate Strate Strate Strate Strate Strate Strate Strate Strate Strate Strate Strate Strate Strate Strate Strate Strate Strate Strate Strate Strate Strate Strate Strate Strate Strate Strate Strate Strate Strate Strate Strate Strate Strate Strate Strate Strate Strate Strate Strate Strate Strate Strate Strate Strate Strate Strate Strate Strate Strate 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Probe SEQ ID	2700		2744	2745	2718	2721	2721	2724	2727	2728	2763	2788	27,80	279	2792	2797	2800	2801	2803	2803	2804	2805	2806	9087 7800	2810	2810	2813	, 6	2818	2827	2828

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Top Hit Descriptor	Homo saniens chondrolitin sulfate proteoclivean 4 (melanoma-associated) (CSPG4), mRNA	A CANCO MANAGEMENT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONT	Homo saptens angiopoeuiro (AINC-5), minera	Homo saptens anglopdietlin-3 (ANG-3), mRNA	602085579F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4249915 5	Homo sapiens protein tyrosine phosphatase, receptor type, T (PTPRT), mRNA	AV725534 HTC Hamo sapiens aDNA alone HTCCCA03 5'	AV725534 HTC Homo sapiens cDNA clone HTCCCA03 5'	au§5d04.yf Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2518663 5' similar to SW:R13A HUMAN P40429 60S RIBOSOMAL PROTEIN L13A ;	602071957F1 NCI_CGAP_Bm67 Homo sepiens cDNA clone IMAGE:4214679 5	601450912F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3854642 5	AU131494 NT2RP3 Hano sepiens cDNA clone NT2RP3002672 5	AU131494 NT2RP3 Hamo sapiens aDNA clone NT2RP3002672 5'	600944794F1 NIH_MGC_17 Homo saplens cDNA clone IMAGE:2980806 5'	600944794F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:2960806 5	glycoprotein D≐Duffy group antigen [fruman, blocd, Genomic DNA, 3068 nt]	Homo sapiens BTRCP2 mRNA for F-box and WD-repeats protein isoform C, complete cds	Homo sapiens ALR-like protein mRNA, partial cds	Homo sapiens ALR-like protein mRNA, pertial cds	Homo sapiens cytochrome P450, subfamily I (dioxin-inducible), polypeptide 1 (glaucoma 3, primary infantile) (CYP1B1) mRNA	Homo sapiens cytochrome P450, subfamily I (dioxin-inducible), polypeptide 1 (glaucoma 3, primary infantile) 🖽	IRNA	H. sapiens serine hydroxymethyltransferase pseudogene	Homo sapiens 5-aminolevulinate synthase 2 (ALAS2) gene, complete cds	Homo sapiens mRNA for KIAA1627 protein, partial cds	Homo sepiens chromosome 21 segment HS21C001	Human AHNAK nucleoprotein mRNA, 5' end	PM0-HT0343-281299-003-e02 HT0343 Homo sapiens cDNA	PM0-HT0343-281299-003-e02 HT0343 Homo sapiens cDNA	H. sapiens Id3 gene for HLH type transcription factor	Homo sapiens chromosome 21 segment HS21C068	Homo sapiens zinc finger protein 221 (ZNF221), mRNA	Homo sapiens zinc finger protein 221 (ZNF221), mRNA
	domo sapie		10mo sapre	Homo saple	302085579	Ното sapie	4/725534	4V725534	au55d04.y1 SW:R13A	302071957	301450912	AU131494	4U131494	500944794	300944794	plycoprotein	-lomo sapie	Homo saple	Homo sapie	Homo sapiens cyt (CYP1B1) mRNA	Homo sapie	(CYP1B1) mRNA	H.sapiens s	Homo sapie	Homo saple	Homo sapie	Human AHI	PM0-HT03-	PM0-HT03	H.sapiens	Homo sapie	Homo sapie	Homo sapie
Top Hit Database Source					I_HUMAN		T_HUMAN	EST_HUMAN /	EST HUMAN	Т	EST HUMAN		Г	EST_HUMAN	EST_HUMAN		INT	NT	INT.				IN	L		NT.	μN	EST_HUMAN	L-HUMAN		NT		
Top Hit Acession No.	4503098 NT	20000	7705275	7705275 NT	0.0E+00 BF677694.1	7427522 NT	0.0E+00 AV725534.1	0.0E+00 AV725534.1	0.0F+00 A1879163 1	0,0E+00 BF530661.1	0.0E+00 BE872768.1	0.0E+00 AU131494.1	0.0E+00 AU131494.1	0.0E+00 BE300344.1	0.0E+00 BE300344.1	0.0E+00 S76830.1		0.0E+00 AF264750.1	0.0E+00 AF264750.1	4503202 NT		4503202 NT	0.0E+00 X85980.1	0.0E+00 AF068624.1	0.0E+00 AB040960.1	0.0E+00 AL163201.2	0.0E+00 M80902.1	0.0E+00 BE154504.1	0.0E+00 BE154504,1	X73428.1	0.0E+00 AL163268.2	7019584 NT	7019584 NT
Most Similar (Top) Hit BLAST E	0.05+00		0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.05+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0 0 + 00		0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00 X73428.1	0.0E+00	0.0E+00	0.0E+00
Expression Signal	187		1.08	1.08	50.5	1.33	17.21	17.21	14 75	2.14	71.97	2.42	2.42	64.06	64.06	5.26	1.64	8.	1.89	204		2.04	3.73	1.26	1.91	4.25	6.5	0.93	0.93	2.05	2.6		1.3
ORF SEQ ID NO:			29062	29063	29064	29072	29075			29081	29082	29083	29084	29085	29086					78276		27288				29099							29109
Exon SEQ ID NO:	15040	L	15955	15955	L		<u> </u>	15966	ļ .	<u>1</u>	15972	15974	15974	15975	15975	13415	ı	13933	l	14230	L	14230	16076	16077	16079	Ĺ	L		ĺ	1	1	16097	
Probe SEQ ID NO:	2000	3	2841	2841	2842	2848	2852	2852	2854	2857	2858	2860	2860	2861	2861	2867	2870	2876	2876	2880		2880	2897	2898	2900	2907	2911	2914	2914	2916	2918	2919	2919

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Top Hit Descriptor	ALL AND THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY	Homo sapiens zinc finger protein 221 (ZNF221), mRNA	Human transglutaminase mRNA, complete cds	Homo sapiens gammma-cytoplasmic actin (ACTGP3) pseudogene	Homo sapiens gammma-cytoplasmic actin (ACTGP3) pseudogene	Novel human mRNA from chromosome 1, which has similarities to BAT2 genes	H.sapiens mRNA for nuclear DNA helicase II	Homo sapiens protocadherin alpha C1 (PCDH-alpha-C1) mRNA, complete cds	Homo sapiens eukaryotic translation elongation factor 1 alpha 1 (EEF1A1) mRNA	Homo sapiens eukaryotic translation elongation factor 1 alpha 1 (EEF1A1) mRNA	Homo sapiens serine/threonine kinase 9 (STK9) mRNA	DKFZp586G0621_r1 586 (synonym: hute1) Homo sapiens cDNA clone DKFZp586G0621	Homo sapiens KIAA0054 gene product; Helicase (KIAA0054), mRNA	Homo sapiens KIAA0054 gene product, Helicase (KIAA0054), mRNA	Homo sapiens chondroitin sulfate proteoglycan 4 (melanoma-associated) (CSPG4), mKNA	QV2-BT0636-130400-138-h03 BT0636 Homo sapiens cDNA	QV2-BT0636-130400-138-h03 BT0636 Homo sapiens cDNA	Homo saplens low density lipoprotein-related protein 2 (LRP2), mRNA	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA	Homo saplens chromosome 21 segment HS21C006	Homo sapiens chromosome 21 segment HS21C006	zg6b11.s1 NCI_CGAP_GCB1 Homo saplens oDNA clone IMAGE:683517 3' similar to contains Alu	repetitive element;	Homo sapiens innob gene to that kerauri, exons 1 to 9	Homo sapiens EphA4 (EPHA4) mKNA	Homo sapiens eukaryotic translation elongation factor 1 alpha 1 (EEF141) mKNA	In18d07.x1 NCI_CGAP_Brn25 Homo sapiens cDNA done IMAGE:2167981 3 similar to 1 K:U15247	016247 F44E7.2 PKOLEIN.;	in18d07.x1 NCI_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2167981 3' similar to 1 R:016247	O16247 F44E7.2 PROTEIN.;	ZINC FINGER PROTEIN 132	Homo sapiens protocadherin gamma C4 (PCDH-gamma-C4) mRNA, complete cds	Homo sapiens mRNA for KJA41267 protein, partial cds	Homo sapiens mRNA for KIAA1267 protein, partial cds	Homo saplens mRNA for KIAA1508 protein, partial cds
Top Hit Database Source			LΝ		ᅜ	NT NT	NT	F		NT	TN	EST HUMAN	۲	NT	LN	EST_HUMAN	EST_HUMAN	FZ	NT	IN	. TN		EST_HUMAN	Į.N.	Į.	Z		EST_HUMAN		EST_HUMAN	SWISSPROT	TN	L	ΤN	L
Top Hit Acession No.		7019584 NT							0.0E+00 4503470 NT	4503470 NT	4507280 NT	L047599.1	0.0E+00 7661883 NT	7661883 NT	4503098 NT	0.0E+00 BE081898.1	0.0E+00 BE081896.1	G806918 NT	6806918 NT	0.0E+00 AL163206.2	0.0E+00 AL163205.2		0.0E+00 AA215579.1		4758279 NT	4503470 NT		.0E+00 AI561002.1		.0E+00 AI561002.1	P52740	0.0E+00 AF152338.1	.0E+00 AB033093.1	0.0E+00 AB033093.1	3.0E+00 AB040941.1
Most Similar (Top) Hit BLAST E	, and	0.0E+00	0.0E+00 M98478.1	0.0E+00 D50657.1	0.0E+00 D50657.1	0.0E+00	0.0E+00 Y10658.1	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00/	0.0E+00		0.0E+00	0.0E+00 Y19210.1	٦	0.0E+00		0		0	0.0E+00 P52740		٥		
Expression Signal		1.3	15.94	30.49	30.49	3.42	6.12	1.13	74.83	74.83	254	1.19	96.0	96.0	2.44						2.3					25.96		1.15		1.15	1.18		3.4		6.2
ORF SEQ ID NO:		29110							29122		29134			29140			L		29152			l	29158			29170		1 29171	L		3 29174			29188	
Exan SEQ ID		ľ		ľ		1		1	1	ı		16124	1	1	16126	1	ı	1	1	16138	1		- 1		16148	16150	1	16151	ı		16153	١.	ı		1 1
Probe SEQ ID NO:		2919	2921	2926	2926	2929	2930	2931	2932	2932	2944	2947	2948	2948	2949	2952	2952	2958	2958	2964	2961		2962	2969	2972	2974		2975		2975	2977	2978	2994	2994	2995

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Offigin Living Laboratory in the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the con	ORF SEQ Expression (Top) Hit Top Hit Acession Database ID NO: Signal BLAST E No. Source	29190 6.2 0.0E+00 AB040941.1 NT	29193 3.31 0.0E+00 7661903 NT	29194 3.31 0.0E+00 7661903 NT	29195 4.93 0.0E+00 5174574 NT	29196 4.93 0.0E+00 5174574 NT	29199 1.29 0.0E+00 BF110702.1 EST_HUMAN	. 29200 1.29 0.0E+00 BF110702.1 EST_HUMAN	29211 3.91 0.0E+00 4505084 NT	29212 3.91 0.0E+00 4505084 NT	29218 1.51 0.0E+00 4758827 NT	29221 0.98 0.0E+00 AB033034.1  NT	29223 9.6 0.0E+00 AF106275.1 NT	1.44 0.0E+00 A1149880.1 [EST_HUMAN	29242 0.71 0.0E+00 AF281074.1 NT	29243 0.71 0.0E+00 AF281074.1 NT	29244 0.92 0.0E+00 4506118 NT	29245 2.81 0.0E+00 AB004884.1 NT	29252 1.85 0.0E+00 7862273 NT	29253 1.92 0.0E+00 AW612528.1 EST_HUMAN	29254 2.4 0.0E+00 5729755 NT	29255 2.4 0.0E+00 5729755 NT	29263 1.17 0.0E+00 AF114488.1 NT	29264 1.17 0.0E+00 AF114488.1 NT	0.61 0.0E+00 AL163246.2 NT	29285 1.29 0.0E+00 M74099.1 NT	29292 0.68 0.0E+00 4506882 NT	3.53 0.0E+00 AF195953.1 NT	29303 4.9 0.0E+00 5579469 NT	
		29190	29193	29194	29195	29196	29199	29200	29211	29212	29218	29221	29223		29242	29243	29244	29245	29252		Ì	1	29263	29264						
	Exan D SEQ ID NO:	35 16171	16174	16174			l	3 15178	Ĺ	Ĺ	Ľ			38 16214		ll			57 16233	i i	ı	1	ı	L	<u> </u>	L	L		l	12 16288
	Probe SEQ ID NO:	296	Ř	2998	2999	2990	3003	3003	3011	3011	3019	30	3024	3038	ဇ္တိ	3045	ဇ္ဇ	3047	ဗ္ဗိ	) Ř	ĕ	3059	3067	3067	ဗ္ဗ	3093	3102	3109	3112	31

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Top Hit Descriptor	soform 2 of a novel human mRNA from chromosome 22	Homo sapiens putative transcription factor CR53 (CR53) mRNA, partial cds	Homo sapiens transcription factor IGHM enhancer 3, JM/11 protein, JM4 protein, JM5 protein, T54 protein, JM10 protein, A4 differentiation-dependent protein, triple LIM domain protein 6, and synaptophysin genes,	complete eds; and L-type calcium channel a>	Homo sapiens interleukin 2 receptor, beta (IL2RB) mRNA	Human germline gene 16.1 for Ig lambda L-chain C region (IgL-C16.1)	Homo sapiens F-box protein FBL5 (FBL5) mRNA, complete cds	Homo sapiens melanoma-associated antigen (MAGE-C1) gene, complete cds	Homo saplens SW I-SNF complex protein p270 mRNA, partial cds	Homo saplens NOD1 protein (NOD1) gene, exons 1, 2, and 3	Homo sapiens KIAA0469 gene product (KIAA0469), mRNA	Homo saplens offactory receptor-like protein (OLFR 42B) gene, OLFR 42B-9110 allele, partial cds	xj8Zh07.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2664733 3' similar to	SW:RNP_HYDHY P00677 RIBONUCLEASE PANCREATIC;	Homo sapiens potassium voltage-gated channel, Shab-related subfamily, member 1 (KCNB1) mRNA	Human fertitin heavy chain mRNA, complete cds	Homo saplens mRNA for KIAA0549 protein, partial cds	Homo saplens mRNA for KIAA0549 protein, partial cds	ye32f03.c1 Stratagene lung (#837210) Homo sapiens cDNA clone IMAGE:119453 3' similar to SP:S29539	601878507F1 NIH MGC 55 Homo sepiens cDNA clone IMAGE:4107433 51	Wu12h10.x1 NCI_CGAP_GC6 Homo saplens cDNA done IMAGE:2516803 3'	H.sapiens mRNA for gamma-glutamytransferase	H.sapiens mRNA for gamma-glutamytransferase	tu38g09.x1 NCI_CGAP_Pr28 Homo saplens cDNA clone IMAGE:2253376 3' similar to SW:RASD_DICDI	P03967 RAS-LIKE PROTEIN RASID	Homo saptens neuradn III (NRXN3) mRNA	Homo saplens neurexin III (NRXN3) mRNA	Homo saplens interleukin 1 receptor, type I (IL1R1) mRNA	Homo sapiens nuclecter phosphoprotain B23 (NPM1) mRNA, complete cds	Homo saplens solute carrier family 25 (mitochondrial carrier; adenine nucleotide translocator), member 5 /si C23A5) nuclear nene encoding mitochondrial protein. mRNA	(SECENA), Hudean gale crocking international process, in the
Top Hit Database Source	Į.	NT		F	¥	LN	ΝŢ	IN	F	뉟	占	N		EST HUMAN	Þ	N	N	LN		EST HIMAN	EST HUMAN	N <sub>T</sub>	LN LN		EST HUMAN	TN	LN	LN	Z E	<u> </u>	ž
Top Hit Acesslon No.	Ī	0.0E+00 AF017433.1		0.0E+00 AF196779.1	8	0.0E+00 X03529.1	AF199355,1	AF064589.1	AF265208.1	4F149773.1	0.0E+00 7662139 NT	AF042075.1		0.0E+00 AW188146.1	4826783 NT	0.0E+00 L20941.1	4B011121.1	AB011121.1		0.0E+00 1946/0.1					0.0E+00 Al685950.1	4758827 NT	4758827 NT	4504658 NT	.0E+00 M28699.1	00000	4502098 N
Most Similar (Top) Hit BLAST E Value	0.0E+00/	0.0E+00		0.0E+00/	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00		0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00		0.0E+00 1948/U.1	00+100	0.0E+00	00+30°0		0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	ľ	0.0E+00
Expression Signal	7.27	1.88		2.21	3.78	3.23	1.92	1.75	4.71	10.17	3.92	1.29		1.19	3.61	20.63	1.05	1.05		75.67	- 20		5.36		1.01				4.54	Ì	1.92
ORF SEQ ID NO:		29309			L	29333		29340	29356	29357	29361	29362		29368	29395	29404	l			29415		}	29442		29444				29482		29485
SEQ ID NO:	16290	16295		16298	1	1	l	16330	18350	18351	ı	16357	ı	16362	16384	1	16396		ı	-1	187.10	1_	L.	L.	16426	L		Ĺ	1	İ	16466
Probe SEQ ID NO:	3114	3119		3122	3124	3145	3151	3155	3175	3176	3181	3182		3187	3210	3219	3222	3222		3229	3244	3250	3250		3252	3262	3262	3270	3288		3292

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Top Hit Descriptor	Homo sapiens CREB binding protein (Rubinstein-Taybi syndrome) (CREBBP) mRNA	Homo sepiens CREB binding protein (Rubinstein-Taybi syndrome) (CREBBP) mRNA	П		Homo sapiens angiostatin binding protein 1 mRNA, complete cds	Homo sapiens fibrillin 1 (Marfan syndrome) (FBN1) mRNA	Homo sepiens titin (TTN) mRNA	Human conneyin 43 processed pseudogene	Homo sapiens HLA class III region containing tenascin X (tenascin-X) gene, partial cds, cytochrome P450 21-	hydroxyase (CYP21B), complement comparient of (CPC) GTI, menuses (SN277), N2, comparient mass (Bf), and complement camponent C2 (C2) genes.>	Homo sapiens very large G-protein coupled receptor-1 (VLGR1) mRNA, complete cds	Homo sapiens A kinase (PRKA) anchor protein 1 (AKAP1), mRNA	Homo sapiens A kinase (PRKA) anchor protein 1 (AKAP1), mRNA	Homo sepiens SWI-SNF complex protein p270 mRNA, partial cds	Homo sapiens hypothetical protein FLJ20695 (FLJ20695), mRNA	Homo sapiens death receptor 6 (DR6), mRNA	Homo sapiens G protein-coupled receptor 24 (GPR24), mRNA			Homo sapiens telomerase reverse transcriptase (TERT) gene, exons 1-6	Homo sapiens telomerase reverse transcriptase (TERT) gene, exons 1-6	Homo sapiens hormonally upregulated neu tumor-associated kinase (HUNK), mKNA	Homo sapiens hormonally upregulated neu tumor-associated kinase (HUNK), mRNA	Homo sapiens caspase 8, apoptosis-related cysteine protease (CASP8) mRNA	Homo sapiens caspase 8, apoptosis-related cysteline protease (CASPB) mRNA	Homo sapiens pyrin (MEFV) gene, complete cds	Homo saptens mRNA for KIAA1507 protein, partial cds		Wb10f04.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2305279 3' similar to TR:Q91929 Q91929; N   ZINC FINGER PROTEIN.	Т	I	Homo sapieta ireal objective empirical process (a
Top Hit Database Source	N F	ΤN	EST HUMAN	TN	NT	LN	LΝ	NT		Ż	NT	Ł	Z	N	N	TN	¥	EST HUMAN	EST_HUMAN	ΤN	ΤN	LΝ	LΝ	LΝ	۲N	LN	N	EST_HUMAN	NAMI III FOR	EST HIMAN		Z
Top Hit Acession No.	4758055 NT	4758055 NT	0.0E+00 AA774783.1	).0E+00 AF286598.1	0.0E+00 AF286598.1	4557590 NT	4507720 NT	3.0E+00 M65189.1		0.0E+00 AF019413.1	3.0E+00 AF055084.1	4502014 NT	4502014 NT	3.0E+00 AF265208.1	8923624 NT	7657038 NT	4885312 NT	0.0E+00 AI589294.1	0.0E+00 AW955400.1	0.0E+00 AF128893.1	0.0E+00 AF128893.1	7657213 NT	7657213 NT	4502582 NT	4502682 NT	0.0E+00 AF111163.1	0.0E+00 AB040940.1	0.0E+00 BE779039.1	A CREATER A A LEGISLA A	0.0E + 00 AI W2305. 1		1/06239 N
Most Similar (Top) Hit BLAST E Value	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00		0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00						١	0.0E+00
Expression Signal	0.78	0.76	29.49	8.38	8.38	3.04	1.01	10.18		0.95	4.06	1.34	1.34	3.56	0.95	1.42	0.72	3.14	9.94	2.41	2.41	1.03	1.03	1.20	1.28	11.92	1.02			000	2	1.16
ORF SEQ ID NO:	29493	29494	29495	29503	29504	29610				29524		29535	29536	l					29589	29596	29597	L	29599									29671
Exon SEQ ID NO:	16472	1	1	1	ı	1	16499	16507		16508	1		18464	16535	ı	1	ı	18571	L	١	l_	L	L	1_	16585	1_	L	L	L	5000 P		16659
Probe SEQ ID NO:	3298	3298	3300	3308	3308	3320	3326	3334		2225	3338	3348	3348	3363	3364	3377	3388	3401	3404	3412	3412	3413	3413	3416	3416	3419	3424	3428		3441	2483	3492

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Top Hit Descriptor	Homo sapiens T-type calcium channel alpha1 subunit Alpha11-a Isoform (CACNA11) mRNA, complete cds	MR1-SN0033-100400-001-008 SN0033 Homo sepiens cDNA	Homo sapiens KIAA0952 protein (KIAA0952), mRNA	Homo sapiens KIAA0952 protein (KIAA0952), mRNA	Homo sapiens beaded filament structural protein 1, filensin (BFSP1) mRNA	Homo sapiens leukocyte Immunoglobulin-like receptor, subfamily A (with TM domain), member 2 (LILRA2), mRNA	Homo sapiens skeletal muscle LIM-protein 1 (FHL1) gene, complete cds	Homo sapiens death receptor 6 (DR6), mRNA	Bacteriophage P1 replication region including repA, parA, and parB genes and IncA, incB, and incC incompatibility determinants	Homo sapiens protein tyrosine phosphataso, receptor type, T (PTPRT), mRNA	Homo sapiens met proto-ancogene (hepatocyte growth factor receptor) (MET) mRNA	wp14d10.x1 NCI_CGAP_Lu19 Homo sapiens cDNA clone IMAGE:2464819 3' similar to TR:O73634 O73634 NEURAL CELL ADHESION MOLECULE. ;	wp14d10.x1 NCI_CGAP_LL19 Homo sapiens cDNA clone IMAGE:2464819 3' similar to TR:O73634 O73634 NEURAL CELL ADHESION MOLECULE.;	Homo sapiens mRNA for putative ankyrin-repeat containing protein (ORF1)	Homo sapiens ∿fos FBJ murine osteosarcoma viral oncogene homolog (FOS), mRNA	Homo sapiens v-fos FBJ murine osteosarcoma viral oncogene homolog (FOS), mRNA	Human endogenous retrovirus HERV-K10	Human MDS1A (AML1/MDS1 fusion) mRNA, partial cds	Homo sepiens cell-line KG1 transcriptional regulatory protein p54 mRNA, complete cds	Homo sapiens cell-line KG1 transcriptional regulatory protein p54 mRNA, complete cds	Homo capiens chromosome 21 unknown mRNA	601143853F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:3061373 5'	601143853F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:3051373 5'	Homo sapiens potassium voltage-gated channel, Isk-related family, member 2 (KCNE2) mRNA	TRANSCRIPTION REGULATOR PROTEIN BACH1 (BTB AND CNC HOMOLOG 1) (HA2303)	1835g12.x1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:2088742 3' similar to TR:000499 1000498 MYASTHENIA GRAVIS AUTOANTIGEN GRAVIN ;	Homo sapiens mRNA for KIAA1153 protein, partial cds	Homo sapiens mRNA for KIAA1153 protein, partial cds
Top Hit Database Source	Ä	EST_HUMAN	NT	FN	MT	F	5	NT	ΙN	N	Į.	EST HUMAN	EST_HUMAN	TN	NT	NT	IN	TN	NT	NŢ	TN	EST_HUMAN	M.1 EST HUMAN	LΝ	SWISSPROT	EST HUMAN	LN	NT
Top Hit Acession No.	0.0E+00 AF211189.1	0.0E+00 AW867015.1	7662401 NT	7662401 NT	4502398 NT	5803067 NT	4F110763.1	0.0E+00 7657038 NT	(02380.1	7427522 NT	4557746 NT	0.0E+00 A1935159.1	0.0E+00 AI935159.1	0.0E+00 AJ278120.1	6552332 NT	6552332 NT	M14123.1	0.0E+00 U43293.1	AF045452.1	4F045452.1	0.0E+00 AF231922.1	0.0E+00 BE304791.1	0.0E+00 BE304791.1	4826795	014867	AI384007.1	AB032979.1	0.0E+00 AB032979.1
Most Similar (Top) Hit BLAST E Value	0.0E+90	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00 K02380.1	00E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00 M14123.1	0.0E+00	0.0E+00	0.0E+00	0.0E+00	1	l	0.0E+00				1 1
Expression Signal	1.26	0.94	2.02	202	0.92	2.35	3.08	2.46	5.5	1.38	1,83	4.17	4.17	1.91	5.38	5.38	1.41	5.78	2.57	257	1.18	3.29	3.29	1.04	8.0			0.6
ORF SEQ ID NO:	29672		29687	29688				29703	29708		29714					<u> </u>	L.	29747			L			29777	29780		1	29802
SEQ ID	16680	16665	16677	16677	16678				16697	16700	16703	16709		1	1	1		16731	16739	16739	16747	16758	l		L			16785
Probe SEQ ID NO:	3493	3498	3511	3511	3512	3514	3523	3528	3532	3535	3538	3544	3544	3548	3555	3555	3560	3556	3574	3574	3582	3594	3594	3597	3600	3603	3621	3621

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	_		_	_	_	_	_	_	_			_,	_	_	- 1	_	_	_	- **		2001	#		47	744	т-	- 1		ii	-	3500	1
Top Hit Descriptor	zx89h04.r1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:811927 5'	zx89h04.r1 Scares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:811927 5	AV701889 ADB Homo sapiens cDNA done ADBDAH06 5	Homo saplens semenogetin II (SEMG2) mRNA	Homo sapiens homologous yeast-44.2 protein mRNA, complete cds	Novel human gene mapping to chomosome X	Homo saplens mRNA for KIAA1476 protein, partial cds	Homo sapiens sal (Drosophila)-like 1 (SALL1), mRNA	Homo saplens sal (Drosophila)-like 1 (SALL1), mRNA	Homo sapiens butyrophllin, subfamily 3, member A3 (BTN3A3), mRNA	QV0-CT0225-230300-169-e01 CT0225 Homo sapiens cDNA	Homo sapiens gamma-glutamylcysteine synthetase (GLCLC) gene, partial cds	602084583F1 NIH MGC_83 Homo saptens cDNA clone IMAGE:4248595 5'	602152486F1 NIH_MGC_81 Homo saplens cDNA clone IMAGE:4283645 5	602152486F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4293645 5'	Homo sapiens retinoblastoma-binding protein 2 (RBBP2) mRNA	hi84g01.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2979024 3'	hi84g01.x1 Soares_NFL_T_GBC_S1 Homo saplens cDNA clone IMAGE:2979024 3'	Homo sapiens heparan sulfate (glucosamine) 3-O-sulfotransferase 1 (HS3ST1) mRNA	Homo sapiens KIAA0808 gene product (KIAA0806), mRNA	Homo sapiens midline 1 (Opitz/BBB syndrome) (MiD1) mRNA	Homo eapiens midline 1 (Opitz/BBB syndrome) (MID1) mRNA	Homo sapiens mRNA for G protein-coupled inward rectifier potassium channel, complete cds	Homo sepiens ghyceraldehyde-3-phosphata dehydrogenase (GAPD), mRNA	Homo saplens WAVE2 mRNA for WASP-family protein, complete cds	Homo sapiens mRNA for KIAA0406 protein, partial cds	Homo sapiens SH2-containing protein Nsp2 mRNA, complete cds	Homo sapiens SH2-containing protein Nsp2 mRNA, complete cds	NHTBCae15g09f1 Normal Human Trabecular Bone Cells Homo sapiens cDNA clone NHTBCae15g09	NHTBCae15g08f1 Normal Human Trabecular Bone Cells Homo sapiens cDNA clone NHTBCae15g09	Homo sapiens chromosome 21 segment HS21C004	Homo seplens chromosome 21 segment HS210004
Top Hit Database Source	EST_HUMAN	EST_HUMAN	EST_HUMAN	NT	NT	NT	TN	ΤN	NT	NT	EST_HUMAN	뒫	EST_HUMAN	EST_HUMAN	EST_HUMAN	Ę	EST_HUMAN	EST_HUMAN	TN	LZ	LN	۲N	L.	LN	NT	ΡZ	Į.	FA	EST_HUMAN	EST HUMAN	N N	L
Top Hit Acession No.	0.0E+00 AA456282.1	0.0E+00 AA456282.1	0.0E+00 AV701869.1	4506884 NT	0.0E+00 AF078868.1	0.0E+00 AL133204.1	0.0E+00 AB040909.1	6997248 NT	6997248 NT	6325463 NT	0.0E+00 AW852217.1	0.0E+00 AF118846.1	0.0E+00 BF676393.1	0.0E+00 BF672054.1	0.0E+00 BF672054.1	4826967 NT	0.0E+00 AW684693.1	0.0E+00 AW664693.1	4826763	7662319 NT	4557752 NT	4557752 NT	J87327.1	7669491 NT	0.0E+00 AB026542.1	0.0E+00 AB007866.2	0.0E+00 AF124250.1	0.0E+00 AF124250.1	0.0E+00 AA852743.1	0.0E+00 AA852743.1	0.0E+00 AL163204.2	0.0E+00 AL163204.2
Most Similar (Top) Hit BLAST E Value	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00.0	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00 D87327.1	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00
Expression Signal	0.68	0.68	1.45	4.48	1.17	1.34	1.16	76.0	76.0	1.06	4.28	1.28	7.85	0.59	0.59	66.0	0.76	0.76	0.89	0.93	0.74	0.74	236	6.29	3.98	1.06	5.10	5.16	32.49	32.49	1.95	1.95
ORF SEQ ID NO:	29803	L	Ĺ			29820		29837						29868				29872				L	29901		L	29922					L	23936
Exan SEQ ID NO:	16787			16795	ı	ı	ľ	1	ı	ı			L	ı	16865		16868	_	16872			16881		16902	16918	ı	1_	L	<u> </u>	l	L	1
Probe SEQ ID NO:	3623	3623	3630	3831	3633	3642	3644	3665	3665	3667	3672	3679	3680	3704	3704	3705	3707	3707	3711	3713	3720	3720	3737	3741	3757	3759	3761	3761	3767	3767	3770	3770

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, and the second	35 N
Expression (Top) Hit Top Hit Acession Database Signal BLAST E No. Source	(Top) Hiff Top Hiff Acession BLAST E No.
0.99 0.0E+00 AB002331.1	0.99 0.0E+00 AB002331.1
0.99	0.99 0.0E+00 AB002331.1
2.4	2.4 0.0E+00 AW851714.1 EST
2.37	2.37 0.0E+00
1.15 0.0E+00 AB018339.1	1.15 0.0E+00 AB018339.1
0.74 0.0E+00 O14867	0.74 0.0E+00 O14867
1.02 0.0E+00 AB020717.1	1.02 0.0E+00 AB020717.1
1.02 0.0E+00 AB020717.1	1.02 0.0E+00 AB020717.1
5.42 0.0E+00 AW298134.1	5.42 0.0E+00 AW298134.1
5.42	5.42 0.0E+00 AW298134.1
1.04 0.0E+00 AB004630.1	1.04 0.0E+00 AB004630.1
1.17	1.17 0.0E+00 AA463659.1
3.23	3.23 0.0E+00
0.83	0.83 0.0E+00 AB037835.1
5.72 0.0E+00	5.72 0.0E+00
18.03 0.0E+00	18.03 0.0E+00
1.52 0.0E+00	0.0E+00
1.52 0.0E+00	1.52 0.0E+00
8.94 0.0E+00 4505594	8.94 0.0E+00 4505594
1.96 0.0E+00 AF145712.1	0.0E+00 AF145712.1
0.73 0.0E+00 AF195658.1	0.73 0.0E+00 AF195658.1
2.36 0.0E+00 AF17973	0.0E+00 AF179733.1
2.36 0.0E+00	2.36 0.0E+00
2.36 0.0E+00 7657468	2.36 0.0E+00 7657468
1.74	0.0E+00 AF020091.1
1.05 0.0E+00 AF127851.1	1.05 0.0E+00 AF127851.1
1.05 0.0E+00 AF127851.1	1.05 0.0E+00 AF127851.1
	1.29 0.0E+00 Al377699.1
1 0.0E+00 AF15249	1 0.0E+00 AF15249
5 2.6 0.0E+00 4758199 NT	0.0E+00
15.6 0.0E+00 S78685.1 NT	15.6 0.0E+00 S78685.1
2.14 0.0E+00 7710148	2 1 4 0 0E+00 7710148

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
3943	17102	30099		0.0E+00	0.0E+00 7662183 NT	NT	Homo saplens KIAA0569 gene product (KIAA0569), mRNA
3946	17105	30101	1.62	0.0E+00		NT	Homo sapiens myosin light chain kinase isoform 2 (MLCK) mRNA, complete cds
3946	17105			0.0E+00		TN	Homo sapiens myosin light chain kinase Isoform 2 (MLCK) mRNA, complete cds
3954	17109		1.02	0.0E+00	0.0E+00 AB001523.1	TN	Homo sapiens gene for TMEM1 and PWP2, complete and partial cds
3951	17109			0.0E+00	AB001523.1	NT	Homo saplens gene for TMEM1 and PWP2,complete and partial cds
3952	17110	30109		0.0E+00	0912735 NT	TN	Homo sapiens transient receptor potential channel 5 (TRPC5), mRNA
3957	17115			0.0E+00	4503178 NT	NT	Homo saplens chromosome X open reading frame 5 (CXORF5) mRNA
3957	17115		96.9	0.0E+00	178	NT	Homo septens chromosome X open reading frame 5 (CXORF5) mRNA
3959	17117	30121		0.0E+00		NT	Human zinc finger protein ZNF134 mRNA, complete ods
3960	17118			0.0E+00		NT	Homo saplens intersectin short isoform (ITSN) mRNA, complete cds
3963	17421	30124	1.23	0.0E+00	TN 8828783	. LN	Homo sapiens potassium voltage-gated channel, Shab-related subfamily, member 1 (KCNB1) mRNA
3968	17124	l		0.0E+00	AF012615.1	TN	Homo sapiens familial mental retardation protein 2 (FMR2) gene, exon 11
3967	17125	Ì		0.0E+00	TN 14759171 NT	F	Homo saplens SC35-Interacting protein 1 (SRRP129), mRNA
3989	17127	30130	0.77	0.0E+00	0.0E+00 AF099117.1	NT	Homo sapiens amphiphysin gene, partial cds
							wk01f01.x1 NCI_CGAP_Lym12 Hamo sapiens cDNA clone IMAGE:2411065 3' similar to TR:043340
3979	17136	30140		0.0E+00	0.0E+00 AI864727.1	EST_HUMAN	O43340 R28830_2, ;contains element PTR7 repetitive element;
3980	17137		1.03	0.0E+00	0.0E+00 AL163248.2	NT	Homo sapiens chromosome 21 segment HS21C048
3983	17140			0.0E+00	4506742 NT	NT	Homo sapiens ribosomal protein S8 (RPS8), mRNA
3988	17145		1.33	0.0E+00	0.0E+00 AL040338.1	EST_HUMAN	DKFZp434N0413_r1 434 (synonym: htes3) Home sapiens cDNA clone DKFZp434N0413 5
3994	17151	30158		0.0E+00	6005887 NT	NT	Homo sapiens AP1 gamma subunit binding protein 1 (AP1GBP1), mRNA
3994	17151			0.0E+00	6005887 NT	NT	Homo sapiens AP1 gamma subunit binding protein 1 (AP1GBP1), mRNA
3996	17153			0.0E+00	4504138 NT	NT	Homo sapiens glutamate receptor, metabotropic 3 (GRM3) mRNA
3997	17154	l	2.26	00+30'0	4505078 NT	NT	Homo saplens melanoma antigen, family B, 1 (MAGEB1) mRNA
4004	17158				0.0E+00 AF149412.1	LN	Homo sapiens HBP17 heparin-binding and FGF-binding protein gene, complete cds
4013	17170			0.0E+00	4506758 NT	. LN	Homo saplens nyanodine receptor 3 (RYR3) mRNA
4017	17174			0.0E+00	4585642 NT	NT	Homo saplens zinc finger protein (KIAA0412) mRNA
4026	17182	30191	5.14	0.0E+00	.0E+00 BF355295.1	EST_HUMAN	RC3-HT0860-170800-011-a12 HT0860 Homo sapiens cDNA
							MXRA5 Human matrix tissue expression library Homo sapians cDNA clone Incyte 1996726 similar to MXRA 🔄
4028	17184	30193	1.37	0.0E+00	.0E+00 AW 888221.1	EST_HUMAN	Matrix remodelling associated gene 5
							MXRA5 Human metrix (Issue expression library Homo sapiens cDNA clone Incyte 1996726 similar to MXRA5
4028				ျ	_	EST_HUMAN	Matrix remodeling associated gene 5
4035	17191	30201		ျိ	-	N	Homo sapiens F-box protein Fbi3b (FBL3B) mKNA, partial cds
4038	Į	-	1.14		1.0E+00 U86281.1	L	Homo saplens olfactory receptor (UK/-141) gene, partial cds

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Top Hit Descriptor	Homo sapiens olfactory receptor (OR7-141) gene, partial cds	601236986F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3608800 5'	601153727F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3509743 5	PM3-LT0031-100100-003-h09 LT0031 Homo sapiens cDNA	Homo sapiens iduronate 2-sulfatase (Hunter syndrome) (IDS), transcript variant 1, mRNA	Human G2 proteth mRNA, partial cds	Human G2 protein mRNA, partial cds	Human G2 protein mRNA, partial cds	Homo sapiens cancer-testis antigen CT10 (CT10) gene, complete cds	Homo sapiens cancer-testis antigen CT10 (CT10) gene, complete cds	Human MHC class II lymphcoyte antigen DPw4-beta-2 pseudogene, exon 2	Homo sapiens chromosome 21 segment HS21C103	Homo sapiens chromosome 21 segment HS21C084	Homo sapiens chromosome 21 segment HS21 C068	Homo sapiens eukaryotic translation elongation factor 1 alpha 1 (EEF1A1) mRNA	#55g08.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2244734 3' similar to TR:O60309 O60309	NAMOON FROIEIN.	Homo sapiens KIAA0569 gene product (NIAA0569), minua	Human zinc finger protein ZNF133	Chlorcoebus aethiops mRNA for ribosomal protein S4X, complete cds	Homo sapiens mRNA for UGA suppressor tRNA-associated antigenic protein (tRNA48 gene)	Homo sapiens chromosome 21 segment HS21C003	Homo saplens mRNA for rapa-2 (rapa gene)	Homo saplens mRNA for rapa-2 (rapa gene)	Homo sapiens retinoblastoma-binding protein 4 (RBBP4) mRNA	Homo sapiens retinoblastoma-binding protein 4 (RBBP4) mRNA	Homo sapiens phosphoribosy/glycinamide formyfransferase, phosphoribosy/glycinamide synthefase,	phosphoribosyaminoimidazole synthetase (GART) mRNA	Homo sapiens G protein-coupled receptor 21 (GPR21), mRNA	Homo sapiens mRNA for KIAA0287 gene, partial cds	Horno sapiens ras GTPase activating protein-like (NGAP) mRNA	Homo sapiens IMP (inosine monophosphate) dehydrogenase 1 (IMPDH1), mKNA	Novel human mRNA from chromosome 1, which has similarities to BA I 2 genes
Top Hit Database Source	_LN	EST_HUMAN (	EST_HUMAN	EST_HUMAN F				I		LN		L L		LN TN		Г	HOMAN			N	L		LN	NT				N	LN	ΝΤ	NT.	NT	N <sub>1</sub>
Top Hit Acession No.	Г		0.0E+00 BE313146.1	0.0E+00 AW580740.1	5360215 NT	0.0E+00 U10991.1		110991.1	4F116195.1	0.0E+00 AF116195.1	0.0E+00 M23910.1	0.0E+00 AL163303.2	0.0E+00 AL163284.2	.0E+00 AL163268.2	4503470 NT		0.0E+00 AI65/076.1	7662183 NT	J09366.1	0.0E+00 AB015610.1	0.0E+00 AJZ38617.1	0.0E+00 AL163203.2	0.0E+00 AJ277276.1	.0E+00 AJ277276.1	5032026 NT	5032026 NT		4503914 NT	4885306 NT	1.0E+00 AB006625.1	4758807	11419297 NT	0.0E+00 AL096857.1
Most Similar (Top) Hit BLAST E Value	0.0E+00 U86281.1	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00		0.0E+00	0.0E+00	0.0E+00 U09366.1	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00		0.0E+00	0.0E+00		0.0E+00		
Expression Signal	1.14	3.47	12	1.28	1.83	0.8	8.0	0.8	9.31	9.31	3.51	7.25	2.93	2.13	111.8		0.99	1.91	285	9	3.22	1.58		2.68				0.64		ľ			4.33
ORF SEQ.	30205	30209	30210	30217			L	30240					L	30266					30285	30304		30318		30320				30337					30347
SEQ ID	17194	17198	1_		17208		17233	ı	1	17239	l	17250	١	L	1_		1		17290	17308	17316	L.	<u> </u>		17335	1	1	17344	ı	ı	17355		ШI
Probe SEQ ID NO:	4038	4042	4043	4051	4052	4077	4077	4077	4084	4084	4093	4095	4104	4112	4127		4134	4137	4138	4157	4166	4177	4178	4178	4185	4185		4194	4202	4203	4206	4207	4208

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riptor	one IMAGE:362920 5' smilar to contains Alu				a subunit (60kD) (GABPA), mRNA	a subunit (60kD) (GABPA), mRNA		mRNA	mRNA		IMAGE:2515975 3'	IMAGE:2515975 3'	NA	NA	MAGE:2967690 5'	SNA	GE:2900095 3' stmilar to SW:THI2_BOVIN	Ä;	s cDNA done IMAGE:3063147 5	mRNA	mRNA	EJ (sperm receptor for egg jelly, sea urchin		e IMAGE:743197 3' similar to contains Alu	ent;	e IMAGE:743197 3' sImilar to contains Alu	ent ;	V3) mRNA, complete cds		1		
Top Hit Descriptor	ze55e09.rl Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:362920 5' smilar to contains Alu repetitive element;	Homo sapiens DGCR8 (DGCR8) mRNA, complete cds	Homo saplens protein kinase, X-linked (PRKX) mRNA	Homo sapiens protein kinase, X-finked (PRKX) mRNA	Homo saplens GA-binding protein transcription factor, alpha subunit (60kD) (GABPA), mRNA	Homo sapiens GA-binding protein transcription factor, alpha subunit (60kD) (GABPA), mRNA	Homo sapiens semenogelin II (SEMG2) mRNA	Homo saplens hypothetical protein FLJ10379 (FLJ10379), mRNA	Homo sapiens hypothetical protein FLJ10379 (FLJ10379), mRNA	Homo saplens mRNA for KIAA0895 protein, partial cds	wu04d04x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE 2515975 3*	wu04d04.x1 NCI_CGAP_GC6 Homo capiens cDNA clone IMAGE:2515975 3	MR1-HT0707-100500-001-a02 HT0707 Homo saplens cDNA	MR1-HT0707-100500-001-a02 HT0707 Homo saplens cDNA	601120778F1 NIH_MGC_20 Homo papiens cDNA clone IMAGE:2967690 5	Homo sapiens nuclear receptor coactivator 3 (NCOA3), mRNA	ba51f04.x1 NIH_MGC_10 Homo saplens cDNA clone IMAGE:2900095 3' similar to SW:THI2_BOVIN	Q95108 MITOCHONDRIAL THIOREDOXIN PRECURSOR	UI-HF-BM0-adx-c-02-0-UI.r1 NIH_MGC_38 Homo sapiens cDNA done IMAGE:3063147 5	Homo sapiens hypothetical protein FLJ10498 (FLJ10498), mRNA	Homo sapiens hypothetical protein FLJ10498 (FLJ10498), mRNA	Homo sepiens polycystic kidney disease (polycystin) and REJ (sperm receptor for egg jelly, eea urchin homoloo Hike (PKDREJ) mRNA	Homo sapiens mRNA for KIAA1318 protein, partial cds	zu68h07.s1 Soares_tests_NHT Homo sapiens cDNA clone IMAGE:743197.3' similar to contains Alu	repetitive element; contains element MER35 repetitive element	zu68h07.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:743197 3' sImilar to contains Alu	repetitive element; contains element MER35 repetitive element	Homo sapiens DNA polymerase zata catalytic subunit (REV3) mRNA, complete cds	Homo sapiens desmoplakin (DPI, DPII) (DSP) mRNA	Homo sapiens desmoplakin (DPI, DPII) (DSP) mRNA	Homo sapiens chromosome 21 segment HS21C103	Human apolipoprotein B-100 mRNA, complete cds
Top Hit Database Source	EST_HUMAN	LΝ	NT				NT TN	TN	IN	LN	EST_HUMAN	EST_HUMAN	EST_HUMAN	Г	EST_HUMAN	NT			EST_HUMAN	TN	Ŋ	L Z	L		EST_HUMAN		EST_HUMAN	LNT	IN	NT.	NT	NT
Top Hit Acession No.	0.0E+00 AA018975.1	0.0E+00 AF165527.1	4826947 NT	4826947 NT	4503854 NT	4503854 NT	4506884 NT	8922391 NT	8922391 NT	0.0E+00 AB020702.1	0.0E+00 A1982597.1	0.0E+00 A1982597.1	0.0E+00 BE184856.1	3E184856.1	3E274217.1	0.0E+00 5729725 NT		0.0E+00 AW675599.1	4W408788.1	8922466 NT	8922466 NT	TN 2587748	0.0E+00 AB037739.1		0.0E+00 AA401438.1		0.0E+00 AA401438.1	0.0E+00 AF157476.1	4758199 NT	4758199 NT	0.0E+00 AL163303.2	0.0E+00 J02610.1
Most Similar (Top) Hit BLAST E Value	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00		0.0E+00	0.0E+00	0.0E+00	0.0E+00	00+100	0.0E+00		0.0E+00		0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00
Expression Signal	96'0	5.32	0.7	0.7	1.32	1.32	0.64	16.0	0.91	0.85	5.57	5.57	-	٦	5.89	2.07		5.78	1.12	1.55	1.55	2.25	1.07		11.47		11.47	1.2	8.09	8.09	0.86	5.01
ORF SEQ ID NO:		30356	27373			30370	29812	30372	30373	30377	30388		30389			30396			30410	30411		<u> </u>	30429	L	30438				30461			30512
Exon SEQ ID NO:	17358	17367	14319	14319		<u> </u>	L	Ĺ	_	L		١_	17400		L	17410	L	17417	17422	١.	17423			1	17452	L	17452	17455	l	17481		17531
Probe SEQ ID NO:	4209	4218	4227	4227	4234	4234	4236	4238	4238	4244	4252	4252	4255	4255	4259	4265		4272	4277	4278	4278	7007	4300		4309		4309	4312	4338	4338	4345	4388

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Top Hit Descriptor	PM2-DT0023-080300-004-a08 DT0023 Homo sapiens cDNA	601464995F1 NIH_MGC_67 Homo sapiens cDNA done IMAGE:3868246 5'	Homo sapiens F-box protein FbH (FBL4) mRNA, partial ods	Homo saplens fow density lipoprotein-related protein 2 (LRP2), mRNA	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA	od2306.x1 Soares_placenta_8to9weeks_ZNbHP8to9W Homo sapiens cDNA clone IMAGE:1724579.3' cimilar to contains MFR20 b2 MFR20 renetitive element :	Human CBFA3 (Cbfa3) gene, partial cds	Homo sapiens myeloid/lymphaid or mixed-lineage leukemia (trithorax (Drosophila) homolog); translocated to, 4	(MLL 14) MRNA	Homo sapiens procein kinase C, nu (Prkhov), nikiva	Homo sapiens protein Kinase C, nu (PRKCN), mRNA	Human G2 protein mRNA, partial ods	Human G2 protein mRNA, partial cds	Homo saptens COMPLEMENT COMPONENT C1q RECEPTOR (C1QR), mRNA	Homo sapiens gap junction protein connexin-38 (CX36) gena, complete cds	Homo saplens plasma membrane calclum ATPase isoform 1 (ATP2B1) gene, afternative splice products,		H.sapkens H2B/h gene	H.sapiens H2B/h gene	H.sapiens H4/d gene for H4 histone	H.sepians H4/d gene for H4 histone	Homo sapiens KIAA0390 gene product (KIAA0390), mRNA	Homo sapiens KIAA0390 gene product (KIAA0390), mRNA	Homo sapiens caudal type homeo box transcription factor 4 (CDX4), mRNA	Homo sapiens Xq pseudoautosomal region; segment 2/2	Homo saplens chromosome 21 segment HS21C007	Homo sapiens mRNA for KIAA1360 protein, partial cds	Homo sapiens myosin regulatory light chain interacting protein (MIR), mRNA	Homo sapiens membrane-bound aminopeptidase P (XNPEP2) gene, complete ods	Homo sapiens ACTN2 gene for alpha-Actinin 2, exon 10	Homo sapiens ACTNZ gene for alpha-Actinin 2, exon 10	24g7 Human retina cDNA randomly primed sublibrary Homo sapiens cDNA	24g7 Human retina cDNA randomly primed sublibrary Homo sapiens cDNA
Top Hit Database Source	EST_HUMAN	EST_HUMAN	LNT.			ECT LILIMANI	T					LN	ΝΤ		N F				NT	NT	<u> </u>		F	Ę	Į.	N-	F	닐	LN.	FZ	TN		П
Top Hit Acession No.	0.0E+00 AW936689.1	0.0E+00 BE779039.1	0.0E+00 AF174590.1	6806918 NT	FN 8109089	00-100			5174574 NT	6563384 N	6563384 NT			6912281 NT	0.0E+00 AF153047.2	, ,	14551.1			X60483.1	X60483.1	7662091 NT	7662091 NT	4885126 NT	0.0E+00 AJ271736.1	0.0E+00 AL163207.2	0.0E+00 AB037781.1	7019456 NT	0.0E+00 AF195953.1	0.0E+00 AJ249765.1	0.0E+00 AJ249765.1	0.0E+00 W26179.1	0.0E+00 W26179.1
Most Similar (Top) Hit BLAST E Value	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0	0.0E+00 U14520.1		0.0E+00	0.0E+00	0.0E+00	0.0E+00 U10991.1	0.0E+00 U10991.1	0.0E+00	0.0E+00		0.0E+00 L14561.1	0.0E+00 Z80780.1	0.0E+00 Z80780.1	0.0E+00 X60483.1	0.0E+00 X60483.	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00
Expression Signal	0.81	0.65	5	0.71	0.71	200	2 4		0.96	0.72	0.72	1.08	1.08	10.33	1.06		3.62	6.28	6.28	1.59	1.59	10.05	10.05	14.1	1.16	1.24	1.2	1.9	6.61	278	2.78	0.69	0.69
ORF SEQ ID NO:	30529			L	30545			L		1	30596	30572	30573					30616	30617	30623			30631	30645			30648	L	L	30687		L	Ш
Exen SEQ ID NO:	17545	16596	17552	17560	17560	4.7584	17584	<b>I</b>	1	- [	17585	17591	17691	17600	17620		_ 1	17634	17634	17640	17640	L	17644		L	L	L	L	ı	1	1	1	ш
Probe SEQ ID NO:	4402	4406	4410	4419	4419	2,7	4424		4428	4445	4445	4451	4451	4460	4480		4490	4494	4494	4500	4500	4505	4505	4517	4518	4519	4522	4553	4564	4570	4570	4574	4574

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Table 4
Single Exon Probes Expressed in Placenta

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	Top Hit Descriptor	Homo sapiens HPS1 gene, intron 5	seq1329 b4HB3MA Cot8-HAP-Ft Homo sapiens cDNA clone b4HB3MA-COT8-HAP-Ft205 5'	seq1329 b4HB3MA Cot8-HAP-FI Homo sapiens oDNA clone b4HB3MA-COT8-HAP-Ft205 5'	Human endogenous retrovirus HERV-K10	xx5Be08.x1 NCI_CGAP_Eso2 Homo sapiens cDNA clone IMAGE:25894463' similar to SW:AHNK_HUMAN Q09666 NEUROBLAST DIFFERENTIATION ASSOCIATED PROTEIN AHNAK;	Homo sapiens LIM domain kinase 2 (LIMK2), transcript variant 2a, mRNA	Homo sapiens vascular endothelial cell growth factor 165 receptor/neuropilin (VEGF165) mRNA, complete	cds	Homo sapiens chromosome 21 segment HS21C007	PM1-HT0305-101199-002-d03 HT0305 Homo sapiens dDNA	Homo saplens mRNA for putative ankyrin-repeat containing protein (ORF1)	Homo sapiens mRNA for putative ankyrin-repeat containing protein (ORF1)	Homo sapiens G protein-coupled receptor 50 (GPR50) mRNA	Homo saplens serine-threonine protein kinase (MNBH) mRNA, complete cds	Homo sapiens ATP-sensitive inwardly rectifying K-channel subunit (KCNJ6/BIR1) gene, exon	Homo sapiens pyrin (MEFV) gene, complete cds	Homo saplens pyrin (MEFV) gene, completa cds	Homo sapiens zinc finger protein 195 (ZNF195), mRNA	Homo sapiens syncytin precursor, mRNA, complete cds	Homo sapiens protocadherin gamma C3 (PCDH-gamma-C3) mRNA, complete cds	Homo sapiens zinc finger protein 211 (ZNF211), mRNA	Homo sapiens eukaryotic translation elongation factor 1 alpha 1 (EEF1A1) mRNA	Homo sapiens low density lipoprotein receptor-related protein 6 (LRP6) mRNA, and translated products	Homo sapiens chondrolfin sulfate proteoglycan 4 (melanoma-associated) (CSPG4), mRNA	Homo sapiens calclum/calmodulin-dependent protein kinase IV (CAMK4) mRNA	Homo sapiens iduronate sulphate sulphatase (IDS) gene, complete cds	Homo sapiens KIAA0390 gene product (KIAA0390), mRNA	Homo sapiens KIAA0390 gene product (KIAA0390), mRNA	Homo sapiens PTEN (PTEN) gene, exons 3 through 5	Homo sapiens mRNA for G7c protein (G7c gene located in the class III region of the major histocompatibility (complex)
	Top Hit Database Source	TN	EST_HUMAN	EST_HUMAN	LN L	EST_HUMAN	NT		Į.	IN	EST_HUMAN	NT	IN	NI.	۲	TN	ΝT	F	M	NT	MT	NT	M	¥	Ā	ΙN	LN⊤	IN	NT	ΝΤ	LΝ
Ì	Top Hit Acession No.	4F200629.1		0.0E+00 T10233.1			8051619 NT		0.0E+00 AF016050.1	AL163207:2	0.0E+00 AW381570.1	4,1278120.1	4,1278120.1	4758467 NT	4F108830.1	578684.1	4F111163.1	0.0E+00 AF111163.1	F005973 NT	4F208161.1	4F152337.1	5454175 NT	4503470 NT	4505016 NT	4503098 NT	4502556 NT	L35485.1	7662091 NT	7662091 NT	0E+00 AF143314.1	0.0E+00 AJ245418.1
	Most Similar (Top) Hit BLAST E Value	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00		0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00.0	0.0E+00	0.0E+00	0.0E+00	0.0E+00	00+30'0	ı		0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00				0.0E+00	
	Expression Signal	2.29	0.65	0.65	0.80	27.37	2.97		1.48	8.47	76.0	1.3	1.3	1.06	2.07	1.02	12	1.2	3.19	20.18	2.17	2.17	59.97	0.73	1.84	1.03	3.19	15.03	15.03	287	11.57
	ORF SEQ ID NO:			30727	L	30742			30745		30750	30757	Ì	30760		L	30771		30783	L	30795	30789	30808	30814	30817			30826		30841	30844
	Exan SEQ ID NO:	17728	17747	•	17750	1	(	L	17763	17767	17769	1	[_	1	17779	17787	17788	17788	18471		17806	17809	17820	17828	17832	<u></u>	17842	L	1	17859	17862
	Probe SEQ ID NO:	4591	4610	4610	4613	4623	4625		4627	4631	4633	4640	4840	4642	4643	4651	4652	4652	4661	4666	4671	4674	4685	4693	4697	4702	4707	4709	4709	4724	4727

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. Top Hit Descriptor	Homo sapiens mRNA for G7c protein (G7c gene located in the class III region of the major histocompatibility complex)	zp18g08.s1 Stratagene fetal retina 937202 Homo sapiens cDNA clone IMAGE:609854 3'	Homo sapiens odz (odd Oz/ten-m, Drosophila) homolog 1 (ODZ1), mRNA	Homo saplens chromosome 21 segment HS21C084	Homo sapiens cyclophilin-related protein (NKTR) gene, complete cds	Homo sapiens chromosome 21 segment HS21C100	Homo saplens gene for natriuretic protein, partial cds	Homo saplens DNA mismatch repair protein (MLH3) gene, complete cds	Novel human gene mapping to chomosome 1	Homo sapiens keratin 18 (KRT18) mRNA	Homo sapiens keratin 18 (KRT18) mRNA	Hamo sepiens inwardly-rectffying potassium channel Kir2.1 (KCNJ2) gene, exon 2 and complete cds	Homo sapiens inwardly-rectifying potassium channel Kir2.1 (KCNJ2) gene, exon 2 and complete ods	Mus musculus E-cacherin binding protein E7 mRNA, complete cds	Homo sapiens mRNA for KIAA1047 protein, partial cds	Homo sapiens mRNA for KIAA1047 protein, partial cds	Human endogenous retrovirus type K (HERV-K), gag, pol and env genes	QV2-BT0635-160400-142-h05 BT0635 Homo sapiens cDNA	zv96b07.s1 Scares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:767605 3'	Homo sapiens truncated tenescin XB (TNXB) gene, partial cds and TNXA gene recombination breakpoint. region	Homo saplens chromosome 21 segment HS21 C078	Homo sapiens chromosome 21 segment HS21C078	Homo sapiens mRNA for KIAA1399 protein, partial cds	Homo sapiens mRNA for KIAA1399 protein, partial cds	Human displacement protein (CCAAT) mRNA	Homo caplens butyrophilin, subfamily 2, member A2 (BTN2A2), mRNA	Homo sapiens butyrophilin, subfamily 2, member A2 (BTN2A2), mRNA	ya83g04.r2 Stratagene fetal spleen (#937205) Homo sapiens cDNA clone IMAGE:68310 5	ya83g04.r2 Stratagene fetal spleen (#937205) Homo saplens cDNA done IMAGE:68310 5	601158935F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3305521 5
Top Hit Database Source	NT	EST HUMAN	IN	NT	NT .	IN	ΙΝ	IN	ĮN.	TN	TN	NT	FN.	LΖ	TN	TN	L	EST_HUMAN	EST_HUMAN	L <sub>Z</sub>	뉟	LN.	LZ.	LN	TN	NT	NT	EST_HUMAN	EST_HUMAN	EST_HUMAN
Top Hit Acesslan No.	0.0E+00 AJ245418.1	0.0E+00 AA174072.1	7657410 NT	1L163284.2	0.0E+00 AF184110.1	0.0E+00 AL163300.2	0.0E+00 AB037521.1	4F195658.1	0.0E+00 AL162331.1	4567887 NT	4557887 NT	E+00 AF153819.1	0.0E+00 AF153819.1	AF167441.1	AB028970.1	AB028970.1	Y18890.1	E+00 BE081527.1	0.0E+00 AA418246.1	0 0F+00 AF086841 1	0.0E+00 AL163278.2	0.0E+00 AL163278.2	0.0E+00 AB037820.1	AB037820.1	M74099.1	6453812 NT	6453812 NT	T56945.1	0.0E+00 T56945.1	BE278730.1
Most Similar (Top) Hit BLAST E Value	0.0E+00	0.0E+00/	00+30.0	0.0E+00	0.0E+00/	0.0E+00	0.0E+00	0.0E+00	0.0E+00/	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	l		8	8		0.0E+00	00-B00	0.0E+00	L				0.0E+00		
Expression Signal	11.57	1.68	1.98	3,31	1.33	4.83	1.95	0.69	1.06	31.32	31.32	1.42	1.42						1.37	19	1.3	1.3	2.72		3.06		2.06			1.18
ORF SEQ ID NO:	30845				30868	30869		30870	30876			30881	30882		30895		١.		30911		30921						30928	26400		
Exon SEQ ID NO:	17862	17881	17884	17886	17887	17888	17889	17891	17896	17899	17899	17900	17900		17911		17916	17922	17923	17070	L.	l_	1_	<u>l</u>	17936	L	17939	13367		17943
Probe SEQ ID NO:	4727	4746	4749	4751	4752	4753	4754	4756	4761	4764	4764	4765	4765	4766	47.76	4776	4781	4787	4788	4704	4799	4799	4800	4800	4801	4804	4804	4806	4806	4810

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Juliga Excursions Expressed in Flacenca	Top Hit Descriptor	601285248F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3607067 5'	Homo sapiens ecotropic viral integration site 28 (EVI2B), mRNA	Homo sapiens ecotropic viral integration site 2B (EVI2B), mRNA	Human AHNAK núolcoprotein mRNA, 5' end	Human haptoglobin and haptoglobin-related protein (HP and HPR) genes, complete ods	Human haptoglobin and haptoglobin-related protein (HP and HPR) genes, complete cds	Homo sapiens cyclophilin-related protein (NKTR) gene, complete cds	Homo sapiens KIAA1084 protein (KIAA1084), mRNA	Homo sapiens KIAA0563 gene product (KIAA0583), mRNA	Human proto-carcogene tyrosine-protein kinase (ABL) gene, exon 1a and exons 2-10, complete cds	Novel human mRNA from chromosome 1, which has similarities to BAT2 genes	Homo sapiens bromodomain adjacent to zinc finger domain, 28 (BAZ2B), mRNA	Homo sapiens bromodomain adjacent to zinc finger domain, 28 (BAZ2B), mRNA	Homo sapiens alpha-3 type IX collagen (COL9A3) gene, promoter region, and exons 1-28	Horno sapiens proteinx0008 (AD013), mRNA	Homo sapiens proteinx0008 (AD013), mRNA	UI-H-BI3-ejw-c-04-0-UI.s1 NCI_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2733294 3'	Homo saplens aldehyde dehydrogenase 12 (ALDH12) mRNA, complete cds	Homo sapiens HSPC024-iso mRNA, complete cds	Human cornexin 43 processed pseudogene	xz89d06.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2871371 3'	Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1)	gales, compres one	Homo sapiens nidogen (enecia) (NID) mXNA	M.fascicularis mRNA for metalloprotease-like, disintegrin-like protein, IVa	Homo sapiens Williams-Bauten syndrome deletion transcript 9 (WBSCR9) mRNA, complete cds	Mus musculus zinc finger transcription factor Kalso mRNA, complete cds	Homo sapiens fragile X mental retardation 2 (FMR2) mRNA	Homo saplens actin, alpha, cardiac muscle (ACTC), mRNA	ZINC FINGER PROTEIN 132	Homo saplens hypothetical protein FLJ20073 (FLJ20073), mRNA	Human Tcr-C-delta gene, exons 1-4; Tcr-V-delta gene, exons 1-2; T-cell receptor alpha (Tcr-alpha) gene, J1-13 J01 segments; and Tcr-C-elpha gene, exons 1-4	
ב באסוו בוסמ	Top Hit Database Source	EST_HUMAN	LN	LN	LN	LN	LΝ	LN	IN	LN L	F	۲N	Þ	Ę	ᅜ	NT	LΝ	<b>EST_HUMAN</b>	LN	IN	Ł	<b>EST_HUMAN</b>	. !	<u> </u>	Į.	٦	N	ΙN	IN	NT	SWISSPROT	LΝ	Ę	
igliic	Top Hit Acession No.	0.0E+00 BE390050.1	5729817 NT	5729817 NT	M80902.1	M69197.1	M69197.1	0.0E+00 AF184110.1	7662479 NT	7662181 NT	J07,583.1	0.0E+00 AL096857.1	7304922 NT	7304922 NT	0.0E+00 AF026801.1	7019320 NT	7019320[NT	0.0E+00 AW 444637.1	0.0E+00 AF303134.1	0.0E+00 AF083242.1	VIG5189.1	0.0E+00 AW339253.1		0.0E+00 AF 240 / 86.1	4505394 NT	X87205.1	0.0E+00 AF084479.1	0.0E+00 AF097416.1	4503766 NT	4885048 NT	P52740	TN 8923080 NT	M94081.1	WOTON:
	Most Similar (Top) Hit BLAST E Value	0.0E+00	0.0E+00	0.0E+00	0.0E+00 M80902.1	0.0E+00 M69197.1	0.0E+00 M69197.1	0.0E+00	0.0E+00	0.0E+00	0.0E+00 U07583.1	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00/	0.0E+00 M65189.1	0.0E+00	200	0.05+00	0.0E+00	0.0E+00 X87205.1	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00 P52740	0.0E+00	0.0E+00 M94081.1	
	Expression Signal	1.13	0.95	0.95	50.79	3.07	3.07	2.07	1.05	1.73	1.15	1.29	0.74	0.74	1.25	0.82	0.82	1.29	1.18	2.01	1.33	0.64		79.9	1.95	1.09	66.0	1.04	4.54	9.88	•	3.41	1.35	lan:
	ORF SEQ ID NO:		30951	30952			30960	30985		30968	30972			30988		31000	31001		31031								31077		31079		31082	İ		١
	Exon SEQ ID NO:	17947	17963	17963	17968	1	17971	17975		17979	17984	l	l	1	18012	18016	18016	ı	18041	18043	18054		ļ	18035	18098	18099	18101	18102			ı	18111		-
	Probe SEQ ID NO:	4814	4830	4830	4835	4838	4838	4842	4844	4846	4851	4856	4872	4872	4882	4886	4886	4907	4911	4913	4924	4925		4500 200 200	4967	4970	4972	4973	4974	4976	4977	4982	4985	3

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Most Signal Most Sinilar Top Hit Acession ID NO: Signal BLASTE No. Source Source	31092 1.35 0.0E+00 M94081.1 NT	31094 1.3	16 31095 1.3 0.0E+00 X94628.1 NT H.saplens MeCP-2 gene	31098 1.46 0.0E+00 M55582.1 INT	31099 2.55	31104	31110 1.19		31113 1.39 0.0E+00 AB014533.1 NT	31114 2.74 0.0E+00 6677648 NT	31115 1.02 0.0E+00 5174560 NT	31116 0.94 0.0E+00 BE007935.1 EST_HUMAN	31117 0.94 0.0E+00 BE007935.1 EST_HUMAN	31118 4.26 0.0E+00 4758199 NT	31120 1.79 0.0E+00 5174560 NT	31121 1.79 0.0E+00 5174560 NT	31122 0.98	31127 11.02 0.0E+00 AF055066.1 NT	2.46 0.0E+00 4505508 NT	31130 2.77		31140 1.56 0.0E+00 4503684 NI	1.17 0.0E+00 AL163285.2 NT	31145 1.14 0.0E+00 D15050.1 NT	31146 1.14 0.0E+00 D15050.1 NT	31147 7.67	31148 7.67 0.0E+00 AB006625.1 NT	31154 1.39 0.0E+00 4504082 NT	31155 1.39 0.0E+00 4504082 NT	31169 1.28 0.0E+00 AL163284.2 NT	31173 0.71 0.0E+00 7662319 NT	31182 1.15
													L										6			_		L	Ĺ			
e Exon ID SEQ ID NO:	4985 18114	87 18116	87 18116	90 18119	91 18120	00 18129	L	<u> </u>	10 18139	11 18140	12 18141	Ĺ	ĺ	5014 18143	16 18145	5016 18145	17 18146	20 18149	5022 18151	23 18152	1	5036 18164		5042 18170	42 18170	18171	5043 18171	Ĺ.,	5049 18177	(	5073 18201	1
Probe SEQ ID NO:	   §	4987	4987	4990	4991	5000	5007	5009	8	. 5011	5012	5013	ន	8	5016	ଝ	5017	(Š	8	8		2	20	ß	ક્ષ	2	22	2	lg	윱	ន	ြင္သ

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Top Hit Descriptor	Human ribosomal protein L21 mRNA, complete cds	Human endogenous retroviral DNA (4-1), complete retroviral segment	601303729F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3638118 6'	Homo saplens desmoplakin (DPI, DPII) (DSP) mRNA	Homo sapiens mRNA for KIAA1043 protein, partial cds	Homo sapiens hypothetical protein FLJ20477 (FLJ20477), mRNA	Homo sapiens hypothetical protein FLJ20477 (FLJ20477), mRNA	no14g09.st NCI_CGAP_Phe1 Homo sapiens cDNA clone iMAGE:1100704 3' similar to TR:E239140 E239140 SPALT PROTEIN ;	no14g09.s1 NCI_CGAP_Phe1 Homo sapiens cDNÁ clone IMAGE:1100704 3' similar to TR:E239140 E239140 SPALT PROTEIN :	no14g09.s1 NCI_CGAP_Phe1 Homo sapiens cDNA ckne IMAGE:1100704 3' similar to TR:E239140 E239140 SPALT PROTEIN;	Homo saciens chromosome Xq28 melanoma antigen family A2a (MAGEA2A), melanoma antigen family A12 (MAGEA12), melanoma antigen family A2b (MAGEA2B), melanoma antigen family A3 (MAGEA3), caltractin (CALT), NAD(P)H dehydrogenase-like protein (NSDHL), and LI>	Horno sapiens chromosome Xq28 melanoma antigen family A2a (MAGEA2A), melanoma antigen family A12 (MACEA12), melanoma antigen family A2b (MAGEA2B), melanoma antigen family A3 (MAGEA3), caltractin (CALT), NAD(P)H dehydrogenase-like protein (NSDHL), and LI>	Homo sapiens DNA mismatch repair protein (MLH3) gene, complete cds	Homo sapiens E2F transcription factor 2 (E2F2) mRNA	Homo sapiens MHC class 1 region	Homo capiens chromosome 21 segment HS21C009	Homo sapiens gammma-cytoplasmic actin (ACTGP3) pseudogene	Homo sapiens titin (TTN) mRNA	Bacillus amyloliquefaciens sacB gene for levansucrase (EC 2.4.1.10)	Human endogenous retrovirus mRNA for gag protein	Homo sapiens vascular endothelial cadherin 2 mRNA, complete cds	Homo sapiens vascular endothelial cadherin 2 mRNA, complete cds	Homo sepions cyclophilin (USA-CYP) mRNA	Homo sapiens ring finger protein (RNF), mRNA	Human cellular fibronectin mRNA	Human cellular fibronectin mRNA	Human endogenous retrovirus-K, LTR U5 and gag gene
Top Hit . Database Source	LN	TN	EST_HUMAN	TN	F	TN	LN.	EST_HUMAN	EST_HUMAN	EST_HUMAN	LN	FZ	NT	LZ	NT	TN	L	LΝ	TN	⊥N	LΝ	LN	TN	LN	⊥N	LN	NT
Top Hit Acession No.	0.0E+00 U14967.1	.0E+00 M10976.1	0.0E+00 BE408863.1	4758199 NT	.0E+00 AB028966.1	8923441 NT	8923441 NT	0.0E+00 AA601246.1	0.0E+00 AA601246.1	.0E+00 AA601246.1	0E+00 U82671.2	0.0E+00 U82671.2	0.0E+00 AF195658.1	4758225 NT	U53588.1	0.0E+00 AL163209.2	D50657.1	4507720 NT	X52988.1	X72791.1	0.0E+00 AF240635.1	0.0E+00 AF240635.1	5454153 NT	5902055 NT	0.0E+00 M10905.1	0.0E+00 M10905.1	Y080321
Most Similar (Top) Hit BLAST E Value	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00 U53588.1	0.0E+00	0.0E+00 D50657.1	0.0E+00	0.0E+00 X52988.1	0.0E+00 X72791.1	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00 Y080321
Expression Signal	7.66	1.25	2.97	4.85	1.43	2:32	2:32	0.72	0.72	0.72	2.09	2.09	0.72	1.09	0.64	1.69	18.98	0.92	3.55	0.61	1.82	1.82	1.18	0.82	4.58	4.58	8.0
ORF SEQ ID NO:		31197		31201	31205	31212	31213	31225	31226	31227	31229	31230			31247							31306	31307	31322			31327
Exon SEQ ID NO:	18215	18225	18227	18230	18238	18247	18247	18259	18259	18259	18262		l	ľ	18282	18289	18292				18334	18334	18335		18356		18358
Probe SEQ ID NO:	5087	5097	5099	5102	5110	5121	5121	5135	5135	5135	5139	5139	5146	5148	5160	5167	5170	5182	5196	5197	5213	5213	5214	5232	5234	5234	5236

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Homo capiene interfeukin 1 receptor accessory protein (IL1RAP) gene, exon 4
AML1-EVI-1=AML1-EVI-1 fusion protein {rearranged translocation} [human, leukemic cell line SKH1, mRNA
Mutant, 5938 nt] 1038g09.X1 NCI\_CGAP\_Pr28 Homo sapiens cDNA done IMAGE:2253376 3' similar to SW:RASD\_DICDI P03967 RAS-LIKE PROTEIN RASD ; Homo saplens polycystic kidney disease (polycystin) and REJ (sperm receptor for egg jelly, sea urchin Homo sapiens core1 UDP-galactose:N-acetylgalactosamine-aipha-R beta 1,3-galactosyltransferase (C1GALT1) mRNA, complete cds Homo sepiens potassium Inwardly-rectifying channel, subfamily J, member 16 (KCNJ16), mRNA exon zw44f12.7 Soares\_total\_fetus\_Nb2HF9\_9w Homo saplens oDNA clone IMAGE:772943 67 zw44f12.1 Soares\_total\_fetus\_Nb2HF9\_9w Homo saplens oDNA clone IMAGE:772943 57 Homo sapiens chromosome 21 segment HS21C006 Homo sapiens placental growth hormone (soform hGH-V3 (hGH-V) mRNA, complete cds member 16 (KCNJ16) Homo sapiens solute carrier family 5 (inositol transporters), member 3 (SLC5A3), mRNA Hamo sapiens aconitase (ACO2) gene, nuclear gene encoding mitochondrial protein, wp06g08 x1 NCI\_CGAP\_Kid12 Homo saplens cDNA clone IMAGE:2464094 3' Homo capient catopate 8, apoptosit-related cysteine protease (CASP8) mRNA Multiple sciencsis associated retrovirus polyprotein (pol) mRNA, partial cds Multiple sciencsis associated retrovirus polyprotein (pol) mRNA, partial cds Homo sapiens SH2-containing protein Nsp2 mRNA, complete cds Homo sapiens potassium inwardly-rectifying channel, subfamily J, Homo sapiens glypican 3 (GPC3) mRNA Homo sapiens acidic 82 kDa protein mRNA (HSU15552), mRNA Top Hit Descriptor Homo sapiens toll-like receptor 8 (TLR8) mRNA, complete cds Homo septens toll-like receptor 8 (TLR8) mRNA, complete cds AV726632 HTC Homo sepiens cDNA done HTCCEA03 Homo saplens keratin 12 (KRT12) gene, complete cds Homo sapiens keratin 12 (KRT12) gene, complete cds Homo sapiens chromosome 21 segment HS21C079 Homo saplens protocadherin 11 (PCDH11), mRNA Homo sapiens 4F2 light chain (LOC51597), mRNA Homo sapiens 4F2 light chain (LOC51597), mRNA nomolog)-like (PKDREJ) mRNA EST\_HUMAN HUMAN EST\_HUMAN EST\_HUMAN HUMAN Top Hit Database Source EST 8923822 NT 7706245 NT Ę ¥ 5174632 NT 5360213 4502582 5902091 8923822 Top Hit Acession 0.0E+00 AL163279.2 0.0E+00 AA425183.1 0.0E+00 AA425183.1 0.0E+00 AF137286.1 0.0E+00 AF137286.1 0.0E+00 A/834954.1 0.0E+00 S690021 0.0E+00 AF009668.1 0.0E+00 AF009688.1 0.0E+00 AF245703.1 0.0E+00 AF245703.1 0.0E+00 AL163206.2 0.0E+00 AF006061.1 0.0E+00 AV726632.1 0.0E+00 AF093093.1 AF124250.1 AF155582.1 0.0E+00 AF167336.1 0.0E+00 AIG85950.1 Š 0.0E+00/ 0.0E+00 0.0E+00/ 0.0E+00 0.0E+00 0.0E+00 0.0E+00 0.0E+00 0.0E+00 Most Similar (Top) Hit BLAST E Value 0.59 110.9 ষ্ 1.21 1.93 24.35 0.85 0.96 8 1.47 1.84 2 Expression Signal ORF SEQ ID NO: 31386 31387 31390 31393 31405 31423 31424 31436 31562 31353 31378 20444 31410 31419 31437 31364 31365 31382 31421 18441 18446 18569 18569 18412 18417 18418 18418 18420 18423 18435 16426 18457 18459 18482 SEG ID 18393 18441 18451 18453 18590 18371 18385 18386 18397 18472 5388 5388 5388 5388 5300 5301 5305 5319 5328 5328 5333 5338 5266 5267 5267 5274 5278 5278 5290 5344 Probe SEQ ID 5250 5253 5266 5294 5297 ö

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Top Hit Descriptor	HUM418D05B Clontech human fefal brain polyA+ mRNA (#6535) Homo sapiens cDNA clone GEN-418D05 5*	HUM418D05B Clontech human fetal brain polyA+ mRNA (#8535) Homo sapiens cDNA clone GEN-418D05 5:	602042322F1 NCI_CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4178988 5	602042322F1 NCI_CGAP_Bm67 Homo saplens cDNA clone IMAGE:4179988 5	601897658F1 NIH_MGC_19 Homo septens cDNA clone IMAGE:4126815 5	Homo saplens calclum channel, voltage-dependent, alpha 1G subunit (CACNA1G), mRNA	wo95b02.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2463051 3' similar to TR:O75054 O75064 KIAA0466 PROTEIN ;	wo95b02.x1 NCJ_CGAP_Kid11 Homo saplens cDNA clone IMAGE:2463051 3' sImilar to TR:O75054 O75054 KIAA0466 PROTEIN;	601150252F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3502909 5	MR0-SN0037-030400-001-h07 SN0037 Homo saplens cDNA	601105291F1 NIH_MGC_15 Hamo sapiens cDNA clane IMAGE:2987903 5'	601105291F1 NIH_MGC_15 Homo sapiens dDNA clone IMAGE:2987903 5'	Homo sapiens olfactory receptor, family 2, subfamily F, member 1 (OR2F1), mRNA	Homo sapiens offactory receptor, family 2, subfamily F, member 1 (OR2F1), mRNA	Homo saplens very long-chain acyl-CoA synthetase homolog 1 mRNA, complete cds	Homo sapiens very long-chain acyl-CoA synthetase homdog 1 mRNA, complete cds	Homo sapiens Surf-5 and Surf-6 genes	Homo sapiens Surf-5 and Surf-6 genes	qf94g10.x1 Soares_placenta_8to9weeks_2NbHP8to9W Homo sapiens cDNA clone IMAGE:1757730 3' shrilar to SW:CADC_HUMAN P55289 BRAIN-CADHERIN PRECURSOR;	EST02238 Fetal brain, Stratagene (cat#936206) Homo sapiens cDNA clone HFBCM48	UI-HF-BL0-adh-d-02-0-UI.r1 NIH_MGC_37 Homo sapiens cDNA clone IMAGE:3061658 5'	H.sapiens isoform 1 gene for L-type calcium channel, exon 14 adnd 15	PM3-CT0263-091299-007-h05 CT0263 Homo saplens cDNA	PM3-CT0263-091299-007-h05 CT0263 Homo sapiens cDNA	PM3-CT0263-091289-007-h05 CT0263 Homo sapiens cDNA	Homo sapiens mRNA for neurexin II, complete cds	Homo sapiens mRNA for neurexin II, complete cds	Human beta-prime-adaptin (BAM22) gene, exon 13	Homo sepiens mRNA for KIAA1641 protein, partial cds
Top Hit Database Source	EST_HUMAN	NAMIN TRE	T	П	EST_HUMAN	NT	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST HUMAN	EST_HUMAN	NT	NT	N	NT	LN	LN	EST_HUMAN	EST_HUMAN	EST_HUMAN	L	EST_HUMAN	EST_HUMAN	EST_HUMAN	TN	LN	ΙN	NT
Top Hit Acession No.	061564.1	161564 4	0.0E+00 BF529031.1	0.0E+00 BF529931.1	0.0E+00 BF313139.1	11434392 NT	.0E+00 A!928181.1	0.0E+00 Al928181.1	0.0E+00 BE260777.1	0.0E+00 AW867316.1	.0E+00 BE292889.1	.0E+00 BE292889.1	11420819 NT	11420819 NT	0.0E+00 AF064254.1	0.0E+00 AF064254.1	.0E+00 AJ224639.1	.0E+00 AJ224639.1	0.0E+00 AI198515.1	0.0E+00 M85719.1	.0E+00 AW 405472.1	),0E+00 Z26269.1	17.1	).0E+00 AW361877.1	0.0E+00 AW361877.1	0.0E+00 AB035266.1	0.0E+00 AB035266.1	3.0E+00 U36261.1	3.0E+00 AB046861.1
Most Similar (Top) Hit BLAST E Value	0.0E+00 D61564.1	0.05+00.061564.1	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00.0	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00		Ĭ		
Expression Signal	0.73	0.79	292	2.92	2.62	4.23	0.59	0.59	1.3	3.95	2.49	2.49	1.7	1.7	4.16	4.16	2.64	2.64	-		4.52							1.67	
ORF SEQ ID NO:	31898		31903	L					32105		32190			32213			32232			1		١	32297	L	١.				
Exan SEQ ID NO:	18824	1007	18827	18827		1	18858	18858	18876	18885	ı	L	1	18918	18926		1	18933	18961	١	18972	ı	1	ı	1	l _			
Probe SEQ ID NO:	5630	2630	5633	5633	5638	5649	5664	5664	5682	5691	5705	5705	5725	5725	5733	5733	6740	5740	5769	5773	5780	5793	5804	5804	5804	5807	5807	2809	5840

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	Top Hit Descriptor	Homo saplens KVLQT1 gene	Homo sapiens KVLQT1 gene	HA2981 Human fetal liver cDNA library Homo sapiens cDNA	Homo saplens protocadherin beta 2 (PCDHB2), mRNA	601584032F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3938551 5'	Homo sapiens amiloride-sensitive cation channel 1, neuronal (degenerin) (ACCN1), mRNA	601345141F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3677843 5'	Mus musculus aczonin (Acz), mRNA	Human L-type calcium channel beta-1 subunit (CACNLB1) gene, exon 13B and isoform beta-1B, complete	spo	Human L-type calcium channel beta-1 subunit (CACNLB1) gene, exon 13B and Isoform beta-1B, complete	COS.	602036272F1 NCI_CGAP_Bm64 Hamo appiens cDNA clone IMAGE:4184321 5	Homo sapiens calcium channel gamma 5 subunit (CACNG5) gene, exon 4 and complete cds	601104462F1 NIH_MGC_14 Homo sapiens cDNA clone IMAGE:3347463 57	hz83d11x1 NCI_CGAP_Lu24 Homo saplens cDNA clone IMAGE:3214581 3' similar to TR:Q62084 Q62084	PHOSPHOLIPASE C NEIGHBORING;	602185852F1 NIH_MGC_45 Homo sapiens cDNA clone IMAGE:4310076 5'	zx89d06.s1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:811883.3'	Homo sapiens cadherin 20 (CDH20) mRNA, complete cds	RC5-ET0027-210600-022-G10 ET0027 Homo saplens cDNA	601645287F1 NIH_MGC_56 Homo saplens cDNA clone IMAGE:3930453 5/	7d72e11.x1 NCI_CGAP_Lu24 Homo sapiens cDNA done IMAGE:3278540 3' similar to SW:DAX1_HUMAN P51843 ORPHAN NUCLEAR RECEPTOR DAX-1. [1];	7472e11.x1 NCI_CGAP_Lu24 Homo saplens oDNA clone IMAGE:3278540 3' similar to SW:DAX1_HUMAN	P51843 ORPHAN NUCLEAR RECEPTOR DAX-1. [1];	xp65f03.x1 NCI_CGAP_Ov39 Homo sapiens cDNA clone IMAGE:2745245 3' similar to TR:P78335 P78335 GUANYLATE KINASE ASSOCIATED PROTEIN. :	801558080F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:3827775 5'	601558060F1 NIH_MGC_58 Homo capiens cDNA clone IMAGE:3827775 5	ha34d06.x1 NCI_CGAP_Kid12 Homo sepiens cDNA clone IMAGE:2875595 3' similar to TR:Q9Z1N3 Op71N3 MYOSIN-RHOGAP PROTEIN, MYR 7	OVA HTOROW 200 and HTOROW Home collans of NA		QV4+H10894-250800-388-410 H10894 Homo sapiens CDNA
	Top Hit Database Source	. TN	LN	EST_HUMAN		EST_HUMAN	Ā	EST_HUMAN			NT			HOMAN	NT	EST_HUMAN		EST_HUMAN	EST_HUMAN	EST_HUMAN			EST_HUMAN	EST HUMAN	Г	EST HUMAN	FST HIMAN		EST HUMAN	FST HIMAN	FOT LIMAN	NAMOR ISS	EST HUMAN
	Top Hit Acession No.	Γ		0.0E+00 A1207616.1	11416801 NT	E+00 BE791173.1	8943	E+00 BE560082.1	10048478 NT		E+00 U86961.1					0.0E+00 BE273983.1		BE503096.1	BF569905.1	0.0E+00 AA454642.1		Γ	E+00 BE958636.1	E+00 BE673986,1		0.0E+00 BE673986.1	0 0F+00 AW 278760 1		0.0E+00 BF031742.1	l _	l		E+00 BF155670.1
	Most Similar (Top) Hit BLAST E Value	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00		0.0E+00	00.700	0.0E+00 066861.1	0.0E+00	0.0E+00	0.0E+00		0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00		0.0E+00	0 0F+00	0.0E+00	0.0E+00	000	00.100	0.0=+00	0.0E+00
	Expression Signal	1.49	1.49	1.23	4.63	1.19	1.1	7.24	2.46		3.06	0	3,00	2.96	0.92	3.07		1.12	2.09	66'0	2.15	4.69	1.19	85.0		0.58	o c	0.96	0.90	, C	3 8	8	60:
	ORF SEQ ID NO:	32400	32401	32410				32442	32443		32444	37700	32443	32466	32469	32470		32484	32491	32495	32524	32526	32531	32550		32551	32555	32565	32568	٠.			32593
	Exan SEQ ID NO:	19088		1.	19114	19119	L	L	19130		19131	,0,0,				ı		19164	19169	19174	19204	19206	19211	19227		19227	19231			1	70007	-	19264
	Probe SEQ ID NO:	5899	5899	5906	5928	5933	5942	5943	5944		5945	2,02	2845	5962	2968	2969		5979	5984	5983	6021	6023	6028	6044		6044	6048	8909	6058	8070	200	8	6082

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	Top Hit Descriptor	zc08h06.r1 Soares_parathyroid_tumor_NbHPA Homo sapiens cDNA clone IMAGE:321755 5'	zc08h06.r1 Soares_parathyroid_tumor_NbHPA Homo sapiens cDNA clone IMAGE:321755 5	Homo sapiens familial mental retardation protain 2 (FMR2) gane, exon 14	601158515F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3505323 5'	601512630F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3914238 5'	601286320F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3613085 5'	II.3-CT0220-111199-028-E04 CT0220 Homo sepiens cDNA	Homo sapiens KIAA0735 gene product; synapilc vesicle protein 28 homolog (KIAA0735), mRNA	Homo sapiens KIAA0735 gene product; synaptic vesícle protein 2B homolog (KIAA0735), mRNA	601677735F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3960200 5'	601677735F1 NIH_MGC_21 Hamo sapiens cDNA clone IMAGE:3960200 5'	601677735F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3960200 5'	Homo sapiens potassium voltage-gated channel, Shal-related subfamily, member 2 (KCND2), mRNA	240h01 r1 Soares_NhHMPu_S1 Homo sepiens cDNA clone IMAGE:685905 5' similar to sex system in IMAM based ut porture to constant in IME prometry is	SWITTO TOWARD PAZOS HITOINE IICAL MITECUL CELL LINE TAOLEIN S.	z/40h01.r1 Soeres_NtHMPu_S1 Hamo sepiens cDNA clone IMAGE:665905 5' similar to SW:YY05_HUMAN P42694 HYPOTHETICAL MYELOID CELL LINE PROTEIN 5, ;	Human T cell surface glycoprotein CD-6 mRNA, complete cds	Human T cell surface glycoprotein CD-6 mRNA, complete cds	601114823F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3355565 5'	QV0-HT0368-090200-099-e09 HT0368 Homo sapiens cDNA	Human neurofibromatosis type 1 (NF-1) mRNA, 3' end of cds	601236276F1 NIH_MGC_44 Homo sepiens cDNA clone IMAGE:3608490 5'	AU137772 PLACE1 Homo sepiens cDNA clone PLACE1007201 5'	Human G protein-coupled receptor GPR-9-6 gene, complete cds	zq81d03.r1 Stratagene hNT neuron (#937233) Homo sepiens cDNA clone IMAGE:648005 5' similar to TR:G854195 G854195 LEUKOCYTE SURFACE PROTEIN ;	Homo sapiens xylosyltransferase II (XTZ), mRNA	Homo capiens xylosyltransferase II (XT2), mRNA	Homo sapiens carcinoembryonic antigen-related cell adhesion molecule 8 (CEACAM8), mRNA	601109532F1 NIH_MGC_16 Homo saplens cDNA clone IMAGE:3350622 5	#91f10.x1 NC_CGAP_Pr28 Homo sapiens cDNA clone IMAGE:2248939 3' similar to TR:Q14839 Q14839 MI-2 PROTEIN. ;
	Top Hit Database Source	EST_HUMAN	EST_HUMAN	LN TA	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	ΓZ	NT	EST_HUMAN	EST_HUMAN	EST_HUMAN	۲	MANAU TOO	EST_HUMAN	EST_HUMAN	N	LN	EST_HUMAN	EST_HUMAN	ΙN	EST_HUMAN	EST_HUMAN	L	EST HUMAN	NT	ĮN.	NT	EST_HUMAN	EST_HUMAN
6	Top Hit Acession No.	V33069.1	V33069.1	0.0E+00 AF012618.1	3E280197.1	3E889610.1	0.0E+00 BE388673.1	1W752848.1	11433071 NT	11433071 NT	3E901608.1	3E901608.1	3E901608.1	9789986 NT	9 00000	0.0E+00 AA193505.1	0.0E+00 AA193506.1	J34625.1	J34625.1	0.0E+00 BE258330.1	0.0E+00 BE156561.1	0.0E+00 M38107.1	3E379007.1	0.0E+00 AU137772.1	345982.1	0.0E+00 AA204740.1	11545913 NT	11545913 NT	11426367 NT	0E+00 BE257173.1	0.0E+00 AI686048.1
	Most Similar (Top) Hit BLAST E Value	0.0E+00	0.0E+00	0.0E+00/	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	20.10	0.0E+00/	0.0E+00/	0.0E+00 U34625.1				0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00
	Expression Signal	1.67	1.67				0.58				1.15	1.15	1.15	10.17		1.28	1.28	10.44	10.44	1.06	1.15	99.0	1.6	1.35	3.33		3.89			3.15	
	ORF SEQ ID NO:	32599	32600				32615					32638	32639	32656		32659	32660	32685		32729		İ					1			32885	
	Exon SEQ ID NO:	Ĺ	19271	19272	19275	1						19300	19300	25819		19318	19318	19339	l	1		19398	19433	ı	1		19489	l	<u> </u>	19527	. I
	Probe SEQ ID NO:	0609	0609	1609	6094	6100	6102	6117	6120	6120	6121	6121	6121	6137	3	6140	6140	. 6163	6163	6203	6213	6223	6229	6265	6287	6316	6317	6317	ශන	6357	6371

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	Top Hit Descriptor	Human anion exchanger (AE1) gene, exons 1-20	601587971F1 NIH_MGC_7 Homo saplens cDNA clone IMAGE:3942329 5'	601687971F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3942329 5'	qt80b11.x1 NCI_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:1859901 3' similar to TR:Q12838 Q12838 TFIIIC ALPHA SUBUNIT;	qi50b11.x1 NCI_CGAP_Bm25 Homo sepiens cDNA clone IMAGE:1859901 3' sImilar to TR:Q12838 Q12838	TFIIIC ALPHA SUBUNIT;	WR0-HT0923-220800-102-b05 HT0923 Homo sapiens cDNA	Homo sapiens peptide transporter 3 (LOC51296), mRNA	Human mRNA for alpha mannosidase II Isozymo, complete cds	IL3-HT0062-010999-014-A04 HT0062 Homo saplens cDNA	7e02c12.xi NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3281302,3' similar to SW:Y176_HUMAN Q14681 HVPOTHETICAL PROTEIN KIAA0176;	Homo sapiens KIAA0285 gene product (KIAA0285), mRNA	AV650020 GLC Homo sapiens cDNA clone GLCCAD09 3'	UI-HF-BLO-acc-g-12-0-UI.s1 NIH_MGC_37 Homo sapiens cDNA clone IMAGE:3058751 3'	y/27b03.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:149933 5	Homo sapiens amiloride sensitive cation channel 1, neuronal (degenerin) (ACCN1), mRNA	Human gene for the light and heavy chains of myeloperoxidase	aa14e07.r1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:813252 5'	T57408.XI NCI_CGAP_OV35 Homo saplens cDNA clone IMAGE:2292087.3' similar to SW:NTCS_HUMAN INCOME AND CHILD AND CHILD AND CHILD AND CHILD AND CHILD AND CHILD AND CHILD AND CHILD AND CHILD AND CHILD AND CHILD AND CHILD AND CHILD AND CHILD AND CHILD AND CHILD AND CHILD AND CHILD AND CHILD AND CHILD AND CHILD AND CHILD AND CHILD AND CHILD AND CHILD AND CHILD AND CHILD AND CHILD AND CHILD AND CHILD AND CHILD AND CHILD AND CHILD AND CHILD AND CHILD AND CHILD AND CHILD AND CHILD AND CHILD AND CHILD AND CHILD AND CHILD AND CHILD AND CHILD AND CHILD AND CHILD AND CHILD AND CHILD AND CHILD AND CHILD AND CHILD AND CHILD AND CHILD AND CHILD AND CHILD AND CHILD AND CHILD AND CHILD AND CHILD AND CHILD AND CHILD AND CHILD AND CHILD AND CHILD AND CHILD AND CHILD AND CHILD AND CHILD AND CHILD AND CHILD AND CHILD AND CHILD AND CHILD AND CHILD AND CHILD AND CHILD AND CHILD AND CHILD AND CHILD AND CHILD AND CHILD AND CHILD AND CHILD AND CHILD AND CHILD AND CHILD AND CHILD AND CHILD AND CHILD AND CHILD AND CHILD AND CHILD AND CHILD AND CHILD AND CHILD AND CHILD AND CHILD AND CHILD AND CHILD AND CHILD AND CHILD AND CHILD AND CHILD AND CHILD AND CHILD AND CHILD AND CHILD AND CHILD AND CHILD AND CHILD AND CHILD AND CHILD AND CHILD AND CHILD AND CHILD AND CHILD AND CHILD AND CHILD AND CHILD AND CHILD AND CHILD AND CHILD AND CHILD AND CHILD AND CHILD AND CHILD AND CHILD AND CHILD AND CHILD AND CHILD AND CHILD AND CHILD AND CHILD AND CHILD AND CHILD AND CHILD AND CHILD AND CHILD AND CHILD AND CHILD AND CHILD AND CHILD AND CHILD AND CHILD AND CHILD AND CHILD AND CHILD AND CHILD AND CHILD AND CHILD AND CHILD AND CHILD AND CHILD AND CHILD AND CHILD AND CHILD AND CHILD AND CHILD AND CHILD AND CHILD AND CHILD AND CHILD AND CHILD AND CHILD AND CHILD AND CHILD AND CHILD AND CHILD AND CHILD AND CHILD AND CHILD AND CHILD AND CHILD AND CHILD AND CHILD AND CHILD AND CHILD AND CHILD AND CHILD AND CHILD AND CHILD AND CHILD AND CHILD AND CHILD AND CHILD AND CHILD AND CHILD AND CHILD AND CHILD AND CHILD AND CHILD AND CHILD AND CHILD AND CHILD AND CHILD	R01305368F1 NIH MGC 38 Homo sepiens cDNA clone IMAGE:3639616 51	601305368F1 NIH_MGC_39 Homo saplens cDNA clone IMAGE:3639816 5'	WRO-BT0284-221199-002-f11 BT0284 Homo saplens cDNA	WR0-BT0264-221199-002-f11 BT0264 Homo sapiens cDNA	AU119245 HEMBA1 Homo sapiens cDNA done HEMBA1005360 5'	AU119245 HEMBA1 Homo sapiens cDNA clone HEMBA1005350 5'	601468712F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3871899 5'	H.sapiens germline immunoglobulin heavy chain, variable region, (13-2)	ws25c07.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2498220 3'	601105344F1 NIH_MGC_15 Homo saplens cDNA clone IMAGE.2987963 5'	601105344F1 NIH MGC 15 Homo sapiens cDNA clone IMAGE:2987963 5'	601443175F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3847291 5
	Top Hit Database Source	LN L	EST_HUMAN	EST_HUMAN	EST HUMAN		EST_HUMAN	EST_HUMAN	LN	NT.	EST_HUMAN	EST HUMAN	¥	EST_HUMAN	EST_HUMAN	EST_HUMAN	N	Z.	EST_HUMAN		EST HIMAN	EST HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	LN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN
	Top Hit Acession No.	L35930.1	0.0E+00 BE797385.1	0.0E+00 BE797385.1	0.0E+00 A1198025.1		0.0E+00 AI198025.1	0.0E+00 BF357123.1	11435630 NT	D55649.1	0.0E+00 AW178142.1	0.0E+00 BE674544.1	7662039 NT	0.0E+00 AV650020.1	0.0E+00 AW 575598.1	H01255.1	11426293 NT	X15377.1	0.0E+00 AA456375.1		0.0E+00 AI612841.1	0.0E+00 BE735989.1	0.0E+00 AW748596.1	0.0E+00 AW748596.1	0.0E+00 AU119245.1	0.0E+00 AU119245.1	0.0E+00 BE780453.1	0.0E+00 X92217.1	0.0E+00 AI989483.1	0.0E+00 BE293153.1	0.0E+00 BE283153.1	0.0E+00 BE867657.1
	Most Similar (Top) Hit BLAST E Value	0.0E+00 L35930.1	0.0E+00	0.0E+00	0.0E+00		0.0E+00	0.0E+00	0.0E+00	0.0E+00 D55849.1	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00 H01255.1	0.0E+00	0.0E+00 X15377.1	0.0E+00		0.05+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00
	Expression Signal	1.32	96.0	0.96	0.71		0.71	1111	1.3	0.59	1.07	0.6	0.77	9.28	3.46	4.53	0.71	1.67	1.17		1.04	4.27	0.86	0.86	52.21	52.21	0.8	0.84	1.71	4.06	4.06	1.07
	ORF SEQ ID NO:		32908		32922					32943		32980			33006		33018			L	33024	L	33037	33038		33041		33048				
	SEQ ID NO:	ı	1	1	19562	1			l l	ı	1	19817	19621		1	İ			L	l	19661				19673	19673		19678	1	1	ΙI	19735
	Probe SEQ ID NO:	6375	6383	883	6393		6393	6395	6403	6413	6428	6450	6454	6468	6477	6480	6488	6492	6494		0490 8504	6501	6505	9202	6507	9207	6512	6513	6527	6541	6541	6573

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Top Hit Descriptor	UI-HF-BL0-acc-h-02-0-UI.r1 NIH_MGC_37 Homo sapiens cDNA clone IMAGE:3059931 5'	UI-HF-BL0-acc-h-02-0-UI.r1 NIH_MGC_37 Homo sapiens cDNA clone IMAGE:3059931 5'	AV719444 GLC Homo capiens cDNA clone GLCEHC06 5'	601681150F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3951301 5'	601681150F1 NIH_MGC_9 Homo seplens cDNA clone IMAGE:3951301 5'	Homo capiens low voltage-activated T-type calcitum channel alpha 1G spilce variant CavT.1a (CACNA1G)	ministry, complete cus	Homo septens when (1502) gene, exans 36, 59, 40 and 41	Homo sapiens transformation/transcription domain-associated protein (TRRAP), mRNA	au96h08.y1 Schnelder fetal brain 00004 Homo saplens cDNA clone IMAGE:2784159 5' similar to TR:015390 015390 GT24. [3] TR:043840 TR:043206 ;	au96h08.yl Schneider fetal bratn 00004 Homo saplens cDNA clone IMAGE:2784159 5' simitar to TR:O15390 O15390 GT24. [3] TR:O43840 TR:O43206 ;	zb20e06.r1 Soares, fetal lung, NbHL19W Homo sapiens cDNA clone IMAGE:302626 5' similar to SW:ZN45 HUMAN Q02386 ZINC FINGER PROTEIN 45	zb20e06.r1 Soares feta Jung NbHL19W Homo sapiens cDNA clone IMAGE:302626 5' similar to	SW:ZN45_HUMAN Q02386 ZINC FINGER PROTEIN 45;	601589371F1 NIH_MGC_7 Homo saplens cDNA clone IMAGE:3943504 5'	601587561F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3941847 5'	QV1-GN0065-140800-318-h02 GN0065 Homo sapiens cDNA	QV1-GN0065-140800-318-h02 GN0065 Homo sapiens cDNA	601512058F1 NIH_MGC_71 Hamo saplens cDNA clane IMAGE:3913311 5*	601512058F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3913311 5'	Human antigen CD27 gene, exons 1;2	Homo sapiens chromosome 21 segment HS21C004	Homo saplens chramosome 21 segment HS21C004	Homo sapiens zona pellucida glycoprotein 3A (sperm receptor) (ZP3A), mRNA	tt31f11.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2242413 3' similar to SW:WNT3_MOUSE P17553 WNT-3 PROTO-ONCOGENE PROTEIN PRECURSOR	Homo capiens zinc finger homeodomain protein (ATBF1-A) mRNA, complete cds	UI-HF-BN0-ama-c-01-0-UI:r1 NIH_MGC_50 Homo sapiens oDNA clone IMAGE:3081217 5'	zw52c03.r1 Scares_total_fetus_Nb2HF8_9w Homo saplens cDNA clone IMAGE:773668 5	601885317F1 NIH_MGC_57 Homo saplens cDNA clone IMAGE:4103693 5'	QV3-BN0047-300800-278-c06 BN0047 Homo sapiens cDNA
Top Hit Database Source	П	EST_HUMAN (	EST_HUMAN	EST_HUMAN	EST_HUMAN					EST_HUMAN	EST_HUMAN		Τ	EST_HUMAN		EST_HUMAN	EST_HUMAN	EST_HUMAN		T_HUMAN		NT	NT		EST HUMAN	Г	EST HUMAN	П	HUMAN	П
Top Hit Acession No.	0.0E+00 AW406348.1	AW406348.1	qV719444.1	3E898340.1	3E898340.1		U.UE+UU AFTSUBBU.T	-48545.1	11420658 NT	0E+00 AW163640.1	0E+00 AW163640.1	0F+00 W37163.1		0.0E+00 W37163.1	BE794853.1	BE799873.1	BE767955.1	BE767955.1	BE889813.1	0.0E+00 BE889813.1	L24493.1	AL163204.2	AL163204.2	G005983 NT	A1638412 1	1,32832.1	AW505430.1	AA434584.1	0.0E+00 BF217200.1	BE925875.1
Most Similar (Top) Hit BLAST E Value	0.0E+00/	0.0E+00	0.0E+00	0.0E+00	0.0E+00	100	0.0E+00	0.0E+00 L48546.1	0.0E+00	0.0E+00	0.0E+00	0.05+00		0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	00+400	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00
Expression Signal	1.81	1.81	0.94	0.74	0.74	,	2.13	0.64	0.99	3.5	3.5	1.08		1.06	1.21	5.1	1.38	1.38	6.83	6.83	4.51	2.62	2.62	3.68	4 12	1.46	0.82	4.11	1.13	1.63
ORF SEQ ID NO:	33158	33159	33188		1		33199	33202	33203	33210	33211	33214		33215	33232	33239	33240	33241	33244		33253			33265	33268	33270				33307
Exon SEQ ID NO:	19769	1	Ι.	19808	1		1981	- [	19816	19823	19823	19827		19827	19842	19849						19868		19874	ſ	Ĺ	(	Ĺ	1 1	19912
Probe SEQ ID NO:	6099	6099	6640	6649	6649		2000	6655	6657	6664	6664	9999		8999	6684	1699	6692	6692	9699	9699	6705	6710	6710	6716	6720	6722	6735	6737	6751	6756

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Top Hit Descriptor	Homo sepiens solute carrier family 1 (high affinity aspartate/glutamate transporter), member 6 (SLC1A6), mRNA mRNA	Homo sepiene solute carrier family 1 (high affinity aspartate/glutamate transporter), member 6 (SLC1A6), mRNA	hg62e04.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE.2952126 3'	AU125928 NT2RM4 Homo saplens cDNA clone NT2RM4002430 5	PM2-NN0174-260700-001-h10 NN0174 Homo sapiens cDNA	PM2-NN0174-260700-001-h10 NN0174 Homo sapiens cDNA	CN0-HT0143-270999-062-d08 HT0143 Homo sapiens cDNA	RC0-BN0121-280300-032-e04 BN0121 Homo sapiens cDNA	RC0-BN0121-280300-032-e04 BN0121 Homo sapiens cDNA	PN/3-HT0520-230200-002-c08 HT0520 Homo sapiens cDNA	IL5-GN0032-180900-145-d07 GN0032 Homo sapiens cDNA	тр88e03.r1 Stratagene HeLa cell s3 937216 Homo sapiens cDNA clone IMAGE:627292 5	Human salivary peroxidase mRNA, complete cds	7a49b07.x1 NCL_CGAP_GC6 Homo sapiens cDNA clone IMAGE:3222037 3' similar to TR:Q9Z285 Q9Z285	TEKTIN.;	I.3-ST0024-230799-001-B01 ST0024 Homo sapiens cDNA	IL3-ST0024-230799-001-B01 ST0024 Homo saplens cDNA	Homo sapiens CD6 antigen (CD6), mRNA	DKFZp434D2021_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434D2021 6'	H.saplens immunoglobulin heavy chain gene, variable region	oo10001.x1 Soares_NSF_F8_9W_DT_PA_P_S1 Homo sapiens cDNA clone IMAGE:1565761 3' sImilar to	RECEDES CECOES IEN II OI.	601567370F1 NIH_MGC_21 Hamo sapiens cDNA cione IMAGE:3642080 5	601339977F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3682267 57	601443667F1 NIH_MGC_65 Homo saplens cDNA clone IMAGE:3847697 5'	601443657F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE;3847697 5'	7249f03.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3231581 3' similar to SW:GG95_HUMAN	Q083/9 GOLGIN-95.	7549f03.x1 NCI_CGAP_Lu24 Homo sepiens oDNA clone IMAGE:3231581 3' similar to SW:GG85_HUMAN_ Coss2to COL CINLOS	CM1-HT0877-060900-397-011 HT0877 Homo sapiens cDNA	-24402 14 Comes NEUNDI C1 Homo conjens CINA clime IMACE 685332 5	TOTACO I OCERCE MILLIAME LE OLI FIGURO SEPRETA COLLA CICILIO CONTROLLA COLLA CICILIO COLLA CICILIO COLLA CICILIO COLLA CICILIO COLLA CICILIO COLLA CICILIO COLLA CICILIO COLLA CICILIO COLLA CICILIO COLLA CICILIO COLLA CICILIO COLLA CICILIO COLLA CICILIO COLLA CICILIO COLLA CICILIO COLLA CICILIO COLLA CICILIO COLLA CICILIO COLLA CICILIO COLLA CICILIO COLLA CICILIO COLLA CICILIO COLLA CICILIO COLLA CICILIO COLLA CICILIO COLLA CICILIO COLLA CICILIO COLLA CICILIO COLLA CICILIO COLLA CICILIO COLLA CICILIO COLLA CICILIO COLLA CICILIO COLLA CICILIO COLLA CICILIO COLLA CICILIO COLLA CICILIO COLLA CICILIO COLLA CICILIO COLLA CICILIO COLLA CICILIO COLLA CICILIO COLLA CICILIO COLLA CICILIO COLLA CICILIO COLLA CICILIO COLLA CICILIO COLLA CICILIO COLLA CICILIO COLLA CICILIO COLLA CICILIO COLLA CICILIO COLLA CICILIO COLLA CICILIO COLLA CICILIO COLLA CICILIO COLLA CICILIO COLLA CICILIO COLLA CICILIO COLLA CICILIO COLLA CICILIO COLLA CICILIO COLLA CICILIO COLLA CICILIO COLLA CICILIO COLLA CICILIO COLLA CICILIO COLLA CICILIO COLLA CICILIO COLLA CICILIO COLLA CICILIO COLLA CICILIO COLLA CICILIO COLLA CICILIO COLLA CICILIO COLLA CICILIO COLLA CICILIO COLLA CICILIO COLLA CICILIO COLLA CICILIO COLLA CICILIO COLLA CICILIO COLLA CICILIO COLLA CICILIO COLLA CICILIO COLLA CICILIO COLLA CICILIO COLLA CICILIO COLLA CICILIO COLLA CICILIO COLLA CICILIO COLLA CICILIO COLLA CICILIO COLLA CICILIO COLLA CICILIO COLLA CICILIO COLLA CICILIO COLLA CICILIO COLLA CICILIO COLLA CICILIO COLLA CICILIO COLLA CICILIO COLLA CICILIO COLLA CICILIO COLLA CICILIO COLLA CICILIO COLLA CICILIO COLLA CICILIO COLLA CICILIO COLLA CICILIO COLLA CICILIO COLLA CICILIO COLLA CICILIO COLLA CICILIO COLLA CICILIO COLLA CICILIO COLLA CICILIO COLLA CICILIO COLLA CICILIO COLLA CICILIO CICILIO CICILIO CICILIO CICILIO CICILIO CICILIO CICILIO CICILIO CICILIO CICILIO CICILIO CICILIO CICILIO CICILIO CICILIO CICILIO CICILIO CICILIO CICILIO CICILIO CICILIO CICILIO CICILIO CICILIO CICILIO CICILIO CICILIO CICILIO CICILIO CICILIO CICILIO CICILIO CICILIO CICILIO CICILIO CICILIO CICILIO
Top Hit Database Source	۲	Ŀ	T_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	<b>EST_HUMAN</b>	EST_HUMAN	EST_HUMAN	EST HUMAN	LN		EST_HUMAN	<b>EST_HUMAN</b>	EST_HUMAN	N	EST_HUMAN	NT		ESI_HOWAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST HUMAN		EST HOMAN	1444	EST DIMAN	101	EST HOMAN
Top Hit Acession No.	11426768 NT	11428758 NT	0.0E+00 AW611964.1	3.0E+00 AU125928.1	0.0E+00 BE701434.1	3.0E+00 BE701434.1	0.0E+00 BE142363.1	3.0E+00 BE006012.1	3.0E+00 BE006012.1	1.0E+00 BE169131.1	0.0E+00 BF085667.1	0.0E+00 AA190755.1	0.0E+00 U39573.1		0.0E+00 BE671987.1	0.0E+00 AI940621.1	0.0E+00 AI940621.1	11435626 NT	0.0E+00 AL042443.1	0.0E+00 X56163.1		0.0E+00 AI1682/0.1	0.0E+00 BE734087.1	0,0E+00 BE566381.1	0.0E+00 BE867889.1	0.0E+00 BE867889.1		0.0E+00 BE550162.1		0.0E+00 BE089278 4	Dr.00037.0. 1	0.0E+00 AA195106.1
Most Similar (Top) Hit BLAST E Value	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00		0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00		0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00		0.0E+00	L	0.0E+00	2011	0.05.+00
Expression Signal	0.76	0.76	0.59	1.64	0.58	0.58	1.27	2.43	2.43	7.79	2.04	3.33	0.83		0.76	5.73	6.73	2.15	0.73	11.05		0.92	0.85	1.28	13.63	13.63		1.74	,	1./4	00.	1.4
ORF SEQ ID NO:	33342	33343	33345	33366	33368	33369	33393	33416		33438		33663	33676		33678				33617	33618						31510	<u> </u>	33558				33594
SEO ID	19944	<u> </u>		19962	_	L	<u>.</u>	l_	L		<u>L.</u>	L		1		L	L	<u> </u>	L	L			20200	1	l	1		8148	l			20172
Probe SEQ ID NO:	6789	6780	6790	8089	6810	6810	6832	6854	6854	6876	82/8	6915	6926		9830	6940	6940	6951	6963	6964		6967	6972	6994	8669	8669		7004		2004	0507	7036

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Top Hit Descriptor	Homo sapiens catenin (cadherin-associated protein), data 2 (neural plakophilin-related arm-repeat protein) (CTNND2), mRNA	Homo sapiens sodium channel, nonvoltage-gated 1, beta (Liddle syndrome) (SCNIN1B), mRNA	802185852F1 NIH_MGC_45 Homo sapiens cDNA clone IMAGE:4310076 57	Homo saplens Bloom syndrome (BLM) mRNA	Human MYCL2 gene, complete cds	Homo sapiens cadherin 20 (CDH20) mRNA, complete cds	Homo saplens cadherin 20 (CDH20) mRNA, complete cds	Human neurofibromatosis type 1 gene, exon x6	Homo sapiens melanoma antigen, family B, 2 (MAGEB2), mRNA	601115515F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3356330 57	wf21c09.x1 Scares_Dieckgreafe_colon_NHUC Homo sapiens cDNA clone IMAGE:2351248 3' similar to gb:M74297 HOMEOBOX PROTEIN HOX.44 (HUMAN);contains PTR5.b1 MER22 MER22 repetitive	element;	wf21c09.x1 Soares_Dleckgraefe_colon_NHUC Homo saptens cDNA clone IMAGE:2351248 3' similar to gb:M74297 HOMEOBOX PROTEIN HOX-A4 (HUMAN);contains PTR5,b1 MER22 MER22 repetitive	element;	AU118478 HEMBA1 Homo sapiens cDNA clone HEMBA1003679 5	601148954F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3501829 5'	H.saplens mRNA for latent transforming growth factor-beta binding protein (LTBP-2)	H.sapiens mRNA for latent transforming growth factor-beta binding protein (LTBP-2)	Homo sapiens ciliary dynein heavy chain 9 (DNAH9) mRNA, complete cds	Homo sapiens ciliary dynein heavy chain 9 (DNAH9) mRNA, complete cds	Homo sapiens NALP1 mRNA, complete cds	QV3-NT0022-140600-223-f01 NT0022 Homo sapiens cDNA	602185852F1 NIH_MGC_45 Homo sapiens cDNA clone IMAGE:4310076 5'	Homo sapiens mRNA for dynein heavy chain (DNAH9 gene)	Homo sapiens mRNA for dynein heavy chain (DNAH9 gene)	Human type IV sodium channel alpha polypeptide (SCN4A) gene, exon 19	UI-HF-BR0p-aka-d-10-0-UI.r1 NIH_MGC_52 Homo capiens cDNA clone IMAGE:3076290 5	UI-HF-BR0p-aka-d-10-0-UI.r1 NIH_MGC_52 Homo sepiens cDNA clone IMAGE:3076290 5	DKFZp434D2211_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434D2211 5	DKFZp434D2211_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434D2211 5'	601889823F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4123948 5
Top Hit Database Source	Į	NT	EST_HUMAN	NT	N	N	NT	LN	Z	EST_HUMAN		EST_HUMAN		EST_HUMAN	EST_HUMAN	EST_HUMAN	TN	IN	٦	TN	IN	EST_HUMAN	EST_HUMAN	LN LN	LN	ΙN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN
Top Hit Acession No.	11034810 NT	11431474 NT	3F569905.1	4557384 NT	0.0E+00 J03069.1	0.0E+00 AF217289.1	AF217289.1	M38113.1	11420775 NT	BE256708.1		0.0E+00 AI660911.1				BE262941.1	237976.1	237976.1	AF257737.1	0.0E+00 AF257737.1	AF310105.1	BE762770.1	BF569905.1	AJ404468.1	AJ404468.1	L01978.1	AW502362.1	0.0E+00 AW502362.1	.0E+00 AL039581.1	0.0E+00 AL039581.1	.0E+00 BF306996.1
Most Similar (Top) Hit BLAST E Value	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00		0.0E+00		0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00
Expression Signal	11.81	1.41	2.69	0.68	2.06	2.56	2.56	1.07	3.59	0.7		0.62		0.62	1.21	7.52	2.72	2.72	3.01	3.01	1.28	0.61	2.56	0.78	0.78	3.25	0.72	0.72	0.87	0.87	5.81
ORF SEQ ID NO:			33529				33600		31515			31493		31494		31461	31462	31463	31464	31465					33720					33739	-
SEO ID NO:	1	l		1	20129	ı	1	20178	18522	l	ļ .	18537		18537	18546	18549	1		ŀ	18551	1	I	ı	ı	l l	ı	ļ.		İ	ı	
Probe SEQ ID NO:	7044	7048	7061	7068	7076	7083	7083	7084	7095	7099		7111		7111	7120	7123	7124	7124	7125	7125	7132	7137	7142	7144	7144	7148	7153	7153	7162	7162	7171

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				_	_		_				_	_	_	_	_	_					_			_				
Top Hit Descriptor	Human chromosome 16 creatine transporter (SLC6A8) and (CDM) paralogous genes, complete cds	Novel human gene mapping to chomosome 13	xodobūz.x1 NCI_CGAP_Ut1 Homo sapiens cDNA done IMAGE:2706458 3' similar to TR:094895 094895 KIAA0803 PROTEIN ;	Homo sapiens mRNA for vascular cadherin-2, complete cds	Homo sapiens mRNA for vascular cadherin-2, complete cds	AU137738 PLACE1 Homo sapiens cDNA clone PLACE1007120 5'	AU137738 PLACE1 Homo sapiens cDNA clane PLACE1007120 5'	EST388878 MAGE resequences, MAGC Homo saplens cDNA	601113958F1 NIH_MGC_16 Homo saplens cDNA clone IMAGE:3354566 5'	Human type VI sodium channel alpha polypeptide (SCN4A) gene, exon 14	Homo sapiens mRNA for KIAA0466 protein, partial cds	Homo saplens mRNA for KIAA0466 protein, partial cds	AU133213 NT2RP4 Homo sapiens cDNA clone NT2RP4001556 5'	Homo saplens membrane protein CH1 (CH1), mRNA	AU143706 Y79AA1 Homo sapiens cDNA clone Y79AA1002365 5'	Homo sapiens netrin 1 (NTN1), mRNA	601431819F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3917164 5'	801431819F1 NIH_MGC_72 Hamo saplens aDNA clone IMAGE:3917164 5'	Homo sapiens keratin 12 (KRT12) gene, complete cds	Homo sapiens keratin 12 (KRT12) gene, complete cds	601580948F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3929722 5'	801580948F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3929722 5'	Homo sapiens vitamin D (1,25- dihydroxyvitamin D3) receptor (VDR), mRNA	Homo sapiens vttamin D (1,25- dihydroxyvitamin D3) receptor (VDR), mRNA	Homo sapiens voltage-dependent calcium channel alpha 1G subunit isoform ae (CACNA1G) mRNA, complete cds	qe67a07.x1 Soares_placenta_8to9weeks_2NbHP8to9W Homo sapiens cDNA clone IMAGE:1714644.3' similar to SW-ARSD_HIMAN P61689 ARYLSULFATASE D PRECURSOR contains element HGR	repetitive element;	qc87a07.x1 Soares_placenta_8tb9weeks_2NbHP8tb9W Homo sapiens cDNA done IMAGE:1714844.3' similar to SW-ARSD_HUMAN P51689 ARYLSULFATASE D PRECURSOR ;contains element HGR repetitive element;
Top Hit Database Source	TN	LN	EST_HUMAN	L	NT	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	IN	LN	NT	EST_HUMAN	LN	EST_HUMAN	FN	EST_HUMAN	EST_HUMAN	TN	TN	EST_HUMAN	EST_HUMAN	LΝ	FZ	Ę		EST_HUMAN	EST_HUMAN
Top Hit Acession No.	141302.1	0.0E+00 AL049784.1	0.0E+00 AW513069.1	0.0E+00 AB026893.1	0.0E+00 AB026893.1	0.0E+00 AU137738.1	0.0E+00 AU137738.1	0.0E+00 AW954806.1	0.0E+00 BE254103.1	.01973.1	0.0E+00 AB007935.1	0.0E+00 AB007935.1	0.0E+00 AU133213.1	11428081 NT	0.0E+00 AU143706.1	TN 628839	0.0E+00 BE891286.1	0.0E+00 BE891286.1	0.0E+00 AF137286.1	0.0E+00 AF137286.1	0.0E+00 BE747231.1	0.0E+00 BE747231.1	11436699 NT	11436699 NT	0.0E+00 AF227744.1		0.0E+00 AI128344.1	0.0E+00 AI128344.1
Most Similar (Top) Hit BLAST E Value	0.0E+00 U41302.1	0.0E+00	0.0E+00.	0.0E+00	0.0E+00/	0.0E+00	0.0E+00/	0.0E+00	0.0E+00	0.0E+00 L01973.1	0.0E+00/	0.0E+00/	0.0E+00/	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00		0.0E+00	0.0E+00
Expression Signel	2.13	1.15	0.64	0.62	0.62	0.84	0.84	1.16	0.72	1	1.03	1.03	1.47	1.06	2.82	0.71	1.25	1.25	2.43	2.43	29'0	0.67	4.07	4.07	0.63		36.37	36.37
ORF SEQ ID NO:	33752	33499	33606	33790	33791	33797	33798	33804	33805	33819	33829	33830	33837	33857		33864	33872	33873				33902	33913	33914	33927		33952	
Exon SEQ ID NO:	20309	20084	20089	20340	20340	20345	20345	20351	20352	20366	20373	20373	20379	20385	l	ı	1	1	18569	18569	20440	20440	20450	20450	1	ł	20484	
Probe SEQ ID NO:	7177	7219	7225	7257	7257	7262	7262	7268	7269	7283	7291	7231	7297	7313	7319	7320	7329	7329	7350	7350	7361	7361	7371	7371	7385		7406	7406

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Top Hit Descriptor	Homo saplens candidate taste receptor T2R9 gene, complete cds	Homo saplens candidate taste receptor T2R9 gene, complete cds	Homo sapiens myosin, heavy polypeptide 8, skeletal muscle, perinatal (MYH8), mRNA	Homo sapiens myosin, heavy polypeptide 8, skeletal muscle, perinatal (MYHB), mRNA	602035089F1 NCI_CGAP_Brn64 Hamo saplens cDNA clone IMAGE:4182839 5'	zn60f09.r1 Stratagene muscle 937209 Homo sapiens cDNA clone IMAGE:562601 5' similar to TR:CB06562 Cranasso nest it in	DKFZp434B0226 r1 434 (synonym: htes3) Homo saplens cDNA clone DKFZp434B0226 5	DKFZp434B0226 r1 434 (synchym: htes3) Homo sapiens cDNA clone DKFZp434B0226 5	Homo sapiens partial mRNA for LTRPC5 protein (LTRPC5 gene)	601174576F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3529794 5'	Homo sapiens hypothetical protein (FLJ20261), mRNA	AU118607 HEMBA1 Homo sapiens cDNA clone HEMBA1003969 5'	Homo sapiens ankyrin 1 (ANK1) mRNA, complete cds	Homo sapiens ankyrin 1 (ANK1) mRNA, complete cds	Homo saplens adlican mRNA, complete cds	H.sapiens DNA for ZNGP2 pseudogene, exon 4	Human P2x1 receptor mRNA, complete cds	Human P2x1 receptor mRNA, complete cds	EST368573 MAGE resequences, MAGD Horiro sapiens oDNA	EST362586 MAGE resequences, MAGA Homo sapiens cDNA	AF001543 Human cDNA (Chandrasekharappa,S.C.) Homo sapiens cDNA clone kappa_200	AF001543 Human cDNA (Chandrasekharappa,S.C.) Homo sapiens cDNA clone kappa_200	AF001543 Human cDNA (Chandrasekharappa,S.C.) Homo sapiens cDNA clone kappa_200	Human BTF3 protein homologue gene, complete cds	601302679F1 NIH_MGC_21 Homo saplens cDNA clone IMAGE:3637434 5'	ym88h10,r1 Soares adult brain N2b4HB55Y Homo saplens cDNA clone IMAGE:166051 5'	x539a05,y1 NCI_CGAP_Lu31 Homo sapiens cDNA clone IMAGE:2578640 5' similar to TR:Q08050 Q08050	HNF3/FH TRANSCRIPTION FACTOR GENESIS;	AU117553 HEMBA1 Homo seplens oDNA clone HEMBA1001661 6'	Homo sapiens glucagon-like peptide 2 receptor (GLP2R), mRNA	zn5602.r1 Stratagene muscle 937209 Homo sapiens cDNA clone IMAGE:562203 5' similar to gb:X03740 MYOSIN HEAVY CHAIN, SKELETAL MUSCLE (HUMAN);	WR0-AN0083-270900-004-f07 AN0083 Homo saplens cDNA
Top Hit Database Source	LN	LN L	IN	۲	EST_HUMAN	MAN ILL FOR	EST HUMAN	EST HUMAN	L	EST_HUMAN	11427965 NT	EST HUMAN	٦	NT	۲	ΝΤ	NT	NT	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	NT.	EST HUMAN	EST_HUMAN		EST_HUMAN	EST_HUMAN	IN	EST_HUMAN	EST_HUMAN
Top Hit Acession No.	0.0E+00 AF227135.1	4F227135.1	11426392 NT	11426392 NT	0.0E+00 BF337375.1	A 4.004E0 4	0.0E+00.AI 079497.1	AL 079497.1	4.1270996.1	3E295489.1	0.0E+00 11427965	0.0E+00 AU118607.1	0.0E+00 AF005213.1	.0E+00 AF005213.1	0.0E+00 AF245505.1	X70172.1	J45448.1	U45448.1	0.0E+00 AW956503.1	0.0E+00 AW950516.1	.0E+00 AF001543.1	0.0E+00 AF001543.1	0.0E+00 AF001543.1	0.0E+00 M90354.1	0.0E+00 BE408293.1	.0E+00 R87430.1		0.0E+00 AW239326.1	0.0E+00 AU117553.1	11427135 NT	).0E+00 AA211663.1	3.0E+00 BF229235.1
Most Similar (Top) Hit BLAST E Value	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	000	00.0	0 0F+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00 X70172.1	0.0E+00 U45448.1	0.0E+00 U45448.1	00+30.0	0.0E+00	00+30.0	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00		0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00
Expression Signal	0.74	0.74	5.41	5.41	13.11	9	77.0	0 77	0.69	1.13	0.91	1.33	1.71	1.71	0.83	6.47	5.81	5.81	0.89	2.31	1.03	1.03	1.03	0.58	0.8	1.09		1.81	1.5	3.8	0.62	
ORF SEQ ID NO:	33955				l		33067	33968	33980			١	34015										34080		34101			34129		34146		
SEQ ID NO:	20486			Į.	1		20493	i		ı	ı	20541		20542	1_	L	!	L	l	ı	20504			!	20625	L	L	20653	20670	1	1	1
Probe SEQ ID NO:	7408	7408	7410	7410	7413	7446	0672	7420	7431	7461	7463	7466	7467	7467	7479	7487	7489	7489	7502	7504	7531	7531	7531	7552	7553	7580		7581	7600	7602	7622	7629

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Olligie Excl. 1 1000 Explosed III 1 1000 Explosed III 1 1000 Explosed III 1 1000 Explosed III 1 1000 Explosed III 1 1000 Explosed III 1 1000 Explosed III 1 1000 Explosed III 1 1000 Explosed III 1 1000 Explosed III 1 1000 Explosed III 1 1000 Explosed III 1 1000 Explosed III 1 1000 Explosed III 1 1000 Explosed III 1 1000 Explosed III 1 1000 Explosed III 1 1000 Explosed III 1 1000 Explosed III 1 1000 Explosed III 1 1000 Explosed III 1 1000 Explosed III 1 1000 Explosed III 1 1000 Explosed III 1 1000 Explosed III 1 1000 Explosed III 1 1000 Explosed III 1 1000 Explosed III 1 1000 Explosed III 1 1000 Explosed III 1 1000 Explosed III 1 1000 Explosed III 1 1000 Explosed III 1 1000 Explosed III 1 1000 Explosed III 1 1000 Explosed III 1 1000 Explosed III 1 1000 Explosed III 1 1000 Explosed III 1 1000 Explosed III 1 1000 Explosed III 1 1000 Explosed III 1 1000 Explosed III 1 1000 Explosed III 1 1000 Explosed III 1 1000 Explosed III 1 1000 Explosed III 1 1000 Explosed III 1 1000 Explosed III 1 1000 Explosed III 1 1000 Explosed III 1 1000 Explosed III 1 1000 Explosed III 1 1000 Explosed III 1 1000 Explosed III 1 1000 Explosed III 1 1000 Explosed III 1 1000 Explosed III 1 1000 Explosed III 1 1000 Explosed III 1 1000 Explosed III 1 1000 Explosed III 1 1000 Explosed III 1 1000 Explosed III 1 1000 Explosed III 1 1000 Explosed III 1 1000 Explosed III 1 1000 Explosed III 1 1000 Explosed III 1 1000 Explosed III 1 1000 Explosed III 1 1000 Explosed III 1 1000 Explosed III 1 1000 Explosed III 1 1000 Explosed III 1 1000 Explosed III 1 1000 Explosed III 1 1000 Explosed III 1 1000 Explosed III 1 1000 Explosed III 1 1000 Explosed III 1 1000 Explosed III 1 1000 Explosed III 1 1000 Explosed III 1 1000 Explosed III 1 1000 Explosed III 1 1000 Explosed III 1 1000 Explosed III 1 1000 Explosed III 1 1000 Explosed III 1 1000 Explosed III 1 1000 Explosed III 1 1000 Explosed III 1 1000 Explosed III 1 1000 Explosed III 1 1000 Explosed III 1 1000 Explosed III 1 1000 Explosed III 1 1000 Explosed III 1 1000 Explosed III 1 1000 Explosed III 1 1000 Explo	Top Hit Descriptor	UFHF-BL0-abs-d-07-0-ULr1 NIH_MGC_37 Homo sapiens cDNA clone IMAGE:3057469 5'	Homo sapiens zinc finger homeodomain protein (ATBF1-A) mRNA, complete cds	601889823F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4123948 5'	601889823F1 NIH_MGC_17 Home saplens cDNA clone IMAGE:4123948 6'	AU118767 HEMBA1 Homo sapiens cDNA clone HEMBA1004314 5	cn17d05x1 Normal Human Trabecular Bone Cells Homo sapiens cDNA clone NHTBC_cn17d03 random	cn17d05.x1 Normal Human Trabecular Bone Cells Homo saplens cDNA clone NHTBC_cn17d05 random	DKFZp434J087_r1 434 (synanym: htes3) Hamo sapiens cDNA clone DKFZp434J087 5	Homo sapiens dynactin 1 (DCTN1) gene, atternatively spliced products, exons 7 through 32 and complete cds	Homo sapiens dynactin 1 (DCTN1) gene, atternatively spliced products, exons 7 through 32 and complete ods	HSU74315 Human chromosome 14 Homo sapiens cDNA clone 1-4	Homo sapiens sema domain, seven thrombospondin repeats (type 1 and type 1-like), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 5A (SEMA5A), mRNA	wb17g05.x1 NCI_CGAP_GC6 Homo sapiens cDNA chone IMAGE:2305976 3' similar to TR:O75363 O75363 ABC1.;	wb17g05.x1 NCI_CGAP_GC6 Homo saplens cDNA ckne IMAGE:2305976 3' similar to TR:078363 075363 AIBC1 ;	Homo sapiens transient receptor potential channel 5 (TRPC5), mRNA	za86e05.s1 Soares_fetal_bing_NbHL19W Homo sapiens cDNA clone IMAGE:299456 3'	601885455F1 NIH_MGC_57 Homo saplens cDNA clone IMAGE:4103729 5	602185808F1 NIH_MGC_45 Homo sapiens cDNA clone IMAGE:4310256 5'	AU129622 NT2RP2 Hamo sapiens cDNA clone NT2RP2005913 5	cr42e09.x1 Jia bone marrow stroma Homo sapiens cDNA clone HBMSC_cr42e093	cr42e09.x1 Jia bane marrow stroma Hamo saplens cDNA clone HBMSC_cr42e093'	Homo sapiens ATP-binding cassette, sub-family A (ABC1), member 3 (ABCA3), mKNA	AV758467 BM Homo sapiens cDNA done BMFBGG05 5	601593156F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3947365 5	601593156F1 NIH_MGC_9 Homo sapiens dDNA clone IMAGE:3947365 5	Homo sapiens atrophin-1 interacting protein 1; activin receptor interacting protein 1 (KIAA0705), mRNA
באטון רוטאבי	Top Hit Database Source	T_HUMAN	Η		EST_HUMAN 60	EST_HUMAN A	EST_HUMAN cn	EST_HUMAN cr	EST_HUMAN D	Horr NT cds	Horn NT	THUMAN		THUMAN			HUMAN	EST_HUMAN 6			EST_HUMAN  c	EST_HUMAN or				EST_HUMAN 6	
aigiilo	Top Hit Acession No.	17.7		0.0E+00 BF306996.1	0.0E+00 BF306996.1	.0E+00 AU118767.1	.0E+00 AI752561.1	0.0E+00 AI752561.1	0.0E+00 AL046347.2	.0E+00 AF064205.1			11417342 NT	.0E+00 AI825504.1		12735	0.0E+00 N76128.1	0.0E+00 BF217905.1	0.0E+00 BF569862.1	0.0E+00 AU129622.1	0.0E+00 AW069274.1	0.0E+00 AW069274.1	4501848 NT	0.0E+00 AV758487.1	0.0E+00 BE739870.1	0.0E+00 BE739870.1	6912461 NT
	Most Similar (Top) Hit BLAST E Value	0.0E+00	0.0E+00 L32832.1	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00
	Expression Signal	0.67	9.0	6.0	6.0	1.09	4.41	4.41	9.0	1.79	1.79	1.34	-	0.7	0.7	1,84	0.88	6.1	0.62	3.52	0.95	0.95	29'9	0.92	5.78	5.78	0.76
	ORF SEQ ID NO:	34182	34189	34209	34210	34220	34281	34282	34344	34363	34364	34375	34392	34422	34423		34435					<u> </u>	34472	34479		34481	34482
	Exon SEQ ID NO:	20703	20710	8733	20733	20740	20794	20794	20852	20368	20868	20876	1	1	20017	20925	20929	20933	1	1	1	L	1			L	20975
·	Probe SEQ ID NO:	7634	7641	7667	7667	7675	7733	7733	7796	7813	7813	7821	7835	7863	7863	7871	7877	7881	7886	7891	7911	7911	7915	7922	7924	7924	7925

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					6		
Probe SEQ ID NO:	SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acesslon No.	Top Hit Database Source	Top Hit Descriptor
7925	20975	34483	92.0	0.0E+00	6912461 NT	μ	Homo saplens atrophin-1 interacting protein 1; activin receptor interacting protein 1 (KIAA0705), mRNA
7926				0.0E+00	0.0E+00 AU120424.1	EST_HUMAN	AU120424 HEMBB1 Homo sapiens cDNA clone HEMBB1000655 5'
7926		Ì	1.05	0.0E+00	0.0E+00 AU120424.1	EST_HUMAN	AU120424 HEMBB1 Homo sepiens oDNA clone HEMBB1000655 5'
	l			L	7 1000	1400	hab22c04.x1.Soares_NSF_F8_9W_OT_PA_P_S1 Homo septens cDNA clone IMAGE:3263214.31 similar to accepting department.
7948	l	١		0.0=+00	0.0E+00 BF59026/.1	ESI HUMAN	Contains element I ANT I repetitive element.
7959	ı	١	1.86	0.0E+00		EST HUMAN	601481/13F1 NIH MIGC 08 Homo sapiens alive cione in/Alde: 3064230 3
7959		34520		0.0E+00	-	EST_HUMAN	601481/13F1 NIH MGC D8 HOMO SEDIENS CLINA CIONE IMAGE: 3004200 3
7998	21048		ග.0	0.0E+00	).0E+00 Y16795.1	LΝ	Homo sapiens psihhaA pseudogene
6662	21049	34562	3.86		0.0E+00 Al346148.1	EST_HUMAN	qp43f05.x1 NCI_CGAP_Co8 Homo saplens cDNA clone IMAGE:1925793 3' simitar to SW:EVX1_HUMAN P49640 HOMEOBOX EVEN-SKIPPED HOMOLOG PROTEIN 1;
8001	1				0.0E+00 W52673.1	EST_HUMAN	zc90f10.r1 Pancreatic Islet Homo sapiens cDNA clone IMAGE:338443 5
8002	21052			0.0E+00	11425128 NT	N	Homo sapiens similar to E.R to nucleus signalling 1 (H. sapiens) (LOC63433), mRNA
8003	1	34566			3.0E+00 AU117333.1	EST_HUMAN	AU117333 HEMBA1 Homo sapiens cDNA clone HEMBA1001175 5'
8004	ı		0.57		.0E+00 BE613963.1	EST_HUMAN	601504084F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3905733 5
							Homo sapiens cystic fibrosis transmembrane conductance regulator, ATP-binding cassette (sub-family C,
8018	21069	34580	0.73	0.0E+00	6995995 NT	٦	member 7) (CFTR), mRNA
	Ì						Homo sapiens cystic fibrosis transmembrane conductance regulator, ATP-binding cassette (sub-family C,
8018	21069	34581	0.73		LN 9665669	Ł	member 7) (CFTR), mRNA
8037	21120	34640	0.49		3.0E+00 AU133187.1	EST HUMAN	AU133187 NT2RP4 Hamo sapiens cDNA clone NT2RP4001507 5'
8083	21165		69'0		3.0E+00 BF217200.1	EST_HUMAN	601885317F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4103693 5
9608	ı				3.0E+00 BE313013.1	EST_HUMAN	601150347F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3503050 5
8108	ŀ		1.36	)	).0E+00 AA149791.1	EST_HUMAN	zo01c06.r1 Stratagene colon (#337204) Homo sapiens cDNA clone IMAGE:566410 5
8121						EST_HUMAN	
8135					0.0E+00 AA017021.1	EST HUMAN	ze33h08.r1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:360831 5
8153	21235		2.06	)	0.0E+00 BE736046.1	EST_HUMAN	601305658F1 NIH_MGC_39 Homo saplens cDNA clone IMAGE:3639903 5
8170	l_				0.0E+00 M34872.1	NT	Human amyloid-beta protein (APP) gene, exon 11
8170	L				0.0E+00 M34872.1	TN	Human amyloid-beta protein (APP) gene, exon 11
	L						bb34d02.y1 NIH_MGC_10 Homo sepiens cDNA clone IMAGE:2885123 5 similar to TR:064652 064652
8200	21282	34604	0.56		0.0E+00 AW674581.1	EST_HUMAN	F17K2.28 PROTEIN.;
	Ш		93.0		0.00 -00 018/02/4504 4	MAN IL	b584d02.yr NIH_MGC_10 Homo sapiens cDNA clone IMAGE:2985123 5' similar to TR:064552 064652
8200	71707	34603		Ì	AWON COOK	ES TOWN	TOTAL AND TOTAL STATE From C44 Home content of Date HAADE-728740 St cimiler to TB-0300489
8207	21289	34811	2.07		0.0E+00 AA397551.1	EST_HUMAN	ZB1D04.r1 Stratagene schzo brain S11 Homo sapiens cuna done Invade: /zz/19 3 similiar to 1 r. Cooudad. G300482 POL=REVERSE TRANSCRIPTASE HOMOLOG (RETROVIRAL ELEMENT);
	ı	l					

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Top Hit Descriptor	601334790F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3688655 5'	Homo sapiens Chediak-Higashi syndrome 1 (CHS1), mRNA	Homo sapiens Chediak-Higashi syndrome 1 (CHS1), mRNA	zv66/02.r1 Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:758619 5' similar to TR:G1304132 G1304132 TPRD.;	zv66702.r1 Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:758619 5' sImilar to TR:01304132 G1304132 TPRD.;	zt73408.s1 Soares_testis_NHT Homo sapiens cDNA done IMAGE:727958 3' similar to gb:S85655 PROHIBITIN (HUMAN);	RC2-FN0094-120600-013-h07 FN0094 Homo sapiens cDNA	QV3-DT0045-221299-046-c07 DT0045 Homo sapiens cDNA	QV3-DT0046-221299-046-c07 DT0045 Homo sapiens cDNA	601452412F1 NIH_MGC_66 Homo saplens cDNA clone IMAGE:3856179 6'	601452412F1 NIH_MGC_66 Homo saplens cDNA clone IMAGE:3856179 5'	Homo saplens chromosome 21 segment HS21C009	Homo sapiens chromosome 21 segment HS21C009	wm33a11.x1 NGI_CGAP_Ut4 Homo sapiens cDNA done IMAGE:2437724 3' similar to TR:075457 075457 CYTOSOLIC PHOSPHOLIPASE A2-GAMMA.;	ne25d10.s1 NCI_CGAP_CG Homo saplens cDNA done IMAGE:882269 3' similar to TR:G1138434 G1138434 KIAA0187 PROTEIN	Homo sapiens protocadhenn beta 3 (PCDHB3), mRNA	ta04f11.x1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:2043117 3	601431238F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3916569 5'	2822701.5prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2822701.5	2822701.5prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2822701 5'	Homo sepiens mitogen-activated protein kinase kinase kinase 13 (MAP3K13), mRNA	Homo sapiens mitogen-activated protein kinase kinase kinase 13 (MAP3K13), mRNA	Human zinc finger protein (ZNF165), gene, exons 2 and 3	Human zinc finger protein (ZNF165), gene, exons 2 and 3	Human Chediak-Higashi syndrome protein short isoform (LYST) mRNA, complete cds	Homo sapiens NESP55, GNAS1 antisense (partial) and XLalphas (partial) genes	H. sapiens mRNA for gemma-glutamytransferase	H.sapiens mRNA for gamma-glutamytransferase	H. sapiens mRNA for gamma-glutamyltransferase
Top Hit Database Source	EST_HUMAN	TN	TN	EST_HUMAN	EST HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST HUMAN	EST_HUMAN	LN	LN.	EST HUMAN	H HMAN	LZ	EST HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	N	NT	NT	NT	NT	NT	TN	NT	NT
Top Hit Acession No.	3E563650.1	11427235 NT	0.0E+00 11427235 NT	0.0E+00 AA403192.1	0.0E+00 AA403192.1	0.0E+00 AA398511.1	BE837593.1	0.0E+00 AW364874.1	AW364874.1	0.0E+00 BE612586.1	BE612586.1	AL163209.2	AL163209.2	0.0E+00 AI884477.1	44502941	11416799 NT	0.0E+00 AI580780.1	BE890797.1			4758695 NT	4758695 NT	0.0E+00 U88084.1	U88084.1	0.0E+00 U84744.1	0.0E+00 AJ251760.1	.0E+00 X98922.1	.0E+00 X98922.1	.0E+00 X98922.1
Most Similar (Top) Hit BLAST E Value	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	001	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00
Expression Signal	1.47	1.72	1.72	0.84	0.84	3.61	0.5	1.34	1,34	1.24	1.24	1.16	1.16	0.93		0.66	0.52	2.08	0.61	0.61	2.13	2.13	0.61	0.61			2,81		
ORF SEQ ID NO:		35102						35156			ļ	35194					35220			35247			35252			35317		35324	Ц
Exan SEQ ID NO:	1		21568	ı	21568	1	l	1	ı		1	21653	1	l .		1	1	١.	ı	1	ì	1	1	ı	21777	ı	ı		ll
Probe SEQ ID NO:	8477	8485	8485	8487	8487	8528	8537	8538	8538	8557	8557	8572	. 8572	8581	8,58	8593	8601	8604	8630	. 8630	8631	8631	8635	8635	8697	8704	8709	8709	8709

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Top Hit Descriptor	Human immunoglobulin-like transcript-3 mRNA, complete cds	Homo sapiens cep250 centrosome associated protein mRNA, complete cds	Homo sapiens cap250 centrosome associated protein mRNA, complete cds	AU131671 NT2RP3 Home sapiens cDNA clone NT2RP3003016 5'	Homo sapiens immunoglobulin superfamily, member 2 (IGSF2), mRNA	xx46e01.x1 NCI_CGAP_Ut1 Home sapiens cDNA clone IMAGE:2707032.3' similar to gb:M14123_cds4 RETROVIRI IS-REI ATED POI, POI YPROTEIN (HUMAN):	601472166F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3874912.5	HUM084C02B Clontech human fetal brain polyA+ mRNA (#6535) Homo saplens cDNA clone GEN-084C02	īo	601238488F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3608709 5'	z32e04.r1 Soares ovary fumor NbHOT Homo sapiens cDNA clone IMAGE:724062 5'	601900571F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4129744 5'	Homo saplens leukocyte Immunoglobulin-like receptor, subfamily B (with TM and ITIM domains), member 3	(LILRB3), mRNA	UI-H-BI1-adr-e-12-0-UI.s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2717687 3'	UI-H-BI1-adr-e-12-0-UI.s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2717687 3'	601150051F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3502836 5	602127664F1 NIH_MGC_56 Hano sapiens cDNA done IMAGE:4284542 5'	602127664F1 NIH_MGC_56 Hamo sapiens cDNA clone IMAGE:4284542 5'	602127664F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4284542 5'	AL449770 Homo sapiens fetal brain (Stavrides GS) Homo sapiens cDNA	o/80g02.s/1 NCI_CGAP_Lu6 Homo sepiens cDNA clone IMAGE:1602194.3' s/milar to gb:M36072.60S RIBOSOMAL PROTEIN L7A (HUMAN);	Homo sepiens ankyrin 1, erythrocytic (ANK1), transcript variant 1, mRNA	Homo sapiens ankyrin 1, enythrocytic (ANK1), transcript variant 1, mRNA	Homo saplens ITGB4 gene for Integrin beta 4 subunit, exons 3-41	601156330F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3139734 5'	AV718377 FHTB Hamo sepiens cDNA done FHTBAAF11 5'	xw73e07.x1 NCI_CGAP_Pen1 Homo sapiens cDNA clone IMAGE.2833644 3' similar to gb:X53587 INTEGRIN BETA-4 SUBUNIT PRECURSOR (HUMAN);	AU124051 NT2RM2 Homo saplens cDNA clone NT2RM2001575 5'	AU140704 PLACE4 Homo sapiens cDNA clone PLACE4000089 5'	Homo sapiens mRNA for KIAA0454 protein, partial cds
Top Hit Database Source	IN	LN T	LN	EST_HUMAN		EST HIMAN	Г	Т	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN						EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST HUMAN			NT	EST_HUMAN	EST_HUMAN	EST HUMAN	Г	T HUMAN	LN
Top Hit Acession No.	J82979.1	0.0E+00 AF022655.1	0.0E+00 AF022855.1	0.0E+00 AU131671.1	11426572 NT	0 0F+00 AW513513 1	0.0E+00 BE783232.1		D52650.1	0.0E+00 BE378495.1	0.0E+00 AA410545.1	0.0E+00 BF313948.1		11424387 NT	0.0E+00 AW139673.1	0.0E+00 AW139673.1	0.0E+00 BE260272.1	0.0E+00 BF700165.1	0.0E+00 BF700165.1	0.0E+00 BF700165.1	0.0E+00 AL449770.1	0.0E+00 AA962527.1	10947037 NT	10947037 NT	Y11107.3	0.0E+00 BE278917.1	0.0E+00 AV718377.1	0.0E+00 AW337277,1	0.0E+00 AU124051.1	0.0E+00 AU140704.1	0.0E+00 AB007923.1
Most Similar (Top) Hit BLAST E Value	0.0E+00 U82979.1	0.0E+00	00+30'0	0.0E+00	0.0E+00	- HO	0.0E+00		0.0E+00 D52650.1	0.0E+00	0.0E+00	0.0E+00		0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00 Y11107.3	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00
Expression Signal	0.78	0.81	0.81	79.0	0.64	1 35	0.54		1.62	4.15	2.15	1.35		0.54	1.41	1.41	2.16	2.91	2.91	2.91	0.84	3.69	3.41	3.41	1.65	1.09	2.88	3.12	1.59	96.0	0.64
ORF SEQ ID NO:	35339								35409		35446			35455	35460	35461		35497		35489		35547			35583			35600	l		35696
Exon SEQ ID NO:	21803		21844	ļ		24867	1	ļ	21870	21902								21963	21963		20022	22009	L.	1	ı	22042	22052	ĺ	1	ı	22/52
Probe SEQ ID NO:	8723	8765	8765	89/8	8784	8788	8790		8791	8823	8829	8831		8838	8843	8843	8879	8884	8884	8884	8923	8930	8836	8936	8961	8963	8973	8980	9868	9063	9073

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Top Hit Descriptor	yg09e09.r1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:31674 5'	yg09e09.r1 Soares Infant brain 1NIB Homo sapiens cDNA clone IMAGE:31674 5'	hf48a09.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE::2935096.3'	hf48a09.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2035096 3'	AV714764 DCB Homo septens cDNA clone DCBAUA06 5'	DKFZp434C1814_s1 434 (synonym: htes3) Homo saplens cDNA clone DKFZp434C1814 3'	DKFZp434C1814_s1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434C1814 3'	Homo saplens killer inhibitory receptor 2-2-1 (KIR221) and killer inhibitory receptor 2-2-2 (KIR222) genes, partial cds	Homo sapiens mRNA for KIAA1512 protein, partial cds	7k29b03.x1 NCI_CGAP_Ov18 Homo sapiens cDNA cbne IMAGE:3476692 3' sImitar to TR:O36448 O36448 S GAG. ;	Homo saplens tumor protein p73 (TP73), mRNA	Human ig rearranged H-chain epsilon-3 pseudogene, constant region	Homo sapiens mRNA for KIAA0823 protein, partial cds	Homo saplens mRNA for KIAA0823 protein, partial cds	AV660739 GLC Homo sapiens cDNA clone GLCGKG12 3'	Homo sapiens polycysth-L (PKDL), mRNA	601588304F1 NIH_MGC_7 Home sapiens cDNA clone IMAGE:3942553 5'	601141119F1 NIH_MGC_9 Hamo sapiens cDNA clone IMAGE:3140740 5'	601141119F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3140740 5	601452562F1 NIH_MGC_66 Homo saplens cDNA clone IMAGE:3856100 51	601452582F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3856100 5'	Human polymorphic loci in Xq28	Human mRNA for GABA-A receptor, alpha 1 subunit	AU127096 NT2RP2 Homo sapiens cDNA clone NT2RP2000579 5'	an 29e04.x1 Gessler Wilms tumor Homo sepiens cDNA clone IMAGE: 1700094 3'	wq34g12.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE::2473150 3' similar to SW:MGB3_HUMAN  O15480 MEI ANOMA-ASSOCIATED ANTIGEN B3 :	Homo caplens protocadherin alpha 8 (PCDHAB), mRNA	EST370381 MAGE resequences, MAGE Homo saplens cDNA	Human endogencus retrovirus, complete gename	AU142662 Y79AA1 Homo capiens cDNA clone Y79AA1000678 5'	Homo sapiens MAP-kinase activating death domain (MADD), mRNA
Top Hit Database Source	EST_HUMAN	П	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	LN	Z	EST_HUMAN	L	NT	TN	TN	EST HUMAN	LN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST HUMAN	EST_HUMAN	IN	NT	EST_HUMAN	EST_HUMAN	NAMIN TOD	L	EST HUMAN	۲	62.1 EST_HUMAN	NT
Top Hit Acession No.	Г			П			0.0E+00 AL040428.1		.0E+00 AB040945.1	0.0E+00 BF058289.1	11422867 NT				0.0E+00 AV660739.1	7706638 NT	BE793326.1	BE315402.1	0.0E+00 BE315402.1	BE612721.1	BE612721.1	M89986.1				0.05400 0.054607.4	9256595INT	0.0E+00 AW958311.1	9635487 NT	0.0E+00 AU142662.1	11436995
Most Similar (Top) Hit BLAST E Value	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00/	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00 K01241.1	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	004300	00+100	0.0E+00	0.0E+00	0.0E+00	0.0E+00
Expression Signal	0.68	99.0	4.78	4.78	0.93	3.17	3.17	1.32	2.12	0.61	2.79	1.59	5.28	5.28	1.84	3.41	0.6	4.22	4.22	9.0	9.0	0.54	1.65	0.53	0.83	1 08	5 69	2.73	1.32	0.84	1.04
ORF SEQ ID NO:	35700							35773			35808	35818	35828	1	i										32909	25042		1	35940		
Exon SEQ ID NO:	22157	22157	22161	22161	22208	22224	22224	22229	22231	l .	ı	ı	22287		ı	1	ı				ı	ı		١.	ı	l	2238B	1	22389	ı	1 1
Probe SEQ ID NO:	18	9078	82	82	ন্ত	45	5	5	9153	9	2	듗	8	8	7.	ន	8	8	346	92	99	529	듒	9279	88	ê	3 8	18	313	328	9344

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Top Hit Descriptor	801301676F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3636163 5'	7g97h12.x1 NCI_CGAP_Co16 Homo sapiens cDNA cone IMAGE:3314471 3' similar to TR:Q9UH62 Q9UH62 HYPOTHETICAL 42.5 KD PROTEIN ;	Homo sapiens mRNA for KIAA0578 protein, partial cds	601589294F1 NIH_MGC_7 Homo saplens cDNA clone IMAGE:3943463 5'	RC3-PT0151-290600-011-c05 PT0151 Homo sapiens cDNA	RC3-PT0151-290600-011-c05 PT0151 Homo sapiens cDNA	AU136229 PLACE1 Homo sapiens cDNA clone PLACE1003804 5'	601510247F1 NIH_MGC_7; Homo sapiens cDNA clone IMAGE:3911986 5'	601510247F1 NIH_MGC_71 Hamo sapiens cDNA cione IMAGE:3911986 6'	Homo seplens mRNA for KIAA0594 protein, partial cds	EST50505 Gall bladder I Homo sapiens cDNA 5' end	EST50505 Gall bladder I Homo caplens cDNA 5' and	ba54d08,y3 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:2900367 5' similar to TR:060275 060275	KAKUSZZ FROTEIN ,	ba64d08.y3 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:2900367 5' similar to TR:060275 060275 KIAA0522 PROTEIN ;	ba09f05.y1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2823873 5' similar to gb:L35049 Mus musculus	Bctxt_mRNA, complete cds (MOUSE);	ba09f05.y1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2823873 5' similar to gb:L35049 Mus musculus	Bctxt_mRNA, complete cas (MOUSE);	602023150F1 NCL_CGAP_Brn67 Homo saplens cDNA clone IMAGE:4158300 5'	QV2-HT0698-250700-282-508 HT0698 Homo sapiens cDNA	601455118F1 NIH_MGC_66 Hama sapiens cDNA clane IMAGE:3859035 5'	601455116F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3859035 5'	RC-BT108-040399-032 BT108 Homo saplens cDNA	Homo sepiens leukocyte immunoglobulin-like receptor, subfamily B (with TM and ITIM domains), member 5 (LILRBS), mRNA	Homo sapiens leukocyte Immunoglobulin-like receptor, subfamily B (with TM and ITIM domains), member 5	(LILRBS), mRNA	DKFZp434L0120_r1 434 (synonym: htec3) Homo sapiens cDNA clone DKFZp434L0120 5	ow60h01.xt Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA cione IMAGE:1651249 3' similar to TR:Q14677 Q14877 KIAAD171 PROTEIN. ;	601892245F1 NIH_MGC_17 Homo sepiens cDNA clone IMAGE:4138066 5'	
Top Hit Database Source	EST_HUMAN	EST_HUMAN		EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN		EST_HUMAN	LZ	EST_HUMAN	EST HUMAN	Г	ESI HUMAN	EST HUMAN	Г	EST_HUMAN		EST_HUMAN		EST_HUMAN		EST_HUMAN	EST_HUMAN	TN			EST_HUMAN	EST_HUMAN	EST_HUMAN	
Top Hit Acessian No.	3.0E+00 BE410768.1		3.0E+00 AB011150.1	0.0E+00 BE794823.1	0.0E+00 BE810292.1	0.0E+00 BE810292.1	0.0E+00 AU136229.1		0.0E+00 BE883843.1	).0E+00 AB011168.1	.0E+00 AA344601.1	.0E+00 AA344601.1		0.0E+00 AW6/3469.1	0.0E+00 AW673469.1	T	0.0E+00 BE207063.1		0.0E+00 BE207063.1	0.0E+00 BF348013.1		0.0E+00 BF034377.1	0.0E+00 BF034377.1	0.0E+00 AI906351.1	5803069 NT		5803069 NT	0.0E+00 AL042278.1	0.0E+00 Al088043.1	0.0E+00 BF309962.1	
Most Similar (Top) Hit BLAST E Value	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	00E+00	0.0E+00	00.70	0.0=+00.	0.0E+00		0.0E+00		0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00		0.0E+00	0.0E+00	0.0E+00	0.0E+00	
Expression Signal	0.76	1.32	1.62	3.42	0.47	0.47	76.0	1.19	1.19	0.57	1.43	1.43		0.96	96.0		0.99		0.99	1.95	3.1	0.49	0.49	0.58	0.77		0.77	0.85	1.3	0.67	
ORF SEO ID NO:		35993		36010		36016		36024	36025	36040	36044	36045	0000	36083	36084		36116			36346								_			
Exam SEQ ID NO:	22421	L	i .	L	L.,	Ĺ	L			l _	L	L	<u>L</u>	22521	22521		22554	L	22554	l	i	ı	22719	L	22728	1	22728	l		21081	
Probe SEQ ID NO:	9345	9359	9373	9374	9378	9378	9381	9386	9386	9403	9407	9407		9464	9464		9498		9498	9509	9545	9577	9577	9583	9288		9286	9656	9631	9638	

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Top Hit Descriptor	Homo sapiens hypothetical C2H2 zinc finger protein FLJ22504 (FLJ22504), mRNA	Homo saplens hypothetical C2H2 zhc finger protein FLJ22504 (FLJ22504), mRNA	qm09a08.x1 NCI_CGAP_Lu5 Home sapiens cDNA clone IMAGE:1881298 3' similar to SW:RL2B_HUMAN P29316 60S RIBOSOMAL PROTEIN L23A ,	qm09a06.X1 NCI_CGAP_Lu5 Homo saplens cDNA cione IMAGE:1881298 3' similar to SW:RL2B_HUMAN Possate ens RIBOSOMA PROTEIN 1.234 ·	EST366026 MAGE resequences, MAGC Homo sepiens cDNA	Homo sepiens polycyclic kidney disease 2-like protein (PKD2L) gene, exon 8	601510882F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3912165 5'	601510882F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3912165 51.	601109942F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3350722 5'	601466828F1 NIH_MGC_67 Homo saplens cDNA clone IMAGE:3870007 5'	601466828F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3870007 5'	au86c04.y1 Schneider fetal brain 00004 Homo sapiens cDNA done IMAGE:2783142 5' similar to gb:M36072 60S RIBOSOMAL PROTEIN L7A (HUMAN);	Homo saplens DNA for amyloid precursor protein, complete cds	601145054F2 NIH_MGC_19 Homo saplens cDNA clone IMAGE:3160477 5'	C06158 Human pancreatic Islet Homo sapiens cDNA clone hbc5605	C06158 Human pancreatic Islet Homo sapiens cDNA clone hbc5605	601578683F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3927548 5'	Homo saplens solute carrier family 21 (organic anion transporter), member 9 (SLC21A9), mRNA	Homo sapiens solute carrier family 21 (organic anion transporter), member 9 (SLC21A9), mRNA	Homo saplens solute carrier family 21 (organic anion transporter), member 9 (SLC21A9), mRNA	601673425F1 NIH_MGC_21 Homo sepiens cDNA clone IMAGE:3956238 5'	AV701829 ADB Homo seplens dDNA clone ADBBYH01 5'	Homo sapiens keratin 2e (KRT2E) gene, complete cds	Homo seplens keratin 2e (KRT2E) gene, complete cds	RC2-BT0642-130300-017-401 BT0642 Homo sepiers cDNA	UI-HF-BN0-akg-b-12-0-UI r1 NIH_MGC_50 Homo sepiens cDNA done IMAGE:3076943 5'	UI-HF-BN0-akg-b-12-0-UI.r1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3076943 5'	Homo sapiens chromosome 9 duplication of the T cell receptor beta locus and trypsinogen gene families	Homo sapiens chromosome 9 duplication of the T cell receptor beta locus and trypsinogen gene families
Top Hit Database Source			EST HUMAN		Т	1	EST_HUMAN 6	EST_HUMAN 6	П	Г	г	EST HUMAN	Г	EST_HUMAN		EST_HUMAN	EST_HUMAN	TN			Г	EST_HUMAN /	Г	±N	EST_HUMAN	Г		TN	NT
Top Hit Acessian No.	11560151 NT	11560151 NT	0.0E+00 Al290909.1		Ţ	0.0E+00 AF153466.1	3E885128.1	3E885128.1			1	0.0E+00/AW163779.1		BE263191.1	0.0E+00 C06158.1	C06158.1	BE746215.1	282	11437282 NT	11437282 NT	BE900549.1	AV701829.1	AF019084.1	AF019084.1	BE082977.1	AW500293.1	0.0E+00 AW500293.1	0.0E+00 AF029308.1	0.0E+00 AF029308.1
Most Similar (Top) Hit BLAST E Value	0.0E+00	0.0E+00	0.0E+00	00-100	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00
Expression Signal	232	2.32	6.52	65.0	2.15	3.95	69.0	0.69	5.87	1.44	4.	5.46	0.58	3.41	4.49	4,49	3.38	203	2.03	2.03	1.91	1.5	2.55	2.55	1.13	1.72	1.72	1.87	1.87
ORF SEQ ID NO:	34595	34596		٠ ا		36201	L			36305	36306	36307	36315	36329	1	36365						ı		İ			36465	36470	36471
Exon SEQ ID NO:	I _	21083	1	l		22632		ļ	1	Į į	22735	22737		22758		ı	ı		i	l			١.		ı	i i	22881	22890	22890
Probe SEQ ID NO:	9640	9640	9642	06.43	9643	9670	9673	9673	9683	9896	9686	9688	2696	9709	9727	9727	9729	9739	9739	9739	9759	9776	9788	82/8	9821	9841	9841	9850	9850

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Top Hit Descriptor	601470824F1 NIH_MGC_67 Hamo sapiens cDNA clone IMAGE:3874037 5'	601470824F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3874037 5'	zd16e11.r1 Soarcs_fetal_heart_NbHH16W Homo sapiens cDNA clone IMAGE:340844 5'	zd18e11.r1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:340844 51	Homo sapiens non-inhibitory killer-cell Ig-lika receptor KIR (KIR2DS5) mRNA, complete cds	Homo sapiens mRNA for neurexin I-alpha protein, complete cds	am56a11.x1 Johnston frontal cortex Homo sapiens cDNA clone IMAGE:1539548 3'	ULHF-BND-akj-c-07-0-UI.r1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3077364 5	Multiple sclerosis associated retrovirus polyprotein (pol) mRNA, partial cds	AIGF-androgen-Induced growth factor AIGF [human, placenta, Genomic/mRNA, 498 nt, segment 6 of 5]	AIGF=androgen-induced growth factor AIGF [human, placenta, Genomic/mRNA, 498 nt, segment 5 of 5]	601334603F1 NIH_MGC_39 Homo saplens cDNA clone IMAGE:3688680 5'	CM2-CT0311-301199-043-h11 CT0311 Homo saplens cDNA	Homo sapiens multimerin (MMRN), mRNA	Homo sapiens leukocyte immunoglobulin-like receptor, subfemily B (with TM and ITIM domains), member 3 (LICRBS), mRNA	bb26c01.x1 NIH_MGC_5 Homo sapiens cDNA clone IMAGE:2964000 3'	AU132349 NT2RP3 Homo sepiens cDNA clone NT2RP3004260 5'	AU132349 NT2RP3 Homo septens cDNA clone NT2RP3004260 5'	UI-HF-BPop-air-f-05-0-UI.11 NIH_MGC_51 Homo sapiens cDNA clone IMAGE:3072897 5'	601595558F1 NIH_MGC_9 Homo saplens cDNA clone IMAGE:3949383 5'	601595558F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3949383 5'	Homo sapiens KIAA0345 gene product (KIAA0345), mRNA	DKFZp434L0120_r1 434 (synchym: htes3) Homo sapiens cDNA clone DKFZp434L0120 5'	DKFZp434B2416_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434B2416 5'	AU132349 NT2RP3 Hamo sapiens cDNA clone NT2RP3004260 5	Homo sapiens protocadherin alpha 12 (PCDH-alpha12) mRNA, complete cds	Homo sapiens leucocyte immunoglobulin-like receptor-1 mRNA, complete cds	Homo sapiens leucocyte immunoglobulin-like receptor-1 mRNA, complete cds	MR4-TN0114-110900-101-e04 TN0114 Homo saplens cDNA	601155227F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3138798 5	601286351F1 NIH_MGC_44 Hamo sapiens cUNA clane IMAGE:3613045 5
 Top Hit Database Source	EST_HUMAN 6	Į į	EST_HUMAN   z	EST_HUMAN   zx		NT TN		LHUMAN		NT	_ K	EST_HUMAN 6	EST_HUMAN C			EST HUMAN b	Г	EST_HUMAN A	EST_HUMAN U	EST_HUMAN 6	EST_HUMAN 6			EST_HUMAN D	EST_HUMAN A		ا NT TN	TN.		T	EST_HUMAN   6
Top Hit Acession No.								1		0E+00 S78466.1		0.0E+00 BE563320.1	0.0E+00 AW363135.1	11436432 NT	11424387 NT	0.0E+00 BE208710.1		Γ	.0E+00 AW500936.1	0.0E+00 BE740490.1	0.0E+00 BE740490.1	82067	0.0E+00 AL042278.1	0.0E+00 AL041084.2	.0E+00 AU132349.1	0.0E+00 AF152308.1	).0E+00 AF009220.1			),0E+00 BE280793.1	,0E+00 BE388700.1
Most Similar (Top) Hit BLAST E Value	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00 S78466.1	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00
Expression Signal	0.52	0.62	0.63	0.63	0.46	1.04	0.64	3	2.65	2.69	269	2.72	1.26	99'0	0.62	0.91	4.49	4.49	0.95	13.26	13.26	1.56	1.54	0.57	2.32	2.16	2.84	2.84	1.13	2.75	6.57
ORF SEQ ID NO:			36485			36500				38585		38591					38658					36692				36724		36752	L	36793	
SEQ ID NO:	ı	l	•	22901	ı	22915			22965	22892		22995	ı			1	23062	ı	ı					Į.		1		ı	Į.	23197	
Probe SEQ ID NO:	9852	9852	1986	9861	9874	9875	9879	9881	9925	8963	89653	9268	9376	2666	8666	10007	10024	10024	10033	10039	10039	10052	10069	10074	10084	10085	10112	10112	10128	10160	10169

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Тop Hit Descriptor	601286351F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3613045 5'	xn72b01.x1 NCI_CGAP_CML1 Homo sapiens cDNA done IMAGE:2899977 3' similar to gb:X02152_cds1 L- LACTATE DEHYDROGENASE M CHAIN (HUMAN);	EST46740 Fetal kidney II Homo sapiens cDNA 5' end	Homo sapiens Chediak-Higashi syndrome 1 (CHS1), mRNA	EST376186 MAGE resequences, MAGH Homo sapiens cDNA	AU143673 Y79AA1 Homo sapiens cDNA clone Y79AA1002307 5	AU143673 Y79AA1 Homo sapiens cDNA done Y79AA1002307 5'	Homo sapiens killer cell inhibitory receptor KIRCI gene, excns 2, 3, and 4	Homo sapiens HEF like Protein (HEFL), mRNA	Homo sapiens HEF like Protein (HEFL), mRNA	AU136637 PLACE1 Homo sapiens cDNA clone PLACE1004737 5'	AU136637 PLACE1 Homo capiens cDNA done PLACE1004737 5'	Homo sapiens partial RANBP7 gene for RanBP7/importin7 and partial ZNF143 gene	Homo sapiens partial RANBP7 gene for RanBP7/importin7 and partial ZNF143 gene	AV695712 GKC Homo sapiens cDNA clone GKCDXA07 5'	AV685712 GKC Homo sapiens cDNA clone GKCDXA07 5'	Homo sapiens killer cell inhibitory receptor KIRCI gene, exons 2, 3, and 4	zp97h11.r1 Stratagene muscle 837209 Homo sapiens cDNA clone IMAGE:628197 5'	2/31/01.r1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:503545 6'	zi31f01.rf Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:503543 5	Homo sapiens KIF4 (KIF4) mRNA, complete cds	601491565F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3893657 5'	601570712F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3845403 51	601570712F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3845403 51	AU127403 NT2RP2 Homo sapiens cDNA clone NT2RP2001212 6	601645134F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:3930177 5	601645134F1 NIH_MGC_56 Homo sepiens cDNA clone IMAGE:3630177 5'	601432317F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3917453 5	EST182353 Jurkat T-cells VI Homo sapiens cDNA 5' end	Homo sapiens neuredn III (NRXN3) mRNA	601432228F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3917598 5'	Homo sapiens hypothetical C2H2 zinc finger protein FLJ22504 (FLJ22504), mRNA	Homo sapiens mKNA for ectin binding protein ABP620, complete cas
Top Hit Database Source	EST_HUMAN	EST HUMAN	EST_HUMAN	NT	EST_HUMAN	EST_HUMAN	EST_HUMAN	TN	IN	IN	EST_HUMAN	EST_HUMAN	M	TN	EST_HUMAN	EST_HUMAN	TN	EST_HUMAN	EST_HUMAN	EST_HUMAN	LN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	l.	EST_HUMAN	Z	TN.
Top Hit Acesston No.	E+00 BE388700.1	0.0E+00 AW236269.1	0.0E+00 AA341305.1	11427235 NT	0.0E+00 AW964113.1	0.0E+00 AU143673.1	1U143673.1	0.0E+00 AF072408.1	11421001 NT	11421001 NT	0.0E+00 AU136637.1	4U136637.1	4,1295844.1	0.0E+00 AJ295844.1	4V695712.1	4V695712.1	4F072408.1	4A196387.1	0.0E+00 AA131248.1	4A131248.1	AF179309.1	3E880658.1	0.0E+00 BE730772.1	0.0E+00 BE730772.1	0.0E+00 AU127403.1	0.0E+00 BE958511.1	0.0E+00 BE958511.1	0.0E+00 BE897487.1	0.0E+00 AA311624.1	4758827 NT	0.0E+00 BE891113.1	0.0E+00 11560151 NT	AB029290.1
Most Similar (Top) Hit BLAST E Vatue	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00/	0.0E+00	0.0E+00/	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00/	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00				0.0E+00		
Expression Signal	6.57	0.87	0.84	0.59	96.0	5.99	5.99	3.31	2.75	2.75	3.07	3.07	2	2	0.73	67.0	0.72	2.42	97.0	0.76			5.34	5.34	0.8	0.89	68.0	0.48		0.65	0.64		1.56
ORF SEQ ID NO:	36800			36819	36834	36845		36849	36851	36852						36918	36925	36928	38959	36960			37057	37058		37073	37074	37094	37107		37121		37130
Exon SEQ ID NO:	23206		ı	23225	23244	23258	1	1	l	23263	Ĺ	23296	23312	ı	ı	23317	ı	1	1	ı	Ι.	1		23452	1		[	L	L		23508	23510	23521
Probe SEQ ID NO:	10169	10178	10179	10188	10208	10222	10222	10225	10228	10228	10261	10261	10277	10277	10282	10282	10288	10290	10317	10317	10359	10404	10417	10417	10422	10432	10432	10450	10460	10461	10473	10475	10486

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Top Hit Descriptor	Homo seriens mRNA for estrogen receptor beta, complete cds	Homo sapiens mRNA for estrogen receptor beta, complete cds	yp01a10.r1 Soares breast 3NbHBst Homo sapiens cDNA done IMAGE:186138 57	Homo sapiens DNA for anyloid precursor protein, complete cds	601308167F1 NIH_MGC_44 Horno saplens cDNA clone IMAGE:3626128 5'	AU125996 NTZRM4 Homo sapiens cDNA clone NT2RM4002536 5	AV711075 Cu Homo sapiens cDNA clone CuAAKG05 5	AV711075 Cu Homo sapiens cDNA clone CuAAKG05 5	RC3-ST0197-120200-015-a03 ST0197 Homo sapiens cDNA	EST375636 MAGE resequences, MAGH Homo sapiens oDNA	Homo sapiens ATP-binding cassette, sub-family A (ABC1), member 3 (ABCA3), mRNA	Homo sapiens ATP-binding cassette, sub-family A (ABC1), member 3 (ABCA3), mRNA	wy61f09.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo capione cDNA clone IMAGE:2553065 3' similar to TRQ60566 Q60566 VDX;	TCAAP3D0917 Pediatric acute myelogenous leukemia cell (FAB M1) Baylor-HGSC project=TCAA Homo	saplens culva clone I caab us 17	wb28a12.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2308974 3' similar to contains dement MSR1 MSR1 repetitive element ;	wb28a12.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2306974 3' similar to contains element	MSR1 MSR1 repetitive element;	601888704F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4122649 5'	601451502F1 NIH_MGC_65 Horno saplens cDNA clone IMAGE:3855289 5'	601451502F1 NIH_MGC_65 Hamo saplens cDNA clone IMAGE:3855289 5	Homo sapiens NOD2 protein (NOD2), mRNA	Homo sapiens NOD2 protein (NOD2), mRNA	UI-FF-BLO-acm-d-04-0-UI.r1 NIH_MGC_37 Homo sapiens cDNA clone IMAGE:3059383 5'	Hamo saplens hypothetical protein FLJ20079 (FLJ20079), mRNA	Homo sapiens 5-hydroxytryptamine (serotonin) receptor 1E (HTR1E) mRNA	Homo sapiens 5-hydroxydryptamine (serotonin) receptor 1E (HTR1E) mRNA	wu32b06.x1 Soares_Dieckgraefe_colon_NHCD Homo sapiens cDNA done IMAGE:2521715 3'	601505204F2 NIH_MGC_71 Hamo sapiens cDNA clone IMAGE:3906865 5'	601434522F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3919636 5'	Homo sapiens myosin, heavy polypeptide 2, skeletal muscle, adult (MYH2), mRNA	Homo sapiens myosin, heavy polypeptide 2, skeletal muscle, adult (MYH2), mRNA
Top Hit Database Source	L	LZ	EST HUMAN	NT	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	TN	FZ	EST HUMAN		ES! HUMAN	EST HUMAN		<b>EST_HUMAN</b>	EST_HUMAN	EST_HUMAN	EST_HUMAN	LN	NT	EST_HUMAN	LΝ	NT	TN	EST_HUMAN	EST_HUMAN	EST_HUMAN	LΝ	Ę
Top Hit Acession No.	O DE+COLABOORSON 1	0.0E+00 AB006590.1	139805.1	387675.1	0.0E+00 BE392276.1	0.0E+00 AU125996.1	0.0E+00 AV711075.1	0.0E+00 AV711075.1	0.0E+00 AW813783.1	0.0E+00 AW963563.1	11431124	11431124 NT	0.0E+00 AW057621.1		0.0E+00 BE243270.1	0.0E+00 Al652239.1		0.0E+00 AI652239.1	0.0E+00 BF306642.1	0.0E+00 BE872908.1	0.0E+00 BE872908.1	11545911 NT	11545911 NT	0.0E+00 AW404795.1	11424829 NT	4504536 NT	4504536 NT	0.0E+00 Al991827.1	0.0E+00 BE882109.1	0.0E+00 BE891630.1	N 65823939 N1	8923939 NT
Most Similar (Top) Hit BLAST E Value	0.04400	0.0E+00	0.0E+00 H39805.1	0.0E+00 D87675.1	0.0E+00	0.0E+00/	0.0E+00	0.0E+00	0.0E+00	0.05+00	0.0E+00	0.0E+00	0.0E+00	200	0.0E+00	0.0E+00		0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00
Expression Signal	0.46	0.46	0.51	0.54	0.59	0.52	1.84	1.84	2.55	5.5	2.52	2.52	1.7		8.59	2.72		2.72	1.48	1.74	1.74	3.59	3.59	1.52	2.85	8.39	8.39	2.68	3.22	6.12	1.55	1.55
ORF SEQ ID NO:	37442		37465	37491	37499	37518	37586	37587		37595					37621	37622		37623		37629	37630								37665			37669
Exan SEQ ID NO:	23810	23819	23842	23868	23870	25866	23957	23957	23959	23968	23979	23979	ļ	ì	23989	23990		23990	23995	23996	23996	24003		ı	1	l	24023	24024	L	Ш	24034	24034
Probe SEQ ID NO:	4078G	10786	10809	10835	10846	10863	10872	10872	10874	10882	10895	10895	10898		10906	10907		10907	10912	10913	10913	10920	10920	10936	10940	10941	10941	10942	10946	10950	10952	10952

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Top Hit Descriptor	601674332F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3957343 5'	zp95b11.r1 Stratagene muscle 937209 Homo saplens cDNA clone IMAGE:627933 5' similar to gb:X03740 MYOSIN HEAVY CHAIN, SKELETAL MUSCLE (HUMAN);	601588829F1 NIH_MGC_7 Homo saplens cDNA clone IMAGE:3943015 6'	601562864F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3832575 5'	601562864F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3832575 5'	AV727362 HTC Homo saplens cDNA clone HTCAQH08 5'	AV727362 HTC Homo sapiens cDNA clone HTCAQH06 5'	yg09e09.r1 Soares infant brain 1NIB Homo saplens cDNA clone IMAGE:31874 5'	yg09e09.r1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:31674 5'	UI-H-BI1-adq-e-06-0-UI s1 NCI_CGAP_Sub3 Homo sapiens cDNA done IMAGE:2717874 3'	xyO4g10.x1 NCI_CGAP_Lym12 Homo sapiens cDNA clane IMAGE:2852226 3' similær to gb:M60854 40S RIBOSOMAL PROTEIN S16 (HUMAN);	AU135741 PLACE1 Homo septens cDNA clone PLACE1002794 5'	hg13d02x1 Soares_NR_T_GBC_S1 Homo septens cDNA clone IMAGE;2845475 3' similar to contains element MSR1 repetitive element.	hg13d02x1 Soares_NFL_T_GBC_S1 Homo sepiens cDNA clone IMAGE:2945475 3' similar to contains	element MSR1 repetitive element ;	hg13d02.x1 Sogres_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2845475 3' simitar to contains element MSR1 repetitive element;	H.saplens mRNA for H1 histamine receptor	HSC3IC031 normalized infant brain cDNA Homo saplens cDNA clone c-3lc03	Homo sapiens RGH1 gene, retrovirus-like element	xw66f01.x1 NC]_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2832985 3' slmiler to gb:X17116 IG MU CHAIN C REGION (HUMAN);	UI-H-Bi3-aih-a-01-0-UI.s1 NCI_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2736649 3'	UI-H-Bi3-alh-a-01-0-UI.s1 NCI_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2736649 3'	Homo sapiens ribosomal protein L31 (RPL31) mRNA	Homo sapiens mRNA for KIAA0667 protein, partial cds	601119248F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3029219.5	Homo sapiens mRNA for KIAA0646 protein, partial cds	EST90347 Synovial sarcoma Homo sapiens cDNA 5' end similar to similar to LERK-2, placenta	601582046F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3936539 5'	602141405F1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4302432 5
Top Hit Database Source	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST HUMAN	EST_HUMAN	EST HUMAN		EST_HUMAN	EST HUMAN	EST HUMAN	FST HUMAN	Г	EST_HUMAN	EST HUMAN			Į.	EST HUMAN	Г	Г		LN	T_HUMAN			EST_HUMAN	
Top Hit Acession No.	0.0E+00 BE903304.1	0.0E+00 AA195905.1	0.0E+00 BE793498.1	0.0E+00 BE729705.1	0.0E+00 BE729706.1	0.0E+00 AV727362.1	0.0E+00 AV727362.1	317132.1	217132.1	0.0E+00 AW139414.1	0.0E+00 AW516055.1	0.0E+00 AU135741.1	0 0E+00 AW59333 1		0.0E+00 AW59333.1	0.0E+00 AW59333.1	734897.1			0.0E+00 AW338094.1	0.0E+00 AW451230.1	0.0E+00 AW451230.1	4506632 NT	0.0E+00 AB014567.1	0.0E+00 BE298449.1	0.0E+00 AB011117.1	0.0E+00 AA377505.1		0.0E+00 BF684061.1
Most Similar (Top) Hit BLAST E Vatue	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00 R17132.1	0.0E+00 R17132.1	0.0E+00	0.0E+00	0.0E+00	0 05+00		0.0E+00	0.0E+00	0.0E+00 Z34897.1	0.0E+00 F13069.1	0.0E+00 D10083.1	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	ľ	Н		0.0E+00
Expression Signal	22.14	1.85	4.49	2.4	24	11.66	11.66	1.6	4.6	2.62	11.81	4.44	2.56		2.56	2.56	1.67	276	2,35	1.7.1	3.75	3.75	9.52	1.79	1.92	1.47	1.39	3.3	76.9
ORF SEQ ID NO:	37680	32399			37711	37712	37713				37732				37742	37743				37767	37768	37769		37771	37787	37797	37803	37813	
Exan SEQ ID NO:	24046	19087	<u>l_</u>	L		24078	24078	24082	l	ı	24093	24099	24105		24105	24105	24107	ı	24116	24131	ı		13443	24136	24148	24161	L	1	24179
Probe SEQ ID NO:	10965	10968	10990	10998	10998	10999	10999	11003	11003	11009	11014	11020	11026		11026	11028	11028	11029	11037	11054	11055	11055	11058	11060	11073	11087	11092	11106	11107

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Top Hit Descriptor	601186342F1 NIH_MGC_B Homo sepiens cDNA clone IMAGE:3544259 5'	ACT 10500 TEMBA 1 Horito septents CONA dulle TEMBA 1003-903 3 xn72b01.x1 NCI CGAP_CML1 Homo septens cDNA done IMAGE:2699977 3' similar to gb:X02152_cds1 L-	LACTATE DEHYDROGENASE M CHAIN (HUMAN);	qf43c03.x1 Soares_testis_NHT Homo saplens cDNA clone IMAGE:1752772.3'	qf43c03.x1 Scares_testis_NHT Homo sapiens cDNA clone IMAGE:1752772 3'	QV4-ST0234-121199-032-b06 ST0234 Homo sepiens cDNA	AU116908 HEMBA1 Homo sapiens cDNA clone HEMBA1000255 5'	Homo saplens insulin receptor (INSR), mRNA	qv85c12.x1 NCI_CGAP_Ut2 Homo sapiens cDNA clone IMAGE:1989334 3' similಡ್ to TR:Q14673 Q14673   KIAA0164 PROTEIN :	qv95c12.x1 NCI_CGAP_Ut2 Homo sapiens cDNA clone IMAGE:1989334 3' similar to TR:Q14673 Q14673	KIAA0164 PROTEIN, ;	602037014F1 NCI_CGAP_Bm64 Homo sapiens cDNA clone IMAGE:4184979 5	601148357F1 NJH_MGC_19 Hamo seplens cDNA clone IMAGE:3163310 5	Homo sapiens mRNA for KIAA117 protein, partial cds	Homo saplens mRNA for KIAA0463 protein, partial cds	Human protein kinase C substrate 80K-H (PRKCSH) gene, exon 15-17	RC1-FT0134-170700-012-f07 FT0134 Homo sapiens cDNA	RC1-FT0134-170700-012-f07 FT0134 Homo sapiens cDNA	ob32e07.s1 NCI_CGAP_Kid5 Homo saplens cDNA clone IMAGE:1328412.3' similar to contains element	Month repeative elerinen. Homo sanians signating lymphocytic activation molecule (SLAM) gene, exon 2	601192748F1 NIH MGC 7 Hamo sapiens cDNA clone IMAGE:3536867 5	601192748F1 NIH_MGC_7 Homo saplens cDNA clone IMAGE:3536867 5'	C05089 Human heart cDNA (YNakamura) Homo saplens cDNA clone 3NHC4817	oa56h01.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1309009 5'	oa56h01.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1309009 5'	EST00596 Fetal brain, Stratagene (catt/936206) Homo sapiens cDNA clone HFBCC26	EST00596 Fetal brain, Stratagene (cat#336205) Homo sapiens cDNA clone HFBCC26	QV2-HT0698-020800-295-d07 HT0698 Homo sapiens cDNA	DKFZp761J2118_r1 761 (synonym: hamy2) Homo sapiens cDNA clone DKFZp761J2116 5'	601336530F1 NIH_MGC_44 Homo saplens cDNA clone IMAGE:3690390 5'	AU116988 HEMBA1 Homo sapiens cDNA clone HEMBA1000424 5'
Top Hit Database Source	EST HUMAN	NEW THOMAIN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	NT	EST HUMAN	  - 	EST_HUMAN	EST_HUMAN	EST HUMAN	TN	NT	NT	EST_HUMAN	EST_HUMAN	1407	ES - HOMAIN	EST HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	<b>EST_HUMAN</b>	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN
Top Hit Acession No.	0.0E+00 BE269288.1	0.0E+00 A0118386.1	0.0E+00 AW236269.1	0.0E+00 A1149809.1	0.0E+00 AI149809.1	0.0E+00 AW391937.1	0.0E+00 AU116908.1	11424726 NT	0.0E+00 Al367350.1		0.0E+00 Al367350.1	0.0E+00 BF340308.1	0.0E+00 BE261209.1	0.0E+00 AB029040.1	0.0E+00 AB007932.1	U50326.1	0.0E+00 BE773036.1	0.0E+00 BE773036.1	, 000	0.0E+00 AA740782.1	0.0E+00 BE266478.1	0.0E+00 BE266478.1	C05089.1	0.0E+00 AA746375.1	0.0E+00 AA746375:1	M78448.1	M78448.1	0.0E+00 BF353625.1	0.0E+00 AL157608.1	0.0E+00 BE562822.1	0.0E+00 AU116988.1
Most Similar (Top) Hit BLAST E Value	0.0E+00	0.05	0.0E+00	0.0E+00	0.0E+00	0.0E+00.	0.0E+00	0.0E+00	0.0E+00		0.0E+00	0.0E+00	0.0E+00(	0.0E+00	0.0E+00	0.0E+00 U50326.1	0.0E+00	0.0E+00	00.70	0.0E+00.0	0.0E+00	0.0E+00	0.0E+00 C05089.1	0.0E+00	0.0E+00	0.0E+00 M78448.1	0.0E+00 M78448.1	0.0E+00	0.0E+00	0.0E+00	0.0E+00
Expression Signal	1.45	3.	1.81	5.71	5.71	2.63	11.83	29.67	2.14		2.14	1.63	13.91	2.19	1.51	3.89	2.43	2.43	1,	27.72	1.71	1.71	4.9	21	2.1	2.69	2.69	1.76	6.5	1.86	6.05
ORF SEQ ID NO:	37814			37820	37821	37822		37827	37828			37835						37856		37800					37915	37926		37930			37942
Exon SEQ ID NO:	24180	24182	24183	24188	24188	24189	24199	24202	24204		24204	24209	24211	24216	24219	24222	24226	24226	3	24240	24268	24268	24270	24277	24277	24287	24287	24290	24291	24303	24305
Probe SEQ ID NO:	11108	סרודור	11111	11116	11116	11117	11127	11130	11132		11132	11137	11139	11144	11147	11151	11165	11155		11186	11199	11199	11201	11208	11208	11218	11218	11221	11222	11234	11236

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Top Hit Descriptor	AV693656 GKC Homo saplens cDNA clone GKCCNC03 5'	II.3-NT0104-200500-143-A07 NT0104 Homo sapiens cDNA	PMC-HT0845-060500-002-E05 HT0645 Hamo sapiens cDNA	PM0-HT0645-060500-002-E05 HT0645 Hamo sapiens cDNA	AV701152 ADA Homo sapiens cDNA clone ADAAAD06 5'	601439092F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3924142 5'	UI-HF-BN0-akg-d-02-0-UI.r1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3077019 51	UI-HF-BNO-akg-d-02-0-UI.r1 NIH_MGC_50 Homo septens obnA clone IMAGE:3077019 5'	bb78c04.y1 NIH_MGC_10 Homo seplens cDNA clane IMAGE:3048486 5' similar to gb:Y00345_cds1 POLYADENYLATE-BINDING PROTEIN (HUMAN); gb:X65553 M.musculus mRNA for paty(A) binding	protein (MOUSE);	MR4-ST0118-041099-010-A12 ST0118 Homo sapiens cDNA	MR4-ST0118-041099-010-A12 ST0118 Homo capiene cDNA	801440446F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3925403 51	ao86g11.x1 Schiller meningioma Homo sapiens cDNA clone IMAGE:1952804 3'	ao86g11.x1 Schiller meningioma Homo sapiens cDNA clone IMAGE:1952804.3'	DKFZp434L0120_r1 434 (synonym: htss3) Homo sapiens cDNA clone DKFZp434L0120 5'	ou61d04x/1 NCI_CGAP_Br2 Homo sapiens cDNA clone IMAGE:1632295 3' similar to SW1LRP1_HUMAN Q07954 LOW-DENSITY LIPOPROTEIN RECEPTOR-RELATED PROTEIN 1 PRECURSOR;	ou61d04x1 NCL_CGAP_Br2 Homo sapiens cDNA clone IMAGE:1632295 3' similar to SW1.RP1_HUMAN Q07954 LOW-DENSITY LIPOPROTEIN RECEPTOR-RELATED PROTEIN 1 PRECURSOR;	ou61d04x1 NCI_CGAP_Br2 Homo sapiens cDNA clone IMAGE:1632295 3' similar to SW:LRP1_HUMAN Q07954 LOW-DENSITY LIPOPROTEIN RECEPTOR-RELATED PROTEIN 1 PRECURSOR;	Homo sepiens neurexin III (NRXN3) mRNA	601870902F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4101433 5'	UI-H-BI2-age-h-01-0-UI.s1 NCI_CGAP_Sub4 Homo sapiens cDNA clone IMAGE:2724312.3'	Homo sapiens mRNA for KIAA0717 protein, partial cds	Homo sapiens mRNA for KIAA0717 protein, partial cds	ba04d07.y1 NIH_MGC_7 Homo septens cDNA clone IMAGE:2823373 5' similar to TR:078022 076022 E1B. 55KDA•ASSOCIATED PROTEIN.;
Top Hit Database Source	EST_HUMAN	EST HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN		EST_HUMAN	EST_HUMAN	EST HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST HUMAN	EST HUMAN	LN	EST_HUMAN	EST_HUMAN	۲N	NT	EST_HUMAN
Top Hit Acession No.	0.0E+00 AV693656.1	0.0E+00 BF368553.1	0.0E+00 BE182360.1	0.0E+00 BE182360.1	0.0E+00 AV701152.1	3.0E+00 BE896423.1	3.0E+00 AW500307.1	3.0E+00 AW500307.1	1	0.0E+00 BE018293.1	0.0E+00 AW387766.1	0.0E+00 AW387766.1	0.0E+00 BE897953.1	).0E+00 Al459545.1	3.0E+00 AI459545.1	3.0E+00 AL042278.1	0.0E+00 AI073917.1	0.0E+00 A1073917.1	0.0E+00 AI073917.1	4758827 NT	3.0E+00 BF206561.1	3.0E+00 AW207734.1	0.0E+00 AB018260.1	0.0E+00 AB018260.1	3.0E+00 BE206846.1
Most Similar (Top) Hit BLAST E Value	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00		0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00/	0.0E+00	0.0E+00	0.0E+00
Expression Signal	1.75	2.97	24	2.4	1.51	3.02	1.83	1.83		2.49	1.45	1.45	3.23	2.24	2.24	1.89	1.37	1.37	1.37	3.8	24.41	11.85	3.93	3.93	2.63
ORF SEQ ID NO:		37969	1	37955		38011	38019	38020			38028		ļ	38073	38074	38087	38112	38113	38114	١.	38131	38137	38141	38142	38144
Exen SEQ ID NO:	24319	24329	24354	24354	24356	24370	24375	24375		24378	25869	25869	24415	24417	24417	24430	24451	24451	24451	24465	24486	24472	24477	24477	24479
Probe SEQ ID NO:	11250	11260	11288	11288	11290	11305	11311	11311		11314	11345	11345	11353	11355	11355	11369	11390	11390	11390	11404	11405	11411	11416	11416	11418

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						777	Single Lyon Flores Lybressed III Flacelina
Probe SEQ ID NO:	Exen SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
11418	24479	38145	2.63	0.0E+00	0.0E+00 BE206846.1	EST_HUMAN	be04d07.yī NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2823373 5' similar to TR:076022 076022 E1B- 56KDA-ASSOCIATED PROTEIN. ;
11429	24490	38155	2.37	0.0E+00	11526409 NT	TN	Homo sapiens KIAA0426 gene product (KIAA0426), mRNA
11438	24499	38166	1.68	0.0E+00	0,0E+00 AI075915.1	EST_HUMAN	ov46g07.x1 Soares_testis_NHT Homo septens cDNA done IMACE:1640412 3' similar to TR:Q14507 Q14507 EPIDIDYMIS-SPECIFIC GENE PRODUCT, ALPHA.;
11445			1.73	0.0E+00	11024711 NT	TN	Homo sapiens myosin, heavy polypeptide 4, skeletal muscle (MYH4), mRNA
11448			1.98	0.0E+00		EST_HUMAN	QV0-UM0091-120900-385-b12 UM0091 Homo saplens cDNA
11448			1.94	0.0E+00		TN	Homo sapiens zinc finger homeodomain protein (ATBF1-A) mRNA, complete cds
11452			4.61	0.0E+00	0.0E+00 BE148076.1	EST_HUMAN	RC3-HT0230-040500-110-h04 HT0230 Homo sapiens cDNA
11452	24612	38179	4.61	0.0E+00	BE148076.1	EST_HUMAN	RC3-HT0230-040500-110-h04 HT0230 Homo saplens cDNA
11475	24534	38204	1.66	0.0E+00	0.0E+00 AW 673469.1	EST_HUMAN	ba54d08,y3 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:2900367 5' similar to TR;O60275 O60275 KIAA0522 PROTEIN;
11475	24534	38205	1.66	0.0E+00	0.0E+00 AW673469.1	EST_HUMAN	ba54d08.y3 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:2900367 5' similar to TR:060275 O60275 KIAA0522 PROTEIN;
11490			4.84	0.0E+00	BF507876.1	EST_HUMAN	UI-H-BI4-aok-b-10-0-UI.s1 NCI_CGAP_Sub8 Homo sapiens cDNA clone IMAGE:3085026 3'
11490	24549	38224	4.84	0.0E+00	0.0E+00 BF507878.1	EST_HUMAN	UI-H-BI4-ack-b-10-0-UI.s1 NCI_CGAP_Sub8 Homo sapiens cDNA clone IMAGE:3085026 3'
11496			4.65	0.0E+00	AU135170.1	EST_HUMAN	AU135170 PLACE1 Homo sapiens cDNA clone PLACE1001381 5'
11501	24559		2.07	0.0E+00	BF576138.1	EST_HUMAN	602132459F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4271630 5'
11501		38235		0.0E+00	BF576138.1	EST_HUMAN	602132459F1 NIH_MGC_81 Homo saplens cDNA done IMAGE-4271630 57
11503	24561	38238		0.0E+00	BE876401.1	EST_HUMAN	601486828F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3889207 5'
11503				0.0E+00	BE876401.1	EST_HUMAN	601486828F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3889207 6
11511			1.61	0.0E+00	0.0E+00 D87682.1	NT	Human mRNA for KIAA0241 gene, partial cds
11518				0.0E+00	BF240536.1	EST_HUMAN	601875630F1 NIH_MGC_55 Home sapiens cDNA done IMAGE:4099710 5'
11531	24587	38262		0.0E+00	AB037737.1	TN	Homo sapiens mRNA for KIAA1316 protein, partial cds
11531				0.0E+00		NT	Homo saplens mRNA for KIAA1316 protein, partial cds
11535		38266		0.0E+00	11430868 NT	TN	Homo sapiens retinoblastoma-like 2 (p130) (RBL2), mRNA
11535	24591	38267	3.09	0.0E+00	11430868 NT	LN	Homo saplens retinoblastome-like 2 (p130) (RBL2), mRNA
11653			6.13	0.0E+00	450354 NT	IN	Homo sapiens eukaryotic translation Initiation factor 5A (EIF5A) mRNA
11560		38294	2.06	0.0E+00	0.0E+00 BF576267.1	EST_HUMAN	602134132F1 NIH_MGC_81 Homo sapiens cDNA done IMAGE:4289502 5'
11562						EST_HUMAN	dr04g05,x1 NIH_MGC_3 Homo sapiens cDNA clone IMAGE:2847177 5'
11567	24622		42.5	0	.0E+00 M55083.1	NT	Human gamma actin-like pseudogene, complete cds
11571	24626	38305	1.76		0.0E+00 AI660968.1	EST HUMAN	wf20e11.x1 Sogres_Dieckgraefe_colon_NHUC Homo saplens cDNA clone IMAGE:2351180 3' similar to gb:M87789 IG GAMMA-1 CHAIN C REGION (HUMAN);
11574				1	BF306996.1	EST HUMAN	801889823F1 NIH MGC 17 Homo saplens oDNA clone IMAGE:4123948 5
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Top Hit Descriptor	601889823F1 NIH_MGC_17 Homo saplens cDNA clone IMAGE:4123948 5'	QV2-NN0054-230800-333-e04 NN0054 Homo sapiens cDNA	Human beta-prime-adaptin (BAM22) gene, exon 16	Human befa-prime-adaptin (BAM22) gene, oxon 16	601439605F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3924577 51	Homo sapiens fyn-related kinase (FRK) mRNA	Homo sapiens golgin-like protein (GLP), mRNA	601861947F1 NIH_MGC_53 Homo saplens cDNA clone IMAGE:4081715 5	ba04d07.yt NIH_MGC_7 Homo saptens oDNA clone IMAGE:2823373 5' similar to TR:076022 076022 E1B- 55KDA-ASSOCIATED PROTEIN ;	ba04d07.71 NIH_MGC_7 Homo saplens oDNA done IMAGE:2823373 5' similar to TR:076022 076022 E1B- 55KDA-ASSOCIATED PROTEIN :	QV0-CT0225-101299-071-106 CT0225 Homo sapiens cDNA	nI42008.s1 NCI_CGAP_Pt4 Homo espiens cDNA clone IMAGE:1043342 similar to gb:M95178 ALPHA- a chinin a cytroskei etta i soneopa, du imaany	wp06g08.x1 NCI_CGAP_Kid12 Home saplens cDNA clone IMAGE:2464094 3'	dr02b08.x1 NIH MGC_3 Homo sapiens cDNA clone IMAGE:2846919 5	UI-H-BW0-aij-d-07-0-UI.s1 NCI_CGAP_Sub6 Homo sapiens cDNA clone IMAGE:2729509 31	Homo saplens neurexin III (NRXN3) mRNA	601113903F1 NIH_MGC_16 Homo sepiens cDNA clone IMAGE:3354600 5'	601659088R1 NIH MGC_70 Homo capiens cDNA clone IMAGE:3895916 3'	601659088R1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3895916 3'	L5-HT0731-020500-077-f05 HT0731 Homo sapiens cDNA	UI-H-BW1-amv-a-05-0-UI.s1 NCI_CGAP_Sub7 Homo sepiens cDNA clone IMAGE:3071121 3'	DKFZp434G178_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434G178 5'	DKFZp434G178_r1 434 (synonym: htes3) Homo sepiens cDNA clone DKFZp434G178 5'	wn83g03.x1 NCI_CGAP_Ut1 Homo sapiens cDNA clone IMAGE:2452458 3° similar to gb:S37431 LAMININ RECEPTOR (HUMAN);	nz11-07.s1 NCI_CGAP_GCB1 Homo saplens cDNA clone IMAGE:1287468 3' similar to TR:Q13686 Q13686 ALKB HOMOLOG PROTEIN.	nz11c07.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1287468 3' similar to TR:Q13686 Q13686 ALKB HOMOLOG PROTEIN. ;	601501090F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3902926 5'
Top Hit Database Source	П	T HUMAN			EST_HUMAN 6			EST_HUMAN 6	EST HUMAN 5	EST HUMAN 5	Т			Г	Т	H	EST_HUMAN 6			П	П		EST_HUMAN D	EST HUMAN		EST_HUMAN C	П
Top Hit Acession No.	П				0.0E400 BE897051.1	4503786 NT	8923698 NT	0.0E+00 BF207662.1	0.0E+00 BE206846.1	0 0E+00 BE 206846 1		000000000000000000000000000000000000000		<u>-</u> -	Γ	8827	0,0E+00 BE254058.1	0.0E+00 BE965909.2	0.0E+00 BE965909.2	0.0E+00 BE185656.1	0.0E+00 BF513960.1	0.0E+00 AL046540.1	0.0E+00 AL046540.1	0.0E+00 AI923116.1	0.0E+00 AA760913.1	0.0E+00 AA760913.1	0.0E+00 BE910546.1
Most Similar (Top) Hit BLAST E Value	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.05+00	0.0E+00	00.00	0.05+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00
Expression Signal	3.37	47.2	2.32	232	4.33	237	234	207	4.53	4.53	3.69	3	2.56	7.51	1.78	1.93	1.35	1.79	1.79	3.81	1.39	7.19	7.19	10.19	4.47	4.47	2.21
ORF SEQ ID NO:	38308	38315	38338				38361		38407				31562	38416				38369		38371			38385	38395			
Exan SEQ ID NO:	24629	24635	24654		L	24860	24672		24718	24716	i_	{	18590	1		23899	24676	24679	ı	l		ı	ı		١.	ı	24753
Probe SEQ (D NO:	11574	11581	11601	11601	11606	11607	11621	11623	11636	11636	11638	30	11644	11645	11664	11671	11677	11680	11680	11681	11682	11696	11696	11706	11708	11708	11713

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Top Hit Descriptor	7127112.x1 NCI_CGAP_CLL1 Homo sapiens cDNA done IMAGE:3295919 3' similar to TR:000409 000409 CHECKPOINT SUPPRESSOR 1.;	togebog.x1'NC]_CGAP_Utt Homo sepiens dDNA clane IMAGE:2274521 3' similar to gb:M55542 INTERFERON-INDUCED GUANYLATE-BINDING PROTEIN 1 (HUMAN);	601279335F1 NIH_MGC_39 Homo saplens cDNA clone IMAGE:3611144 5	601278335F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3611144 5'	AV767420 BM Hamo sepiens cDNA clone BMFAGH03 5'	DKFZp564C187_r1 564 (synonym: hfbr2) Homo saplens cDNA clone DKFZp564C187 6'	Human oxytocinase variant 2 mRNA, complete cds	601509139F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3910833 5'	Human endogenous retrovtrus type K (HERV-K), gag, pol and env genes	Homo saplens polycystic kidney disease-associated protein (PKD1) gene, complete cds	Homo sepiens polyoystic kidney disease-associated protein (PKD1) gene, complete cds	AU138211 PLACE1 Homo sapiens cDNA clone PLACE1008077 5'	601441096F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3916270 5	601572186T1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:3839012 3'	601572186T1 NIH_MGC_55 Homo sepiens cDNA clone IMAGE:3839012 3'	AU141882 THYRO1 Homo sapiens cDNA clone THYRO1001398 5	AU141882 THYRO1 Homo sapiens cDNA clone THYRO1001398 5'	wzs1h01.x1 NCI_CGAP_Brn26 Homo sapiens cDNA clone IMAGE:2566225 3' similar to WP:F53H10.2 CE11040 ZINC FINGER, C2H2 TYPE:	7h22b10.x1 NCI CGAP Co16 Homo sapiens cDNA clone IMAGE:3316699 3' similar to TR:Q13458 Q13458	TRIO.;	C06264 Human pancreatic islet Homo saplens cDNA similar to insulin receptor	601564180F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3833730 5'	tigo a10 x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:21478023' similar to	b:M31681 PROLACTIN RECEPTOR TYPE 2 PRECURSOR (HUMAN);	MR4-ST0118-261099-012-b03 ST0118 Homo saplens cDNA	MR4-ST0118-261099-012-b03 ST0118 Homo saplens cDNA	MR3-SN0010-310300-107-h03 SN0010 Homo sapiens cDNA	Homo sapiens KIAA0247 gene product (KIAA0247), mRNA	Homo sapiens KIAA0247 gene product (KIAA0247), mRNA	Human beta-prime-adaptin (BAW22) gene, exon 5	601237691F1 NIH_MGC_44 Home sepiens cDNA clone IMAGE:3609623 5
Top Hit Database Source	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	NT.	EST_HUMAN	NT	TN	Į.	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST HUMAN		EST_HUMAN	EST_HUMAN		Г	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST HUMAN	L	NT	NT	EST_HUMAN
Top Hit Acession No.	0.0E+00 BE676347.1	0.0E+00 A(683358.1	0.0E+00 BE615666.1	0.0E+00 BE615666.1	0.0E+00 AV757420.1	0.0E+00 ALG37746.1	0.0E+00 U62769.1	0,0E+00 BE883386.1	0.0E+00 Y18890.1		L39891.1	.0E+00 AU138211.1	0.0E+00 BE622317.1	0.0E+00 BE748899.1	0.0E+00 BE748899.1	0.0E+00 AU141882.1	.0E+00 AU141882.1	0E+00 AW006022.1		0.0E+00 BF002333.1	0.0E+00 C06264.1	0.0E+00 BE727811.1		0.0E+00 A/472010.1	0.0E+00 AW387776.1	.0E+00 AW387776.1	0.0E+00 AW863777.1	11435244 NT	11435244 NT	0.0E+00 U36253.1	0.0E+00 BE379254.1
Most Similar (Top) Hit BLAST E Value	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00 L39891.1	0.0E+00 L39891.1	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.05+00		0.0E+00	0.0E+00	0.0E+00		0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00
Expression Signal	11.64	1.47	3.13	3.13	1.59	7.33	4.2	1.33	1.75	3.69	3.59	2.03	6.43	17.72	17.72	4.58	4.58	2.7		2.73	1.32	1.56		2.36	2.84	2.84	1.8	3.67	3.67	4.38	26.74
ORF SEQ ID NO:	37533	37535								38465	38456		38485		38513	38527	38528	38531		38537	38548			38555		38564		38589		38596	
SEO ID NO:	23909	23911			23920			L	l		24761	1	24787	ı	<u> </u>		ł	1	1	25871		<u> </u>	<u></u>	24860	l	l		L.	L	L	Ш
Probe SEQ ID NO:	11723	11725	11727	11727	11734	11739	11740	11745	11766	11769	11769	11784	11797	11833	11833	11845	11845	11848		11853	11864	11868		11872	11878	11878	11889	11901	11901	11907	11911

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Top Hit Descriptor	601237691F1 NIH_MGC_44 Homo saplens cDNA ckne IMAGE:3609623 5'			601491821F1 NIH_MGC_69 Homo saplens cDNA clone IMAGE:3894220 5	Human von Willebrand factor pseudogene corresponding to exons 23 through 34	Homo sapiens neurexin III (NRXN3) mRNA	Homo saplens neurexin III (NRXN3) mRNA	Homo sapiens glutathlone transferase zeta 1 (GSTZ1) gene, exons 6 and 7	601299403F1 NIH_MGC_21 Homo saplens cDNA clone IMAGE:3629544 5'	MR0-HT0241-150500-011-f02 HT0241 Homo sapiens cDNA	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, excins 7-49, and partial cds, alternatively spliced	Homo saplens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively shined	Human name for dibudrolimamide succinultransferase, complete cds (evon 1-15)		Human gene for dihydrolipoamide succinyfransterase, complete cds (exon 1-15)	OUZIDS/ZZFI NIH MCC 35 HOMO SEPTEM CUMA CIGHE IMAGE: 4290/20 5	602155722F1 NH_MGC_83 Homo saptens cDNA clone IMAGE:4236725 5	AU132940 NT2RP4 Hamo sepiens cDNA clone NT2RP4000929 5	601676357F1 NIH_MGC_21 Hamo saplens cDNA clone IMAGE:3958935 5	601897524F1 NIH_MGC_19 Homo saplens cDNA clone IMAGE:4127069 5'	601897524F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4127069 5'	Human tambda-Immunoglobulin constant region complex (germline)	Human lambda-Immunoglobulin constant region complex (germline)	601498653F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3900396 5'	Human endogenous retrovirus, complete genome	601890534F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4131416 5	RC4-NN0025-120600-016-b07 NN0025 Homo sepiens cDNA	RC4-NN0025-120600-016-b07 NN0026 Homo sapiens cDNA	601177407F1 NIH_MGC_17 Homo saplens cDNA done IMAGE:3532968 5'	601576525F1 NIH_MGC_9 Homo saplens cDNA clone IMAGE:3837222 5'	[601576525F1 NIH_MGC_9 Homo saplens cDNA clone IMAGE:3837222 5		601113009F1 NIH_MGC_16 Homo saplens cDNA done IMAGE:3353378 5
Top Hit Database Source	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	F	눌	<u>F</u>	LΝ	EST_HUMAN	EST_HUMAN	ΤΝ	L			LN L	ESI HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	ΝT	ΝΤ	<b>EST_HUMAN</b>		<b>EST_HUMAN</b>	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN
Top Hit Acession No.	0.0E+00 BE379254.1	0.0E+00 AW 500056.1	3E794758.1	BE879633.1	V/60676.1	0.0E+00 4758827 NT	4758827 NT	0.0E+00 AF053543.1	0.0E+00 BE409993.1	3E148650.1	0E+00 AF223391.1	0 05+00	DOEESE 4	250000.1	0.0E+00 D26535.1	81-681641.1	BF681641.1	AU132940.1	BE903372.1	BF312652.1	BF312552.1	X51755.1	X51755.1	0.0E+00 BE906402.1	9635487	BF309120.1	BE698861.1	BE698861.1	0.0E+00 BE297175.1	BE744311.1	BE744311.1	0.0E+00 BE257612.1	BE257612.1
Most Similar (Top) Hit BLAST E Vatue	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	00710	20.0	20.00	0.0E+00	0.05+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00
Expression Signal	26.74	4.87	2.05	65.18	1.6	1.38	1.38	1.68	7.29	2.22	2.89	e c	4 40	2	1.48	11.38	11.38	1.79	4.99	1.56	1.56	3.4	3.4	1.96	1.46	8.57	2.37	2.37	96'09	1.42	1.42	2.02	202
ORF SEQ ID NO:	38601	38606	38621	38622	38623	38629	38630	38635	38642	38643	38644	38848	24004	13015	31832	38647				38671	38672	38675	38676		38700		38713	38714				38741	
Exan SEQ ID NO:	24898	24903	24918	24920	١.,	24927	24927	<u> </u>	١.	24940	24941	l	L	1	1	١			١.	24968	24968	24971	Ĺ.,	24983				J	ł		L		25035
Probe SEQ ID NO:	11911	11917	11932	11934	11935	11941	11941	11946	11953	11954	11955	11055	300	3	11956	11958	11958	11964	11967	11983	11983	11986	11986	11998	12013	12028	12029	12029	12032	12046	12046	12054	12054

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					_		-		_			,	_		_		<u> </u>	11_31		.71-10		•	mur .	M3144	<u>.                                    </u>	71417 7119	49959 - 2164
Top Hit Descriptor	601070391F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3456407 5	283e01.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:729912 5' similar to SW:PMT1_SCHPO P40999 DNA METHYLTRANSFERASE PMT1;	AU117974 HEMBA1 Homo sapiens cDNA clone HEMBA1002612 5	AU117974 HEMBA1 Homo saplens cDNA clone HEMBA1002612 5'	601468712F1 NIH_MGC_67 Homo sapiens cDNA done IMAGE:3871899 57	xv46h03.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2816213 3' shniter to gb:L11706_cds1 HORMONE SENSITIVE LIPASE (HUMAN);	AU132394 NT2RP3 Homo sapiens cDNA clone NT2RP3004339 5'	601105652F1 NIH_MGC_15 Hamo sapiens cDNA done IMAGE: 2988325 57	601150023F1 NIH_MGC_19 Homo sapiens cDNA done IMAGE:3503020 5	Homo sapiens chromosome 21 segment HS21C046	qe17b12.x1 Soares_fetal_lung_NbHL19W Homo sapiens cDNA clone IMAGE:1739231 3'	Homo sapiens gene for AF-6, complete cds	Homo sapiens chromosome 21 segment HS21C046	Homo sapiens ELK1 pseudogene (ELK2) and immunoglobulin heavy chain gamma pseudogene (IGHGP)	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA	Homo sapiens antioxidant protein 1 (AOP1), nuclear gene encoding mitochondrial protein, mRNA	Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1)	DKFZp434K0819 r1 434 (sunonym: htes3) Homo sapiens cDNA clone DKFZp434K0819 5'	Homo saplens G-2 and S-phase expressed 1 (GTSE1), mRNA	DKFZp434G218_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434G218 5	L-BT030-271098-001 BT030 Homo sapiens cDNA	yw40e08.s1 Soares fetal liver spleen 1NFLS Homo saptens cDNA clone IMAGE:245222 3' similar to SW-POL BAEVM P10272 POL POLYPROTEIN :	Homo saplens adenylosuccinate lyase gene, complete cds	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA	Homo saplens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA	Homo sapiens nuclear factor of activated T-cells, cytoplasmic, calcineurin-dependent 2 (NFATC2), mRNA	Homo sapiens X-linked anhidrollic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
Top Hit Database Source	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST HUMAN	EST HUMAN	EST_HUMAN	EST_HUMAN	LN.	EST_HUMAN	LN L	IN	ħ	LN.	Į.	Ę	EST HUMAN	N <sub>T</sub>	EST_HUMAN	EST_HUMAN	EST HIMAN	N	L	N	LN.	NT
Top Hit Acessian No.	0.0E+00 BE545535.1	0.0E+00 AA399001.1	0.0E+00 AU117974.1	0.0E+00 AU117974.1	0.0E+00 BE780453.1	0.0E+00 AW269990.1	0.0E+00 AU132394.1	0.0E+00 BE292840.1	0.0E+00 BE312542.1	0.0E+00 AL163246.2	0.0E+00 AI190993.1	0.0E+00 AB011399.1	0.0E+00 AL163246.2	0.0E+00 AB016195.1	11417862 NT	5802973 NT	0.0E+00.0E98.1	0.0E+00 AL041931.1	11418318 NT	0.0E+00 AL046544.1	0.0E+00 AI903497.1	0 DE+00 N54484 1	0.0E+00 AF108656.1	4507500 NT	4607600 NT	10092587 NT	0.0E+00 AF003528.1
Most Similar (Top) Hit BLAST E Value	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	00+100	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.05+0.0	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00
Expression Signal	2.85	1.34	1.55	1.55	1.72	2.15	1,99	1.35	9.34	3.02	5.49	3.73	6.87	1.35	3.2	4.95	1 47	3.47	3.39	4.77	2.92	1.88	4.08			3.07	4.88
ORF SEQ ID NO:	38770	38773			38778	38792	38803		31540								21787							27106			
SEQ ID NO:	25064	25067	L	25068	25071	25088	l_	L	26185	26005	26013	25134	25149	25151	25156	25170	25073	┸	<u> </u>	25222	26017	26172	L	1		26021	13754
Probe SEQ ID NO:	12084	12087	12088	12088	12091	12108	12118	12131	12147	12160	12162	12172	12192	12194	12201	12220	12254	12267	12295	12304	12317	12356	12371	12374	12374	12383	12415

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Top Hit Descriptor	Homo sapiens low density lipoprofein-related protein 2 (LRP2), mRNA	hg31e08.x1 NCI_CGAP_GC6 Homo sapiens cDNA ctone INAGE:2947234 3' similar to contains Atu repetitive element;	Human gamma-glutamyl transpeptidase mRNA, complete cds	Homo sapiens somatostatin receptor subtype 3 (SSTR3) gene, 5 flanking region and partial cds	Human endogenous retrovirus, complete genome	AV720678 GLC Hamo sepiens cDNA done GLCEPG09 5'	an05h04.x1 Stratagene schizo brain S11 Homo saplens cDNA clone IMAGE:1684759 3'	QV-BT065-020399-103 BT065 Homo sapiens cDNA	HTM1-654F HTM1 Homo sapiens cDNA	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA	Homo sapiens caveolin-3 (CAV3) mRNA, complete cds	yo59e08.r1 Soares breast 3NbHBst Homo saplens cDNA clone IMAGE:182246 5' similar to gb:M64099 GAMMA-GLUTAMYLTRANSPEPTIDASE 5 PRECURSOR (HUMAN);	y699608.r1 Soares breast 3nbHBst Homo sapiens cDNA done IMAGE:182246 5' similar to gb:M64099 GAMMA-GI UTAMYLTRANSPEPTIDASE 5 PRECURSOR (HUMAN);	Homo saplens gene for AF-8, complete cds	Human gamma-cytoplasmic actin (ACTGP9) pseudogene	Homo sapiens thyroid autoantigen 70kD (Ku antigen) (G22P1), mRNA	Homo sapiens thyroid autoantigen 70kD (Ku antigen) (G22P1), mRNA	Hamo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)	Homo sapiens GTP binding protein 1 (GTPBP1) mRNA	hB6e08.x1 Soares_NFL_T_GBC_S1 Hamo sapiens cDNA clone IMAGE:29791543'	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA	Homo sapiens hypothetical protein FLJ10697 (FLJ10697), mRNA	Homo sapiens G protein-coupled receptor 24 (GPR24), mRNA	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA	Homo capiens CST gene for cerebroside sulfotransferase, exon 1, 2, 3, 4, 5	Homo sapiens cleavage and polyadenylation specific factor 1, 160kD subunit (CPSF1), mRNA	Homo sapiens chromosome 21 segment HS21 C046	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA	Homo sapiens calcineurin binding protein 1 (KIAA0330), mKNA
Top Hit Database Source	TN	EST_HUMAN	LN	NT	NT	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	IN	LN L	Ę	EST_HUMAN	NAM H FRE	L	Z.	F	ĽΝ	<u> </u>	Ę	EST_HUMAN	ΤN	LN.	N	Į.	۲	TN	NT	LN	노
Top Hit Acession No.	11430460 NT	).0E+00 AW 590082.1	20493.1	0.0E+00 AF088757.1	9635487 NT	3.0E+00 AV720678.1	3.0E+00 AI204914.1	3.0E+00 A1904646.1	3.0E+00 BE439792.1	6912457 NT	6912457 NT	3.0E+00 AF036365.1	130132.1	000000000000000000000000000000000000000	0.0E+00 AB011399.1	D50659.1	11418189 NT	11418189 NT	0 0E+00 AB0288881	4758489 NT	0.0E+00 AW664999.1	11430460 NT	R922593 NT	4885312 NT	TN 8169089	0.0E+00 AB029900.1	9558724 NT	0.0E+00 AL163246.2	6806918 NT	11417862 NT
Most Similar (Top) Hit BLAST E Value	0.0E+00	0.0E+00	0.0E+00 L20493.1	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00 H30132.1	00+400	0.0E+00/	0.0E+00 D50659.	0.0E+00	0.0E+00	00+40	0.0E+00	0.0E+00	0.0E+00	00+30.0	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00
Expression Signal	3.95	1.64	1.34	2,73	4.61	1.19	3.51	1.33	2.29	1.39	1.39	1.21	3.26	3 28	1.6	33.13	5.44	5.44	7 88	1.7	2.11	1.43	1.74	3.11	2.3	1.88	1.82	2.93	2.46	1.17
ORF SEQ ID NO:	31937									28297	28298				27031	L	31997	١		28420	L	31988					31983		26851	
Exan SEQ ID NO:	25781	Ĺ	<u> </u>	26015		ſ.	l	25462		15187	15187	25490	1	14960	_[_		1_	25514	<u></u>	L	L	L	L	L	İ_		<u> </u>	I	13828	
Probe SEQ ID NO:	12450	12510	12542	12573	12618	12638	12660	12694	12702	12714	12714	12739	12751	42754	12755	12766	12771	12771	42778	12798	12837	12847	12892	12927	12935	12938	12981	13010	13017	13113

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<del></del>	-		_			_	_	_	_
Top Hit Descriptor	Homo saplens DNA for Human P2XM, complete cds	Homo sapiens DKFZp434P211 protein (DKFZP434P211), mRNA	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes,	complete cds)	UI-HF-BN0-aly-g-08-0-UI.r1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3081399 5'	Human endogenous retrovrus pHE.1 (ERV9)	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA	Homo sablens chromosome 12 open reading frame 3 (C12ORF3), mRNA
Top Hit Database Source	LZ	٦		N.	EST_HUMAN	TA	IN	L	ΤN
Top Hit Acession No.		7657020		AB026898.1		X57147.1	6806918	6806918	TN 4480868
Most Similar (Top) Hit BLAST E Value	00+30.0	0.0E+00			ľ	0.0E+00		0.0E+00	0.05+00
Expression Signal	1.4	3,11		5.96	1.16	1.51	1.37	1.37	1 29
ORF SEQ ID NO:							29151	29152	27402
Exan SEQ ID NO:	25728	25731		25740	26207	25774	16135	ļ	14345
Probe SEQ ID NO:	13116	13119		13140	13151	13190	13209	13209	13215
	Exon ORF SEQ Expression (Top) Hit Top Hit Acession Signal BLASTE No. Source Source	Expn         ORF SEQ ID ID NO:         Signal No:         Crop Hit Acession Signal         Top Hit Acession Top Hit Acession Source         Top Hit Acession Database Source         Top Hit Acession Database Source         Top Hit Acession Source         Top Hit Acession Source         Top Hit Acession Database Source         Source         Source         Source         Source         Acethod Aboro2069.1         In More Septions DNA for Human P2XM, complete	Exon SEQ ID NO:         ORF SEQ Signal Signal         Abost Similar (Top) Ht Signal Value         Top Hit Top Hit No.         Top Hit Source Source No.         Top Hit Source Source No.         Top Hit Source No.         Top Hit Source No.         Top Hit Source No.         Top Hit Source No.         Top Hit Source No.         Top Hit Source No.         Top Hit Source No.         Top Hit Source No.         Top Hit Source No.         Top Hit Source No. 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NT	Exon SEQ ID NO:         ORF SEQ Signal Signal         Expression (Top) Hit Value         Top Hit Accession No:         Top Hit Accession Source         Top Hit Accession Source         Top Hit Accession Source         Top Hit Accession Source         Top Hit Accession Source         Database Source           25728         14         0.0E+00 AB002059.1         NT         NT           25731         3.11         0.0E+00 AB026898.1         NT         O           26740         56.96         0.0E+00 AB026888.1         NT         O           26774         1.16         0.0E+00 AW505176.1         EST_HUMAN           26774         1.51         0.0E+00 X57147.1         NT	Exon SEQ ID NO:         ORF SEQ Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal 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CLAIMS

A spatially-addressable set of single exon nucleic acid probes for measuring gene expression in a sample derived
 from human placenta comprising a plurality single exon nucleic probes, said probes comprising any one of the nucleotide sequences set out in SEQ ID NOs: 1 - 13,232 or a complementary sequence, or a portion of such a sequence.

- 10 2. A spatially-addressable set of single exon nucleic acid probes as claimed in claim 1 wherein each of said plurality of probes is separately and addressably amplifiable.
- 3. A spatially-addressable set of single exon nucleic acid 15 probes as claimed in claim 1 wherein each of said plurality of probes is separately and addressably isolatable from said plurality.
- 4. A spatially-addressable set of single exon nucleic acid 20 probes as claimed in any of claims 1 to 3 wherein said probes comprise any one of the nucleotide sequences set out in SEQ ID NOS.: 13,233 - 26,232.
- 5. A spatially-addressable set of single exon nucleic acid 25 probes as claimed in any of claims 1 to 4, wherein each of said plurality of probes is amplifiable using at least one common primer.
- 6. A spatially-addressable set of single exon nucleic acid probes as claimed in any of claims 1 to 5 wherein the set comprises between 50 20,000 single exon nucleic acid probes.
- 7. A spatially-addressable set of single exon nucleic acid probes as claimed in any of claims 1 to 6, wherein the

average length of the single exon nucleic acid probes is between 200 and 500 bp.

- 8. A spatially-addressable set of single exon nucleic acid 5 probes as claimed in any of claims 1 to 7, wherein at least 50% of said single exon nucleic acid probes lack prokaryotic and bacteriophage vector sequence.
- 9. A spatially-addressable set of single exon nucleic acid 10 probes as claimed in any of claims 1 to 8, wherein at least 50% of said single exon nucleic acid probes lack homopolymeric stretches of A or T.
- 10. A spatially-addressable set of single exon nucleic acid probes as claimed in any of claims 1 9 characterised in that said set of probes is addressably disposed upon a substrate.
- 11. A spatially-addressable set of single exon nucleic acid 20 probes as claimed in claim 10 wherein said substrate is selected from glass, amorphous silicon, crystalline silicon and plastic.
- 12. A microarray comprising a spatially addressable set of single exon nucleic acid probes as claimed in any of claims 1 11.
- 13. A single exon nucleic acid probe for measuring human gene expression in a sample derived from human placenta comprising a nucleotide sequence as set out in any of SEQ ID NOs.: 1 13,232 or a complementary sequence or a fragment thereof wherein said probe hybridizes at high stringency to a nucleic acid molecule expressed in the human placenta.

14. A single exon nucleic acid probe as claimed in claim 13 comprising a nucleotide sequence as set out in any of SEQ ID NOs.: 13,233 - 26,232 or a complementary sequence or a fragment thereof.

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- 15. A single exon nucleic acid probe for measuring human gene expression in a sample derived from human placenta which is a nucleic acid molecule having a sequence encoding a peptide comprising a peptide sequence as set out in any
- of SEQ ID NOs.: 26,233 38,837, or a complementary sequence or a fragment thereof wherein said probe hybridizes at high stringency to a nucleic acid expressed in the human placenta.
- 15 16. A single exon nucleic acid probe as claimed in any one of claims 13 to 15 wherein said single exon nucleic acid probe comprises between 15 and 25 contiguous nucleotides of said SEQ ID NO.
- 20 17. A single exon nucleic acid probe as claimed in any one of claims 13 to 15, wherein said probe is between 3 25 kb in length.
- 18. A single exon nucleic acid probe as claimed in any one of claims 13 17, wherein said probe is DNA, RNA or PNA.
  - 19. A single exon nucleic acid probe as claimed in any one of claims 13 18, wherein said probe is detectably labeled.

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- 20. A single exon nucleic acid probe as claimed in any one of claims  $13\,-\,19$ , wherein said probe lacks prokaryotic and bacteriophage vector sequence.
- 35 21. A single exon nucleic acid probe as claimed in any one

of claims 13 - 20, wherein said probe lacks homopolymeric stretches of A or T.

22. A method of measuring gene expression in a sample5 derived from human placenta, comprising:

contacting the microarray of claim 12, with a first collection of detectably labeled nucleic acids, said first collection of nucleic acids derived from mRNA of human placenta; and then

measuring the label detectably bound to each probe of said microarray.

- 23. A method of identifying exons in a eukaryotic genome, comprising:
- algorithmically predicting at least one exon from genomic sequence of said eukaryote; and then detecting specific hybridization of detectably labeled nucleic acids to a single exon probe,

wherein said detectably labeled nucleic acids are derived
from mRNA from the placenta of said eukaryote, said probe
is a single exon probe having a fragment identical in
sequence to, or complementary in sequence to, said
predicted exon, said probe is included within a microarray
according to claim 12, and said fragment is selectively
hybridizable at high stringency.

24. A method of assigning exons to a single gene, comprising:

identifying a plurality of exons from genomic
sequence according to the method of claim 23; and
then

measuring the expression of each of said exons in a plurality of tissues and/or cell types using hybridization to single exon microarrays having a probe with said exon,

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wherein a common pattern of expression of said exons in said plurality of tissues and/or cell types indicates that the exons should be assigned to a single gene.

- 5 25. A nucleic acid sequence as set out in any of SEQ ID NOs: 1 26,232 which encodes a peptide.
  - 26. A peptide encoded by a sequence as set out in any of SEQ ID Nos: 1 26,232.

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27. A peptide comprising a sequence as set out in any of SEQ ID Nos: 26,233 - 38,837.

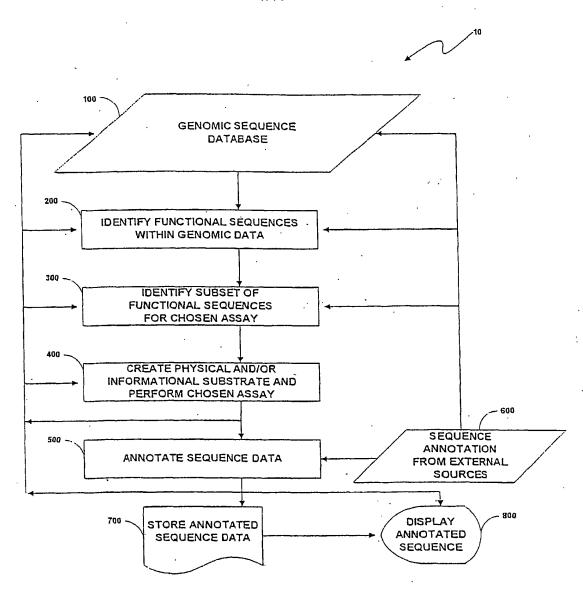


Fig. 1

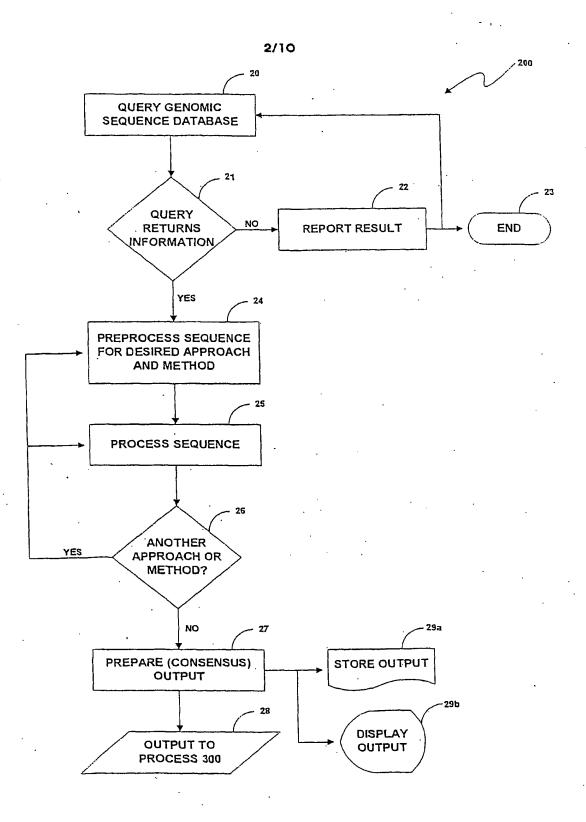


Fig. 2

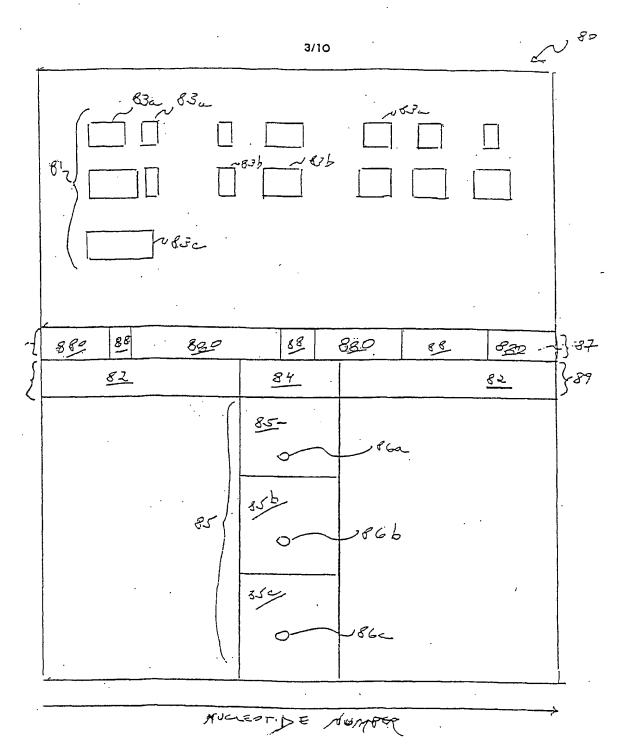


Fig. 3

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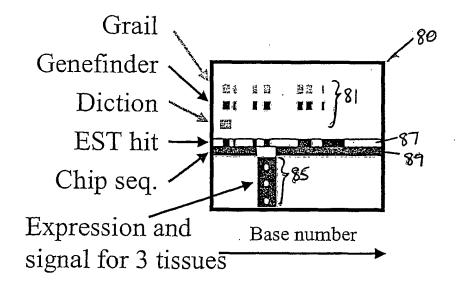


Fig. 4

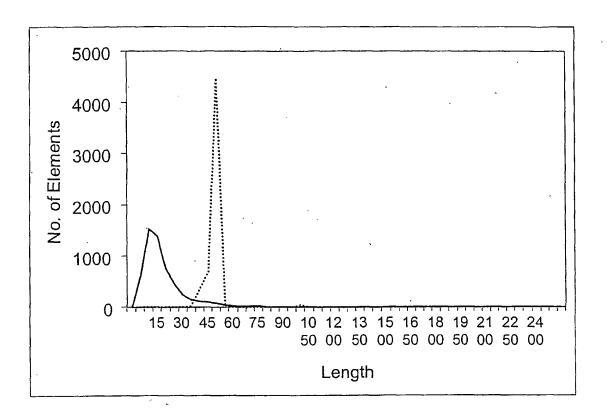


Fig. 5

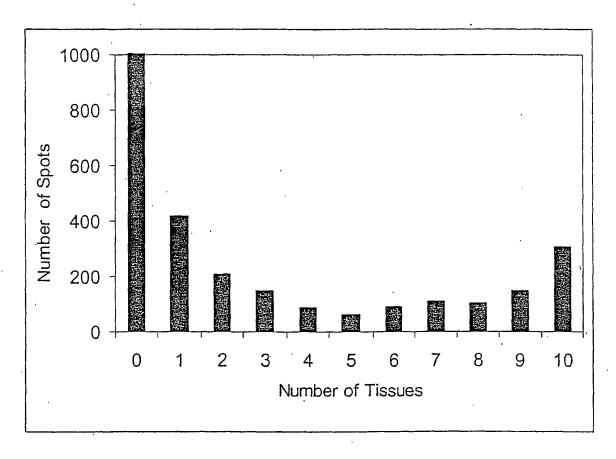
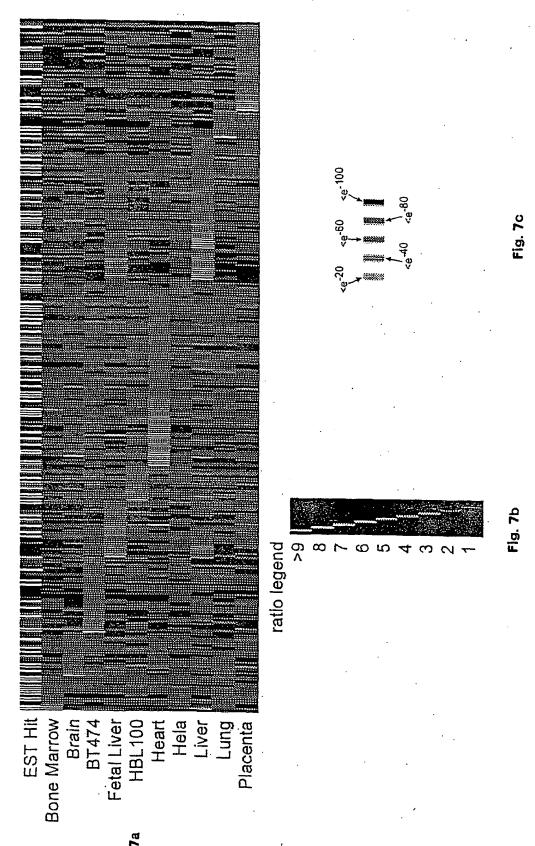
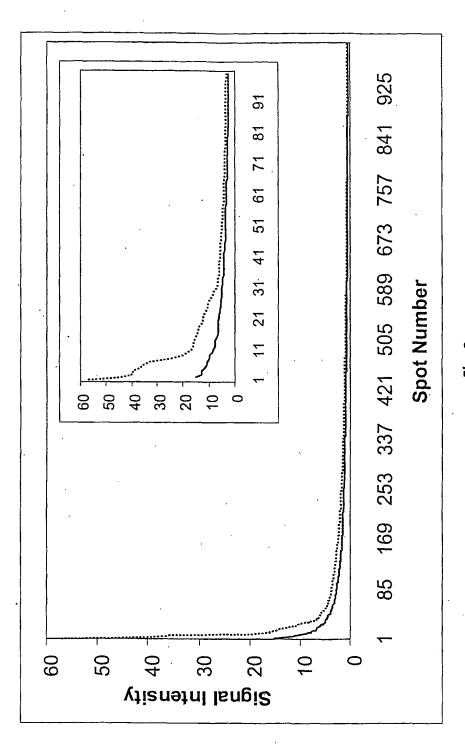


Fig. 6

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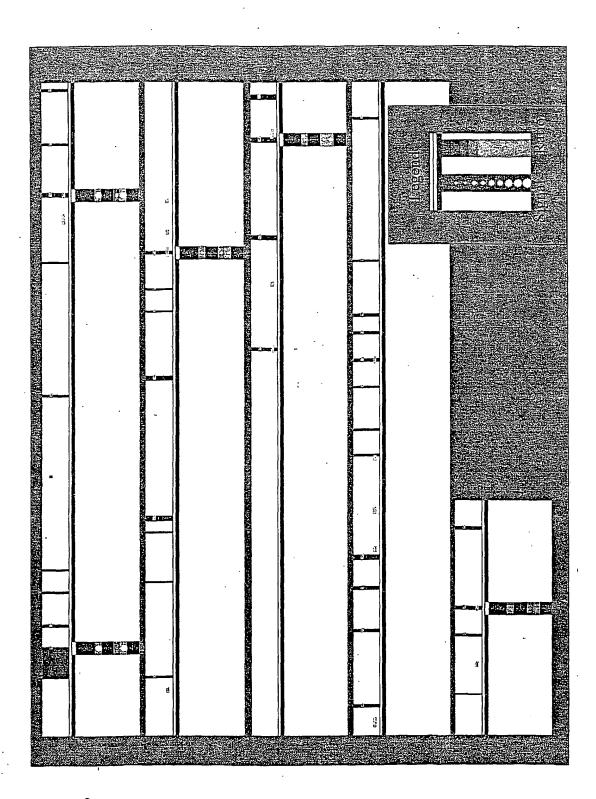


Fig. 9

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Fig. 10

